

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
19 December 2002 (19.12.2002)

PCT

(10) International Publication Number
WO 02/101075 A2

(51) International Patent Classification⁷: **C12Q**

Karen [US/US]; 17 Beacon Street, Natick, MA 01760 (US). **HOERSCH, Sebastian** [DE/US]; 127 Brattle Street, Arlington, MA 02424 (US).

(21) International Application Number: PCT/US02/18638

(22) International Filing Date: 12 June 2002 (12.06.2002)

(74) Agents: **SMITH, DeAnn, F.** et al.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).

(25) Filing Language: English

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(26) Publication Language: English

(30) Priority Data:
60/298,159 13 June 2001 (13.06.2001) US
60/298,155 13 June 2001 (13.06.2001) US
60/335,936 14 November 2001 (14.11.2001) US

(71) Applicant (*for all designated States except US*): **MILLENNIUM PHARMACEUTICALS, INC.** [US/US]; 75 Sidney Street, Cambridge, MA 02139 (US).

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **SCHLEGEL, Robert** [US/US]; 211 Melrose Street, Auburndale, MA 02466 (US). **CHEN, Yan** [CN/US]; 26A Plymouth Street, Apartment 2, Cambridge, MA 02141 (US). **ZHAO, Xumei** [US/US]; 6 Wildwood Lane, Burlington, MA 01803 (US). **MONAHAN, John, E.** [US/US]; 942 West Street, Walpole, MA 02081 (US). **KAMATKAR, Shubhangi** [IN/US]; 655 Saw Mill Brook Parkway, #1, Newton, MA 02459 (US). **GANNAVARAPU, Manjula** [IN/US]; 10 Windemere Drive, Acton, MA 01720 (US). **GLATT,**

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF CERVICAL CANCER

(57) Abstract: The invention relates to newly discovered nucleic acid molecules and proteins associated with cervical cancer including pre-malignant conditions such as dysplasia. Compositions, kits, and methods for detecting, characterizing, preventing, and treating human cervical cancers are provided.



WO 02/101075 A2

NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
CERVICAL CANCER

5 RELATED APPLICATIONS

The present application claims priority to U.S. provisional patent application serial no. 60/298,159, filed on June 13, 2001, U.S. provisional patent application serial no. 60/298,155, filed on June 13, 2001, and U.S. provisional patent application serial no. 60/335,936, filed on November 14, 2001, all of which are expressly incorporated by
10 reference.

FIELD OF THE INVENTION

The field of the invention is cervical cancer, including diagnosis, characterization, management, and therapy of cervical cancer.
15

BACKGROUND OF THE INVENTION

The increased number of cancer cases reported in the United States, and, indeed, around the world, is a major concern. Currently there are only a handful of treatments available for specific types of cancer, and these provide no absolute guarantee
20 of success. In order to be most effective, these treatments require not only an early detection of the malignancy, but a reliable assessment of the severity of the malignancy.

Cancer of the cervix is one of the most common malignancies in women and remains a significant public health problem throughout the world. In the United States alone, invasive cervical cancer accounts for approximately 19% of all
25 gynecological cancers. In 1996, it was estimated that there were 14,700 newly diagnosed cases and 4900 deaths attributed to this disease (American Cancer Society, Cancer Facts & Figures 1996, Atlanta, Ga.: American Cancer Society, 1996). In many developing countries, where mass screening programs are not widely available, the clinical problem is more serious. Worldwide, the number of new cases is estimated to be 471,000 with a
30 four-year survival rate of only 40% (Munoz et al., 1989, *Epidemiology of Cervical Cancer* In: "Human Papillomavirus", New York, Oxford Press, pp 9-39; National Institutes of Health, Consensus Development Conference Statement on Cervical Cancer, Apr.1-3, 1996).

The precursor to cervical cancer is dysplasia, also known in the art as cervical intraepithelial neoplasia (CIN) or squamous intraepithelial lesions (SIL). While it is not understood how normal cells become transformed, the concept of a continuous spectrum of histopathological change from normal, stratified epithelium through CIN to
5 invasive cancer has been widely accepted for many years. A large body of epidemiological and molecular biological evidence has established human papillomavirus (HPV) infection as a causative factor in cervical cancer. HPV is found in 85% or more of squamous cell invasive lesions, which represent the most common histologic type seen in cervical carcinoma. Additional cofactors have also been
10 identified, including oncogenes that have been activated by point mutations and chromosomal translocations or deletions.

In light of this, cervical cancer remains a highly preventable form of cancer when pre-invasive lesions are detected early. Cytological examination of Papanicolaou-stained cervical smears (also referred to as Pap smears) is currently the
15 principle method for detecting cervical cancer. Not surprisingly, the effectiveness of Pap smear screening varies depending not only upon the quality of the sample being used, but also upon subjective parameters that are inherent to the analysis. In addition, despite the historical success of the test, concerns have arisen regarding its ability to reliably predict the behavior of some pre-invasive lesions (Ostor *et al.*, 1993, *Int. J. Gynecol.*
20 *Pathol.* 12: 186-192; and Genest *et al.*, 1993, *Human Pathol.* 24: 730-736).

SUMMARY OF THE INVENTION

The invention relates to cancer markers (hereinafter “markers” or “markers of the inventions”), which are listed in Table 1. The invention provides
25 nucleic acids and proteins that are encoded by or correspond to the markers (hereinafter “marker nucleic acids” and “marker proteins,” respectively). Table 1 provides the sequence identifiers of the sequences of such marker nucleic acids and proteins listed in the accompanying Sequence Listing. The invention further provides antibodies, antibody derivatives and antibody fragments which bind specifically with such proteins
30 and/or fragments of the proteins.

The invention also relates to various methods, reagents and kits for diagnosing, staging, prognosing, monitoring and treating cervical cancer. “Cervical cancer “ as used herein includes carcinomas, (*e.g.*, carcinoma in situ, invasive

carcinoma, metastatic carcinoma) and pre-malignant conditions, (*e.g.*, dysplasia, including CIN or SIL). In one embodiment, the invention provides a diagnostic method of assessing whether a patient has cervical cancer or has higher than normal risk for developing cervical cancer, comprising the steps of comparing the level of expression of a marker of the invention in a patient sample and the normal level of expression of the
5 marker in a control, *e.g.*, a sample from a patient without cervical cancer. A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer or has higher than normal risk for developing cervical cancer.

10 According to the invention, the markers are selected such that the positive predictive value of the methods of the invention is at least about 10%, preferably about 25%, more preferably about 50% and most preferably about 90%. Also preferred for use in the methods of the invention are markers that are differentially expressed, as compared to normal cervical cells, by at least two-fold in at least about 20%, more
15 preferably about 50% and most preferably about 75% of any of the following conditions: stage 0 cervical cancer patients, stage I cervical cancer patients, stage II cervical cancer patients, stage III cervical cancer patients, stage IV cervical cancer patients, grade I cervical cancer patients, grade II cervical cancer patients, grade III cervical cancer patients, squamous cell (epidermoid) cervical cancer patients, cervical adenocarcinoma
20 patients, cervical adenosquamous carcinoma patients, small-cell cervical carcinoma patients, malignant cervical cancer patients, patients with primary carcinomas of the cervix, patients with primary malignant lymphomas of the cervix and patients with secondary malignant lymphomas of the cervix, and all other types of cancers, malignancies and transformations associated with the cervix.

25 In a preferred diagnostic method of assessing whether a patient is afflicted with cervical cancer (*e.g.*, new detection ("screening"), detection of recurrence, reflex testing), the method comprises comparing:

- a) the level of expression of a marker of the invention in a patient sample, and
- 30 b) the normal level of expression of the marker in a control non-cervical cancer sample.

A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer.

The invention also provides diagnostic methods for assessing the efficacy of a therapy for inhibiting cervical cancer in a patient. Such methods comprise comparing:

- a) expression of a marker of the invention in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, and
- 10 b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy.

A significantly lower level of expression of the marker in the second sample relative to that in the first sample is an indication that the therapy is efficacious for inhibiting cervical cancer in the patient.

15 It will be appreciated that in these methods the “therapy” may be any therapy for treating cervical cancer including, but not limited to, chemotherapy, radiation therapy, surgical removal of tumor tissue, gene therapy and biologic therapy such as the administering of antibodies and chemokines. Thus, the methods of the invention may be used to evaluate a patient before, during and after therapy, for

20 example, to evaluate the reduction in tumor burden.

In a preferred embodiment, the diagnostic methods are directed to therapy using a chemical or biologic agent. These methods comprise comparing:

- a) expression of a marker of the invention in a first sample obtained from the patient and maintained in the presence of the chemical or biologic
- 25 agent, and
- b) expression of the marker in a second sample obtained from the patient and maintained in the absence of the agent.

A significantly lower level of expression of the marker in the second sample relative to that in the first sample is an indication that the agent is efficacious for inhibiting cervical

30 cancer, in the patient. In one embodiment, the first and second samples can be portions of a single sample obtained from the patient or portions of pooled samples obtained from the patient.

The invention additionally provides a monitoring method for assessing the progression of cervical cancer in a patient, the method comprising:

- a) detecting in a patient sample at a first time point, the expression of a marker of the invention;
- 5 b) repeating step a) at a subsequent time point in time; and
- c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of cervical cancer in the patient.

A significantly higher level of expression of the marker in the sample at the subsequent time point from that of the sample at the first time point is an indication that the cervical
10 cancer has progressed, whereas a significantly lower level of expression is an indication that the cervical cancer has regressed.

The invention further provides a diagnostic method for determining whether cervical cancer has metastasized or is likely to metastasize in the future, the method comprising comparing:

- 15 a) the level of expression of a marker of the invention in a patient sample, and
- b) the normal level (or non-metastatic level) of expression of the marker in a control sample.

A significantly higher level of expression in the patient sample as compared to the
20 normal level (or non-metastatic level) is an indication that the cervical cancer has metastasized or is likely to metastasize in the future.

The invention moreover provides a test method for selecting a composition for inhibiting cervical cancer in a patient. This method comprises the steps of:

- 25 a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;
- c) comparing expression of a marker of the invention in each of the aliquots; and
- 30 d) selecting one of the test compositions which significantly reduces the level of expression of the marker in the aliquot containing that test composition, relative to the levels of expression of the marker in the presence of the other test compositions.

The invention additionally provides a test method of assessing the cervical carcinogenic potential of a compound. This method comprises the steps of:

- a) maintaining separate aliquots of cervical cells in the presence and absence of the compound; and
- 5 b) comparing expression of a marker of the invention in each of the aliquots.

A significantly higher level of expression of the marker in the aliquot maintained in the presence of the compound, relative to that of the aliquot maintained in the absence of the compound, is an indication that the compound possesses cervical carcinogenic potential.

10 In addition, the invention further provides a method of inhibiting cervical cancer in a patient. This method comprises the steps of:

- a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of compositions;
- 15 c) comparing expression of a marker of the invention in each of the aliquots; and
- d) administering to the patient at least one of the compositions which significantly lowers the level of expression of the marker in the aliquot containing that composition, relative to the levels of expression of the marker in the presence of the other compositions.

20 In the aforementioned methods, the samples or patient samples comprise cells obtained from the patient. The cells may be found in a cervical smear collected, for example, by a cervical brush. In another embodiment, the sample is a body fluid. Such fluids include, for example, blood fluids, lymph, ascitic fluids, gynecological fluids, urine, and fluids collected by vaginal rinsing. In a further embodiment, the patient sample is *in vivo*.

According to the invention, the level of expression of a marker of the invention in a sample can be assessed, for example, by detecting the presence in the sample of:

- 30 • the corresponding marker protein (*e.g.*, a protein having one of the sequences set forth as "SEQ ID NO (AAs)" in Table 1, or a fragment of the protein (*e.g.* by using a reagent, such as an antibody, an antibody derivative,

an antibody fragment or single-chain antibody, which binds specifically with the protein or protein fragment)

- the corresponding marker nucleic acid (*e.g.* a nucleotide transcript having one of the nucleic acid sequences set forth as “SEQ ID NO (nts)” in Table 1, or a complement thereof), or a fragment of the nucleic acid (*e.g.* by contacting transcribed polynucleotides obtained from the sample with a substrate having affixed thereto one or more nucleic acids having the entire or a segment of the nucleic acid sequence of any of the SEQ ID NO (nts), or a complement thereof)
- a metabolite which is produced directly (*i.e.*, catalyzed) or indirectly by the corresponding marker protein.

According to the invention, any of the aforementioned methods may be performed using a plurality (*e.g.* 2, 3, 5, or 10 or more) of cervical cancer markers, including cervical cancer markers known in the art. In such methods, the level of expression in the sample of each of a plurality of markers, at least one of which is a marker of the invention, is compared with the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with cervical cancer. A significantly altered (*i.e.*, increased or decreased as specified in the above-described methods using a single marker) level of expression in the sample of one or more markers of the invention, or some combination thereof, relative to that marker's corresponding normal or control level, is an indication that the patient is afflicted with cervical cancer. For all of the aforementioned methods, the marker(s) are preferably selected such that the positive predictive value of the method is at least about 10%.

In a further aspect, the invention provides an antibody, an antibody derivative, or an antibody fragment, which binds specifically with a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing) or a fragment of the protein. The invention also provides methods for making such antibody, antibody derivative, and antibody fragment. Such methods may comprise immunizing a mammal with a protein or peptide comprising the entirety, or a segment of 10 or more amino acids, of a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing), wherein the protein or peptide may be obtained from a cell or by chemical synthesis. The methods of the invention also encompass producing

monoclonal and single-chain antibodies, which would further comprise isolating splenocytes from the immunized mammal, fusing the isolated splenocytes with an immortalized cell line to form hybridomas, and screening individual hybridomas for those that produce an antibody that binds specifically with a marker protein or a
5 fragment of the protein.

In another aspect, the invention relates to various diagnostic and test kits. In one embodiment, the invention provides a kit for assessing whether a patient is afflicted with cervical cancer. The kit comprises a reagent for assessing expression of a marker of the invention. In another embodiment, the invention provides a kit for
10 assessing the suitability of a chemical or biologic agent for inhibiting cervical cancer in a patient. Such a kit comprises a reagent for assessing expression of a marker of the invention, and may also comprise one or more of such agents. In a further embodiment, the invention provides kits for assessing the presence of cervical cancer cells or treating cervical cancers. Such kits comprise an antibody, an antibody derivative, or an antibody
15 fragment, which binds specifically with a marker protein, or a fragment of the protein. Such kits may also comprise a plurality of antibodies, antibody derivatives, or antibody fragments wherein the plurality of such antibody agents binds specifically with a marker protein, or a fragment of the protein.

In an additional embodiment, the invention also provides a kit for
20 assessing the presence of cervical cancer cells, wherein the kit comprises a nucleic acid probe that binds specifically with a marker nucleic acid or a fragment of the nucleic acid. The kit may also comprise a plurality of probes, wherein each of the probes binds specifically with a marker nucleic acid, or a fragment of the nucleic acid.

In a further aspect, the invention relates to methods for treating a patient
25 afflicted with cervical cancer or at risk of developing cervical cancer. Such methods may comprise reducing the expression and/or interfering with the biological function of a marker of the invention. In one embodiment, the method comprises providing to the patient an antisense oligonucleotide or polynucleotide complementary to a marker nucleic acid, or a segment thereof. For example, an antisense polynucleotide may be
30 provided to the patient through the delivery of a vector that expresses an anti-sense polynucleotide of a marker nucleic acid or a fragment thereof. In another embodiment, the method comprises providing to the patient an antibody, an antibody derivative, or antibody fragment, which binds specifically with a marker protein or a fragment of the

protein. In a preferred embodiment, the antibody, antibody derivative or antibody fragment binds specifically with a protein having one of the amino acid sequences set forth in the Sequence Listing, or a fragment of the protein.

It will be appreciated that the methods and kits of the present invention
5 may also include known cancer markers including known cervical cancer markers. It will further be appreciated that the methods and kits may be used to identify cancers other than cervical cancer.

DETAILED DESCRIPTION OF THE INVENTION

10 The invention relates to newly discovered cancer markers associated with the cancerous state of cervical cells. It has been discovered that the higher than normal level of expression of any of these markers or combination of these markers correlates with the presence of cervical cancer including pre-malignant conditions such as dysplasia, in a patient. Methods are provided for detecting the presence of cervical
15 cancer in a sample, the absence of cervical cancer in a sample, the stage of a cervical cancer, and other characteristics of cervical cancer that are relevant to prevention, diagnosis, characterization, and therapy of cervical cancer in a patient. Methods of treating cervical cancer are also provided.

Table 1 lists the markers of the invention which are over-expressed in
20 cervical cancer cells compared to normal (*i.e.*, non-cancerous) cervical cells and comprises markers listed in Tables 2 and 3. Table 2 lists newly-identified nucleotide and amino acid sequences. Table 3 lists newly-identified nucleotide sequences. Tables 1-3 provide the sequence listing identifiers of the cDNA sequence of a nucleotide transcript and the amino acid sequence of a protein encoded by or corresponding to each
25 marker, as well as the location of the protein coding sequence within the cDNA sequence.

Table 1

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M661	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 1	1	2	223..11946
M662	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 2	3	4	223..11922
M663	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 3	5	6	223..12000
M664	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 4	7	8	223..11976
M1	APOL1: Apolipoprotein L-I mRNA, splice variant A, major form	9	10	213..1364
M2	APOL1: Apolipoprotein L-I mRNA, splice variant B, minor form	11	12	274..1518
M3	APOL3: apolipoprotein L, 3; TNF-inducible protein CG12-1	13	14	418..1413
OV3	AQP5: Aquaporin 5	15	16	519..1316
M4	BC001980: clone MGC:5618	17	18	157..225
M5	BST2: Bone marrow stromal cell antigen 2	19	20	10..552
M6	BTEB1: basic transcription element binding protein 1	21	22	1265..1999
M665	CD74: CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	23	24	8..706
M7	CDC20: CDC20 cell cycle protein	25	26	45..1544
M8	CDKN2C: cyclin-dependent kinase inhibitor 2C, p18	27	28	1216..1722
M9	CKTSF1B1: (cysteine knot superfamily 1, BMP antagonist 1), gremlin	29	30	45..1544
M10	CLDN1: claudin 1	31	32	221..856
M11	CLIC4: chloride intracellular channel 4	33	34	198..959
M12	COL1A1: collagen, type I, alpha 1	35	36	120..4514
M13	COL1A2: collagen, type I, alpha 2	37	38	140..4240
M14	COL8A1: collagen, type VIII, alpha 1	39	40	1..2235
M15	COPA: coatamer protein complex, subunit alpha	41	42	467..4141
M16	CRIP1: cysteine-rich protein 1 (intestinal)	43	44	1..234
M17	CTGF: connective tissue growth factor	45	46	146..1195
M18	DOC: downregulated in ovarian cancer 1	47	48	135..2393
M19	EFNA1: ephrin-A1	49	50	74..691
M481	EPPK1: epiplakin 1	51	52	89..15286
M20	FLJ11350: hypothetical protein FLJ11350	53	54	106..1047
M21	FLJ13809: hypothetical protein FLJ13809	55	56	64..1593
M22	FLJ20500: hypothetical protein FLJ20500	57	58	198..896
M23	FLJ23399: hypothetical protein FLJ23399	59	60	283..1770
M24	FN1: Fibronectin 1, variant 1	61	62	<1..2384
M25	FN1: Fibronectin 1, variant 2	63	64	<1..6988
M482	FOSL2: FOS-like antigen 2, variant 1	65	66	324..1304
M483	FOSL2: FOS-like antigen 2, variant 2	67	66	324..1304
M484	FSHPRH1: FSH primary response (LRPR1, rat) homolog 1	68	69	270..2540
M26	FY: Duffy blood group	70	71	495..1511

M485	G1P3:interferon, alpha-inducible protein (clone IFI-6-16)	72	73	108..500
M486	GW112: GW112 protein	74	75	509..1072
M27	HSKERUV: clone 266, Human radiated keratinocyte mRNA 266 (keratin-related protein)	76	77	<1..801
M28	HSPC121: butyrate-induced transcript 1	78	79	150..1271
M29	HUMCLPB: Coactosin like protein	80	81	150..576
M487	hypothetical protein	82	83	58..8163
M30	IFI27: (interferon, alpha-inducible protein 27	84	85	55..423
OV31	IFI30: interferon, gamma-inducible protein 30	86	87	41..952
M31	IFITM2: interferon induced transmembrane protein 2 (1-8D)	88	89	280..678
M32	IGFBP-3: insulin-like growth factor binding protein 3	90	91	133..1009
M33	IL8RA: interleukin 8	92	93	75..374
M34	INHBA: Inhibin, beta-1	94	95	86..1366
M488	ITGA3: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor), variant a	96	97	74..3229
M454	ITGA3: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor), variant b	98	99	74..3274
M35	ITGB6: integrin, beta 6	100	101	195..2561
M36	KATII: L-kynurenine/alpha-aminoadipate aminotransferase	102	103	454..1731
M666	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 1	104	105	89..1315
M667	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 2	106	107	54..1313
M668	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 3	108	109	28..1233
M37	KIAA0662: KIAA0662 protein	110	111	<1..2035
M38	LAMA3: Laminin, alpha-3 (nicein (150kD), (kalinin (165kD), BM600 (150kD)	112	113	1..5142
M39	LAMC2: laminin, gamma 2	114	115	90..3671
M40	LSM5: U6 snRNA-associated Sm-like protein	116	117	1..276
M41	LUM: lumican	118	119	85..1101
M42	MACMARCKS: macrophage myristoylated alanine-rich C kinase substrate	120	121	14..601
M43	MAGP: microfibrillar-associated protein 2 precursor, transcript variant 1	122	123	115..666
M44	MAGP: microfibrillar-associated protein 2 precursor, transcript variant 2	124	125	100..651
M45	MAPK: mitogen-activated protein kinase 1	126	127	328..1410
M489	MCM6: minichromosome maintenance deficient (mis5, S. pombe) 6	128	129	62..2527
M46	MDK: midkine (neurite growth-promoting factor 2)	130	131	26..457
M47	MGP: matrix Gla protein	132	133	47..358
M48	MMP12: matrix metalloproteinase 12	134	135	13..1425
M49	MMP3: matrix metalloproteinase 3, stromelysin 1, progelatinase	136	137	64..1497
M294	MMP7: matrix metalloproteinase 7 (matrilysin, uterine), PUMP1 proteinase, variant 1	138	139	48..851
OV52	MMP7: matrix metalloproteinase 7 (matrilysin, uterine), PUMP1 proteinase, variant 2	140	139	28..831

M50	MMP9: matrix metalloproteinase 9, gelatinase B, 92kD gelatinase, 92kD type IV collagenase	141	142	20..2143
OV68	MSLN: mesothelin, variant 1	143	144	88..2196
OV69	MSLN: mesothelin, variant 2	145	146	88..1980
OV70	MSLN: mesothelin, variant 3	147	148	88..1950
OV71	MSLN: mesothelin, variant 4	149	150	88..2172
OV72	MSLN: mesothelin, variant 5	151	152	88..1926
OV43	MSLN: mesothelin, variant 6	153	154	88..1956
OV45	MUC1: mucin 1, transmembrane, variant 1	155	156	58..1605
M669	MUC1: mucin 1, transmembrane, variant 2	157	158	74..3841
M51	MYBL2: v-myb avian myeloblastosis viral oncogene homolog-like 2	159	160	128..2230
M52	MYH11: smooth muscle myosin heavy chain 11, isoform SM1	161	162	89..6007
M53	MYH11: smooth muscle myosin heavy chain 11, isoform SM2	163	164	89..5905
M54	NK4: natural killer cell transcript 4 , variant 1	165	166	60..764
M670	NK4: natural killer cell transcript 4 , variant 2	167	168	60..764
M55	NP25: (neuronal protein)	169	170	50..898
OV48	OPN-a (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	171	172	1..942
OV49	OPN-b (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	173	174	88..990
OV50	OPN-c (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	175	176	1..861
M56	OSF-2, osteoblast specific factor 2 (fascin I-like), variant 1	177	178	12..2522
M491	OSF-2, osteoblast specific factor 2 (fascin I-like), variant 2	179	180	28..2367
M57	PIM2: pim-2 oncogene	181	182	186..1190
M58	PLAU: plasminogen activator, urokinase	183	184	77..1372
M59	PLK: polo (Drosophila)-like kinase	185	186	64..1875
M671	PNN: pinin, desmosome associated protein	187	188	31..2262
M60	PRG1: proteoglycan 1, secretory granule	189	190	25..501
M61	PTH1H: parathyroid hormone-like hormone	191	192	304..831
M62	PTN: pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	193	194	1542..2048
M63	RAB6KIFL: RAB6 interacting, kinesin-like (rabkinesin6)	195	196	28..2700
M64	RARRES3: retinoic acid receptor responder (tazarotene induced) 3	197	198	62..556
M65	RBP1: retinol-binding protein 1 (cellular), CRABP-I, CRBP-I	199	200	126..533
M66	RGS16: Regulator of G protein signaling-16	201	202	93..701
M67	S100A2: S100 calcium binding protein A2, variant 1	203	204	72..362
M68	S100A2: S100 calcium binding protein A2, variant 2	205	206	41..334
M69	SCYA20: small inducible cytokine subfamily A (Cys-Cys), member 20	207	208	59..349
M70	SPARC: Osteonectin (secreted protein, acidic, cysteine-rich)	209	210	58..969
M71	STCH: stress 70 protein chaperone, microsome-associated	211	212	37..1452
M492	STK12: serine/ threonine kinase 12	213	214	58..1092

M72	TK1: thymidine kinase 1, soluble	215	216	58..762
OV86	TMPRSS4: transmembrane protease, serine 4	217	218	310..1623
M73	TMSB4X: thymosin, beta 4, X chromosome	219	220	78..212
M74	TOP2A: topoisomerase (DNA) II alpha (170kD)	221	222	37..4632
M493	TPM1: tropomyosin 1 (alpha)	223	224	57..911
M75	TXN: thioredoxin	225	226	64..381
M76	UBCH10: ubiquitin carrier protein E2-C	227	228	41..580
M77	UBD: diubiquitin	229	230	19..516
M78	unnamed gene (1)	231	232	45..1353
M79	unnamed gene (2)	233	234	1..1508
M80	VATD: vacuolar proton pump delta polypeptide	235	236	166..909
M81	ZWINT: ZW10 interactor	237	238	25..858

Table 2

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M661	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 1	1	2	223..1194 6
M662	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 2	3	4	223..1192 2
M663	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 3	5	6	223..1200 0
M664	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 4	7	8	223..1197 6
OV68	MSLN: mesothelin, variant 1	143	144	88..2196
OV69	MSLN: mesothelin, variant 2	145	146	88..1980
OV70	MSLN: mesothelin, variant 3	147	148	88..1950
OV71	MSLN: mesothelin, variant 4	149	150	88..2172
OV72	MSLN: mesothelin, variant 5	151	152	88..1926
M670	NK4: natural killer cell transcript 4, variant 2	167	168	60..764
M67	S100A2: S100 calcium binding protein A2, variant 1	203	204	72..362
OV86	TMPRSS4: transmembrane protease, serine 4	217	218	310..1623
M78	unnamed gene (1)	231	232	45..1353
M79	unnamed gene (2)	233	234	1..1508

Table 3

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M481	EPPK1: epiplakin 1	51	52	89..15286
M482	FOSL2: FOS-like antigen 2, variant 1	65	66	324..1304
M483	FOSL2: FOS-like antigen 2, variant 2	67	66	324..1304
M484	FSHPRH1: FSH primary response (LRPR1, rat) homolog 1	68	69	270..2540
M35	ITGB6: integrin, beta 6	100	101	195..2561
OV43	MSLN: mesothelin, variant 6	153	154	88..1956

Definitions

5 As used herein, each of the following terms has the meaning associated with it in this section.

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.* to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

10 A "marker" is a gene whose altered level of expression in a tissue or cell from its expression level in normal or healthy tissue or cell is associated with a disease state, such as cancer. A "marker nucleic acid" is a nucleic acid (*e.g.*, mRNA, cDNA) encoded by or corresponding to a marker of the invention. Such marker nucleic acids include DNA (*e.g.*, cDNA) comprising the entire or a partial sequence of any of the
15 nucleic acid sequences set forth in the Sequence Listing or the complement of such a sequence. The marker nucleic acids also include RNA comprising the entire or a partial sequence of any of the nucleic acid sequences set forth in the Sequence Listing or the complement of such a sequence, wherein all thymidine residues are replaced with uridine residues. A "marker protein" is a protein encoded by or corresponding to a
20 marker of the invention. A marker protein comprises the entire or a partial sequence of any of the sequences set forth in the Sequence Listing. The terms "protein" and "polypeptide" are used interchangeably.

The term "probe" refers to any molecule which is capable of selectively binding to a specifically intended target molecule, for example, a nucleotide transcript or
25 protein encoded by or corresponding to a marker. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be labeled, as

described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

A "cervical-associated" body fluid is a fluid which, when in the body of a patient, contacts or passes through cervical cells or into which cells or proteins shed
5 from cervical cells are capable of passing. The cells may be found in a cervical smear collected, for example, by a cervical brush. Exemplary cervical-associated body fluids include blood fluids, lymph, ascitic fluids, gynecological fluids, cystic fluid, urine, and fluids collected by vaginal rinsing.

The "normal" level of expression of a marker is the level of expression of
10 the marker in cervical cells of a human subject or patient not afflicted with cervical cancer

An "over-expression" or "significantly higher level of expression" of a marker refers to an expression level in a test sample that is greater than the standard error of the assay employed to assess expression, and is preferably at least twice, and
15 more preferably three, four, five or ten times the expression level of the marker in a control sample (*e.g.*, sample from a healthy subjects not having the marker associated disease) and preferably, the average expression level of the marker in several control samples.

A "significantly lower level of expression" of a marker refers to an
20 expression level in a test sample that is at least twice, and more preferably three, four, five or ten times lower than the expression level of the marker in a control sample (*e.g.*, sample from a healthy subject not having the marker associated disease) and preferably, the average expression level of the marker in several control samples.

As used herein, the term "promoter/regulatory sequence" means a nucleic
25 acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses
30 the gene product in a tissue-specific manner.

A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell under most or all physiological conditions of the cell.

5 An "inducible" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only when an inducer which corresponds to the promoter is present in the cell.

 A "tissue-specific" promoter is a nucleotide sequence which, when
10 operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

 A "transcribed polynucleotide" or "nucleotide transcript" is a polynucleotide (*e.g.* an mRNA, hnRNA, a cDNA, or an analog of such RNA or cDNA)
15 which is complementary to or homologous with all or a portion of a mature mRNA made by transcription of a marker of the invention and normal post-transcriptional processing (*e.g.* splicing), if any, of the RNA transcript, and reverse transcription of the RNA transcript.

 "Complementary" refers to the broad concept of sequence
20 complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid
25 strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably,
30 the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residues of the first portion are capable of base pairing

with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

"Homologous" as used herein, refers to nucleotide sequence similarity
5 between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is
10 expressed in terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue. By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% homology. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and
15 preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue. More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

A molecule is "fixed" or "affixed" to a substrate if it is covalently or non-
20 covalently associated with the substrate such the substrate can be rinsed with a fluid (*e.g.* standard saline citrate, pH 7.4) without a substantial fraction of the molecule dissociating from the substrate.

As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in an organism found
25 in nature.

A cancer is "inhibited" if at least one symptom of the cancer is alleviated, terminated, slowed, or prevented. As used herein, cervical cancer is also "inhibited" if recurrence or metastasis of the cancer is reduced, slowed, delayed, or prevented.

A kit is any manufacture (*e.g.* a package or container) comprising at least
30 one reagent, *e.g.* a probe, for specifically detecting the expression of a marker of the invention. The kit may be promoted, distributed, or sold as a unit for performing the methods of the present invention.

“Proteins of the invention” encompass marker proteins and their fragments; variant marker proteins and their fragments; peptides and polypeptides comprising an at least 15 amino acid segment of a marker or variant marker protein; and fusion proteins comprising a marker or variant marker protein, or an at least 15 amino acid segment of a marker or variant marker protein.

Unless otherwise specified herewithin, the terms “antibody” and “antibodies” broadly encompass naturally-occurring forms of antibodies (*e.g.*, IgG, IgA, IgM, IgE) and recombinant antibodies such as single-chain antibodies, chimeric and humanized antibodies and multi-specific antibodies, as well as fragments and derivatives of all of the foregoing, which fragments and derivatives have at least an antigenic binding site. Antibody derivatives may comprise a protein or chemical moiety conjugated to an antibody.

Description

The present invention is based, in part, on newly identified markers which are over-expressed in cervical cancer cells as compared to their expression in normal (*i.e.* non-cancerous) cervical cells. The enhanced expression of one or more of these markers in cervical cells is herein correlated with the cancerous state of the tissue. The invention provides compositions, kits, and methods for assessing the cancerous state of cervical cells (*e.g.* cells obtained from a human, cultured human cells, archived or preserved human cells and *in vivo* cells) as well as treating patients afflicted with cervical cancer.

The compositions, kits, and methods of the invention have the following uses, among others:

- 1) assessing whether a patient is afflicted with cervical cancer;
- 2) assessing the stage of cervical cancer in a human patient;
- 3) assessing the grade of cervical cancer in a patient;
- 4) assessing the benign or malignant nature of cervical cancer in a patient;
- 5) assessing the metastatic potential of cervical cancer in a patient;
- 6) assessing the histological type of neoplasm associated with cervical cancer in a patient;

- 7) making antibodies, antibody fragments or antibody derivatives that are useful for treating cervical cancer and/or assessing whether a patient is afflicted with cervical cancer;
- 8) assessing the presence of cervical cancer cells;
- 5 9) assessing the efficacy of one or more test compounds for inhibiting cervical cancer in a patient;
- 10 10) assessing the efficacy of a therapy for inhibiting cervical cancer in a patient;
- 11) monitoring the progression of cervical cancer in a patient;
- 10 12) selecting a composition or therapy for inhibiting cervical cancer in a patient;
- 13) treating a patient afflicted with cervical cancer;
- 14) inhibiting cervical cancer in a patient;
- 15 15) assessing the cervical carcinogenic potential of a test compound; and
- 16) preventing the onset of cervical cancer in a patient at risk for developing cervical cancer.

The invention thus includes a method of assessing whether a patient is afflicted with cervical cancer which includes assessing whether the patient has pre-
20 metastasized cervical cancer. This method comprises comparing the level of expression of a marker of the invention (listed in Table 1) in a patient sample and the normal level of expression of the marker in a control, *e.g.*, a non-cervical cancer sample. A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer.

25 Gene delivery vehicles, host cells and compositions (all described herein) containing nucleic acids comprising the entirety, or a segment of 15 or more nucleotides, of any of the nucleic acid sequences set forth in the Sequence Listing, or the complement of such sequences, and polypeptides comprising the entirety, or a segment of 10 or more amino acids, of any of the amino acid sequences set forth in the Sequence
30 Listing, are also provided by this invention.

As described herein, cervical cancer in patients is associated with an increased level of expression of one or more markers of the invention. While, as discussed above, some of these changes in expression level result from occurrence of the

cervical cancer, others of these changes induce, maintain, and promote the cancerous state of cervical cancer cells. Thus, cervical cancer characterized by an increase in the level of expression of one or more markers of the invention can be inhibited by reducing and/or interfering with the expression of the markers and/or function of the proteins

5 encoded by those markers.

Expression of a marker of the invention can be inhibited in a number of ways generally known in the art. For example, an antisense oligonucleotide can be provided to the cervical cancer cells in order to inhibit transcription, translation, or both, of the marker(s). Alternately, a polynucleotide encoding an antibody, an antibody
10 derivative, or an antibody fragment which specifically binds a marker protein, and operably linked with an appropriate promoter/regulator region, can be provided to the cell in order to generate intracellular antibodies which will inhibit the function or activity of the protein. The expression and/or function of a marker may also be inhibited by treating the cervical cancer cell with an antibody, antibody derivative or antibody
15 fragment that specifically binds a marker protein. Using the methods described herein, a variety of molecules, particularly including molecules sufficiently small that they are able to cross the cell membrane, can be screened in order to identify molecules which inhibit expression of a marker or inhibit the function of a marker protein. The compound so identified can be provided to the patient in order to inhibit cervical cancer
20 cells of the patient.

Any marker or combination of markers of the invention, as well as any known markers in combination with the markers of the invention, may be used in the compositions, kits, and methods of the present invention. In general, it is preferable to use markers for which the difference between the level of expression of the marker in
25 cervical cancer cells and the level of expression of the same marker in normal cervical cells is as great as possible. Although this difference can be as small as the limit of detection of the method for assessing expression of the marker, it is preferred that the difference be at least greater than the standard error of the assessment method, and preferably a difference of at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 15-, 20-, 25-, 100-,
30 500-, 1000-fold or greater than the level of expression of the same marker in normal cervical tissue.

It is recognized that certain marker proteins are secreted from cervical cells (*i.e.* one or both of normal and cancerous cells) to the extracellular space surrounding the cells. These markers are preferably used in certain embodiments of the compositions, kits, and methods of the invention, owing to the fact that the such marker proteins can be detected in a cervical-associated body fluid sample, which may be more easily collected from a human patient than a tissue biopsy sample. In addition, preferred *in vivo* techniques for detection of a marker protein include introducing into a subject a labeled antibody directed against the protein. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

It is a simple matter for the skilled artisan to determine whether any particular marker protein is a secreted protein. In order to make this determination, the marker protein is expressed in, for example, a mammalian cell, preferably a human cervical cell line, extracellular fluid is collected, and the presence or absence of the protein in the extracellular fluid is assessed (*e.g.* using a labeled antibody which binds specifically with the protein).

The following is an example of a method which can be used to detect secretion of a protein. About 8×10^5 293T cells are incubated at 37°C in wells containing growth medium (Dulbecco's modified Eagle's medium {DMEM} supplemented with 10% fetal bovine serum) under a 5% (v/v) CO₂, 95% air atmosphere to about 60-70% confluence. The cells are then transfected using a standard transfection mixture comprising 2 micrograms of DNA comprising an expression vector encoding the protein and 10 microliters of LipofectAMINE™ (GIBCO/BRL Catalog no. 18342-012) per well. The transfection mixture is maintained for about 5 hours, and then replaced with fresh growth medium and maintained in an air atmosphere. Each well is gently rinsed twice with DMEM which does not contain methionine or cysteine (DMEM-MC; ICN Catalog no. 16-424-54). About 1 milliliter of DMEM-MC and about 50 microcuries of Trans-³⁵S™ reagent (ICN Catalog no. 51006) are added to each well. The wells are maintained under the 5% CO₂ atmosphere described above and incubated at 37°C for a selected period. Following incubation, 150 microliters of conditioned medium is removed and centrifuged to remove floating cells and debris.

The presence of the protein in the supernatant is an indication that the protein is secreted.

It will be appreciated that patient samples containing cervical cells may be used in the methods of the present invention. In these embodiments, the level of expression of the marker can be assessed by assessing the amount (*e.g.* absolute amount or concentration) of the marker in a cervical cell sample, *e.g.*, cervical smear obtained from a patient. The cell sample can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (*e.g.*, nucleic acid and/or protein extraction, fixation, storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the amount of the marker in the sample. Likewise, cervical smears may also be subjected to post-collection preparative and storage techniques, *e.g.*, fixation.

The compositions, kits, and methods of the invention can be used to detect expression of marker proteins having at least one portion which is displayed on the surface of cells which express it. It is a simple matter for the skilled artisan to determine whether a marker protein, or a portion thereof, is exposed on the cell surface. For example, immunological methods may be used to detect such proteins on whole cells, or well known computer-based sequence analysis methods may be used to predict the presence of at least one extracellular domain (*i.e.* including both secreted proteins and proteins having at least one cell-surface domain). Expression of a marker protein having at least one portion which is displayed on the surface of a cell which expresses it may be detected without necessarily lysing the cell (*e.g.* using a labeled antibody which binds specifically with a cell-surface domain of the protein).

Expression of a marker of the invention may be assessed by any of a wide variety of well known methods for detecting expression of a transcribed nucleic acid or protein. Non-limiting examples of such methods include immunological methods for detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods.

In a preferred embodiment, expression of a marker is assessed using an antibody (*e.g.* a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (*e.g.* an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair {*e.g.* biotin-streptavidin}), or an

antibody fragment (*e.g.* a single-chain antibody, an isolated antibody hypervariable domain, etc.) which binds specifically with a marker protein or fragment thereof, including a marker protein which has undergone all or a portion of its normal post-translational modification.

5 In another preferred embodiment, expression of a marker is assessed by preparing mRNA/cDNA (*i.e.* a transcribed polynucleotide) from cells in a patient sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a marker nucleic acid, or a fragment thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction methods prior to
10 hybridization with the reference polynucleotide; preferably, it is not amplified. Expression of one or more markers can likewise be detected using quantitative PCR to assess the level of expression of the marker(s). Alternatively, any of the many known methods of detecting mutations or variants (*e.g.* single nucleotide polymorphisms, deletions, etc.) of a marker of the invention may be used to detect occurrence of a
15 marker in a patient.

 In a related embodiment, a mixture of transcribed polynucleotides obtained from the sample is contacted with a substrate having fixed thereto a polynucleotide complementary to or homologous with at least a portion (*e.g.* at least 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a marker nucleic
20 acid. If polynucleotides complementary to or homologous with are differentially detectable on the substrate (*e.g.* detectable using different chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of markers can be assessed simultaneously using a single substrate (*e.g.* a "gene chip" microarray of polynucleotides fixed at selected positions). When a method of
25 assessing marker expression is used which involves hybridization of one nucleic acid with another, it is preferred that the hybridization be performed under stringent hybridization conditions.

 Because the compositions, kits, and methods of the invention rely on detection of a difference in expression levels of one or more markers of the invention, it
30 is preferable that the level of expression of the marker is significantly greater than the minimum detection limit of the method used to assess expression in at least one of normal cervical cells and cancerous cervical cells.

It is understood that by routine screening of additional patient samples using one or more of the markers of the invention, it will be realized that certain of the markers are over-expressed in cancers of various types, including specific cervical cancers, as well as other cancers such as breast cancer, ovarian cancer, etc. For example, it will be confirmed that some of the markers of the invention are over-expressed in most (*i.e.* 50% or more) or substantially all (*i.e.* 80% or more) of cervical cancer. Furthermore, it will be confirmed that certain of the markers of the invention are associated with cervical cancer of various stages (*i.e.* stage 0, I, II, III, and IV cervical cancers, as well as subclassifications IA1, IA2, IB, IB1, IB2, IIA, IIB, IIIA, IIIB, IVA, and IVB, using the FIGO Stage Grouping system for primary carcinoma of the cervix (see *Gynecologic Oncology*, 1991, 41:199 and *Cancer*, 1992, 69:482)), and pre-malignant conditions (*e.g.*, dysplasia including CIN or SIL), of various histologic subtypes (*e.g.* squamous cell carcinomas and squamous cell carcinoma variants such as verrucous carcinoma, lymphoepithelioma-like carcinoma, papillary squamous neoplasm and spindle cell squamous cell carcinoma (see *Cervical Cancer and Preinvasive Neoplasia*, 1996, pp. 90-91) serous, mucinous, endometrioid, and clear cell subtypes, as well as subclassifications and alternate classifications adenocarcinoma, papillary adenocarcinoma, papillary cystadenocarcinoma, surface papillary carcinoma, malignant adenofibroma, cystadenofibroma, adenocarcinoma, cystadenocarcinoma, adenoacanthoma, endometrioid stromal sarcoma, mesodermal {Müllerian} mixed tumor, malignant carcinoma, Brenner tumor, mixed epithelial tumor, and undifferentiated carcinoma, using the WHO/FIGO system for classification of malignant cervical tumors; Scully, *Atlas of Tumor Pathology*, 3d series, Washington DC), and various grades (*i.e.* grade I {well differentiated} , grade II {moderately well differentiated}, and grade III {poorly differentiated from surrounding normal tissue}). In addition, as a greater number of patient samples are assessed for expression of the markers of the invention and the outcomes of the individual patients from whom the samples were obtained are correlated, it will also be confirmed that altered expression of certain of the markers of the invention are strongly correlated with malignant cancers and that altered expression of other markers of the invention are strongly correlated with benign tumors. The compositions, kits, and methods of the invention are thus useful for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in patients.

When the compositions, kits, and methods of the invention are used for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in a patient, it is preferred that the marker or panel of markers of the invention is selected such that a positive result is obtained in at least about 20%,
5 and preferably at least about 40%, 60%, or 80%, and more preferably in substantially all patients afflicted with a cervical cancer of the corresponding stage, grade, histological type, or benign/malignant nature. Preferably, the marker or panel of markers of the invention is selected such that a positive predictive value (PPV) of greater than about 10% is obtained for the general population (more preferably coupled with an assay
10 specificity greater than 80%).

When a plurality of markers of the invention are used in the compositions, kits, and methods of the invention, the level of expression of each marker in a patient sample can be compared with the normal level of expression of each of the plurality of markers in non-cancerous samples of the same type, either in a single
15 reaction mixture (*i.e.* using reagents, such as different fluorescent probes, for each marker) or in individual reaction mixtures corresponding to one or more of the markers. In one embodiment, a significantly increased level of expression of more than one of the plurality of markers in the sample, relative to the corresponding normal levels, is an indication that the patient is afflicted with cervical cancer. When a plurality of markers
20 is used, it is preferred that 2, 3, 4, 5, 8, 10, 12, 15, 20, 30, or 50 or more individual markers be used, wherein fewer markers are preferred.

In order to maximize the sensitivity of the compositions, kits, and methods of the invention (*i.e.* by interference attributable to cells of non-cervical origin in a patient sample), it is preferable that the marker of the invention used therein be a
25 marker which has a restricted tissue distribution, *e.g.*, normally not expressed in a non-cervical tissue.

Only a small number of markers are known to be associated with cervical cancer (*e.g.* bcl-2, 15A8 antigen, cdc6, Mcm5, and EGFR). These markers are not, of course, included among the markers of the invention, although they may be used
30 together with one or more markers of the invention in a panel of markers, for example. It is well known that certain types of genes, such as oncogenes, tumor suppressor genes, growth factor-like genes, protease-like genes, and protein kinase-like genes are often involved with development of cancers of various types. Thus, among the markers of the

invention, use of those which correspond to proteins which resemble known proteins encoded by known oncogenes and tumor suppressor genes, and those which correspond to proteins which resemble growth factors, proteases, and protein kinases are preferred.

It is recognized that the compositions, kits, and methods of the invention will be of particular utility to patients having an enhanced risk of developing cervical cancer and their medical advisors. Patients recognized as having an enhanced risk of developing cervical cancer include, for example, patients having a familial history of cervical cancer, patients identified as having a mutant oncogene (*i.e.* at least one allele), and patients of advancing age (*i.e.* women older than about 50 or 60 years).

The level of expression of a marker in normal (*i.e.* non-cancerous) human cervical tissue can be assessed in a variety of ways. In one embodiment, this normal level of expression is assessed by assessing the level of expression of the marker in a portion of cervical cells which appears to be non-cancerous and by comparing this normal level of expression with the level of expression in a portion of the cervical cells which is suspected of being cancerous. Alternately, and particularly as further information becomes available as a result of routine performance of the methods described herein, population-average values for normal expression of the markers of the invention may be used. In other embodiments, the 'normal' level of expression of a marker may be determined by assessing expression of the marker in a patient sample obtained from a non-cancer-afflicted patient, from a patient sample obtained from a patient before the suspected onset of cervical cancer in the patient, from archived patient samples, and the like.

The invention includes compositions, kits, and methods for assessing the presence of cervical cancer cells in a sample (*e.g.* an archived tissue sample or a sample obtained from a patient). These compositions, kits, and methods are substantially the same as those described above, except that, where necessary, the compositions, kits, and methods are adapted for use with samples other than patient samples. For example, when the sample to be used is a paraffinized, archived human tissue sample, it can be necessary to adjust the ratio of compounds in the compositions of the invention, in the kits of the invention, or the methods used to assess levels of marker expression in the sample. Such methods are well known in the art and within the skill of the ordinary artisan.

The invention includes a kit for assessing the presence of cervical cancer cells (*e.g.* in a sample such as a patient sample). The kit comprises a plurality of reagents, each of which is capable of binding specifically with a marker nucleic acid or protein. Suitable reagents for binding with a marker protein include antibodies, antibody derivatives, antibody fragments, and the like. Suitable reagents for binding with a marker nucleic acid (*e.g.* a genomic DNA, an mRNA, a spliced mRNA, a cDNA, or the like) include complementary nucleic acids. For example, the nucleic acid reagents may include oligonucleotides (labeled or non-labeled) fixed to a substrate, labeled oligonucleotides not bound with a substrate, pairs of PCR primers, molecular beacon probes, and the like.

The kit of the invention may optionally comprise additional components useful for performing the methods of the invention. By way of example, the kit may comprise fluids (*e.g.* SSC buffer) suitable for annealing complementary nucleic acids or for binding an antibody with a protein with which it specifically binds, one or more sample compartments, an instructional material which describes performance of a method of the invention, a sample of normal cervical cells, a sample of cervical cancer cells, and the like.

The invention also includes a method of making an isolated hybridoma which produces an antibody useful for assessing whether patient is afflicted with an cervical cancer. In this method, a protein or peptide comprising the entirety or a segment of a marker protein is synthesized or isolated (*e.g.* by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein or peptide *in vivo* or *in vitro* using known methods). A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the protein or peptide. The vertebrate may optionally (and preferably) be immunized at least one additional time with the protein or peptide, so that the vertebrate exhibits a robust immune response to the protein or peptide. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the marker protein or a fragment thereof. The invention also includes hybridomas made by this method and antibodies made using such hybridomas.

The invention also includes a method of assessing the efficacy of a test compound for inhibiting cervical cancer cells. As described above, differences in the level of expression of the markers of the invention correlate with the cancerous state of cervical cells. Although it is recognized that changes in the levels of expression of certain of the markers of the invention likely result from the cancerous state of cervical cells, it is likewise recognized that changes in the levels of expression of other of the markers of the invention induce, maintain, and promote the cancerous state of those cells. Thus, compounds which inhibit an cervical cancer in a patient will cause the level of expression of one or more of the markers of the invention to change to a level nearer the normal level of expression for that marker (*i.e.* the level of expression for the marker in non-cancerous cervical cells).

This method thus comprises comparing expression of a marker in a first cervical cell sample and maintained in the presence of the test compound and expression of the marker in a second cervical cell sample and maintained in the absence of the test compound. A significantly reduced expression of a marker of the invention in the presence of the test compound is an indication that the test compound inhibits cervical cancer. The cervical cell samples may, for example, be aliquots of a single sample of normal cervical cells obtained from a patient, pooled samples of normal cervical cells obtained from a patient, cells of a normal cervical cell line, aliquots of a single sample of cervical cancer cells obtained from a patient, pooled samples of cervical cancer cells obtained from a patient, cells of an cervical cancer cell line, or the like. In one embodiment, the samples are cervical cancer cells obtained from a patient and a plurality of compounds known to be effective for inhibiting various cervical cancers are tested in order to identify the compound which is likely to best inhibit the cervical cancer in the patient.

This method may likewise be used to assess the efficacy of a therapy for inhibiting cervical cancer in a patient. In this method, the level of expression of one or more markers of the invention in a pair of samples (one subjected to the therapy, the other not subjected to the therapy) is assessed. As with the method of assessing the efficacy of test compounds, if the therapy induces a significantly lower level of expression of a marker of the invention then the therapy is efficacious for inhibiting cervical cancer. As above, if samples from a selected patient are used in this method,

then alternative therapies can be assessed *in vitro* in order to select a therapy most likely to be efficacious for inhibiting cervical cancer in the patient.

As described above, the cancerous state of human cervical cells is correlated with changes in the levels of expression of the markers of the invention. The invention includes a method for assessing the human cervical cell carcinogenic potential of a test compound. This method comprises maintaining separate aliquots of human cervical cells in the presence and absence of the test compound. Expression of a marker of the invention in each of the aliquots is compared. A significantly higher level of expression of a marker of the invention in the aliquot maintained in the presence of the test compound (relative to the aliquot maintained in the absence of the test compound) is an indication that the test compound possesses human cervical cell carcinogenic potential. The relative carcinogenic potentials of various test compounds can be assessed by comparing the degree of enhancement or inhibition of the level of expression of the relevant markers, by comparing the number of markers for which the level of expression is enhanced or inhibited, or by comparing both.

Various aspects of the invention are described in further detail in the following subsections.

I. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules, including nucleic acids which encode a marker protein or a portion thereof. Isolated nucleic acids of the invention also include nucleic acid molecules sufficient for use as hybridization probes to identify marker nucleic acid molecules, and fragments of marker nucleic acid molecules, *e.g.*, those suitable for use as PCR primers for the amplification or mutation of marker nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Preferably, an "isolated" nucleic acid molecule is free of sequences (preferably protein-encoding sequences) which naturally flank the nucleic acid (*i.e.*,

sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kB, 4 kB, 3 kB, 2 kB, 1 kB, 0.5 kB or 0.1 kB of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention can be isolated using standard molecular biology techniques and the sequence information in the database records described herein. Using all or a portion of such nucleic acid sequences, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, ed., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, nucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which has a nucleotide sequence complementary to the nucleotide sequence of a marker nucleic acid or to the nucleotide sequence of a nucleic acid encoding a marker protein. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise only a portion of a nucleic acid sequence, wherein the full length nucleic acid sequence comprises a marker nucleic acid or which encodes a marker protein. Such nucleic acids

can be used, for example, as a probe or primer. The probe/primer typically is used as one or more substantially purified oligonucleotides. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150,
5 175, 200, 250, 300, 350, or 400 or more consecutive nucleotides of a nucleic acid of the invention.

Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. The probe comprises a label group attached thereto, *e.g.*, a
10 radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit for identifying cells or tissues which mis-express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, *e.g.*, detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

15 The invention further encompasses nucleic acid molecules that differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing), and thus encode the same protein.

It will be appreciated by those skilled in the art that DNA sequence
20 polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist
25 that may affect the overall expression level of that gene (*e.g.*, by affecting regulation or degradation).

As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic
30 acid molecules comprising an open reading frame encoding a polypeptide corresponding to a marker of the invention. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be

readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.

5 In another embodiment, an isolated nucleic acid molecule of the invention is at least 7, 15, 20, 25, 30, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, 3500, 4000, 4500, or more nucleotides in length and hybridizes under stringent conditions to a marker nucleic acid or to a nucleic acid encoding a marker protein. As
10 used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% (65%, 70%, preferably 75%) identical to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in sections 6.3.1-6.3.6 of *Current Protocols in Molecular Biology*, John Wiley & Sons,
15 N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

 In addition to naturally-occurring allelic variants of a nucleic acid molecule of the invention that can exist in the population, the skilled artisan will further
20 appreciate that sequence changes can be introduced by mutation thereby leading to changes in the amino acid sequence of the encoded protein, without altering the biological activity of the protein encoded thereby. For example, one can make nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues. A "non-essential" amino acid residue is a residue that can be altered from
25 the wild-type sequence without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity and thus would be likely targets for alteration.
 Alternatively, amino acid residues that are conserved among the homologs of various
30 species (*e.g.*, murine and human) may be essential for activity and thus would not be likely targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a variant marker protein that contain changes in amino acid residues that are not essential for activity. Such variant marker proteins differ in amino acid sequence from the naturally-occurring marker proteins, yet retain biological activity. In one embodiment, such a variant marker protein has an amino acid sequence that is at least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of a marker protein.

An isolated nucleic acid molecule encoding a variant marker protein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of marker nucleic acids, such that one or more amino acid residue substitutions, additions, or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

The present invention encompasses antisense nucleic acid molecules, *i.e.*, molecules which are complementary to a sense nucleic acid of the invention, *e.g.*, complementary to the coding strand of a double-stranded marker cDNA molecule or complementary to a marker mRNA sequence. Accordingly, an antisense nucleic acid of the invention can hydrogen bond to (*i.e.* anneal with) a sense nucleic acid of the invention. The antisense nucleic acid can be complementary to an entire coding strand,

or to only a portion thereof, *e.g.*, all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can also be antisense to all or part of a non-coding region of the coding strand of a nucleotide sequence encoding a marker protein. The non-coding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences
5 which flank the coding region and are not translated into amino acids.

An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an
10 antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which
15 can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-
20 methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-
25 methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense
30 orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a marker protein to thereby inhibit expression of the marker, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. Examples of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site or infusion of the antisense nucleic acid into an ovary-associated body fluid. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α -units, the strands run parallel to each other (Gaultier *et al.*, 1987, *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.*, 1987, *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach, 1988, *Nature* 334:585-591) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity for a nucleic acid molecule encoding a marker protein can be designed based

upon the nucleotide sequence of a cDNA corresponding to the marker. For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved (see Cech *et al.* U.S. Patent No. 4,987,071; and Cech *et al.* U.S. Patent No. 5,116,742).

- 5 Alternatively, an mRNA encoding a polypeptide of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (see, *e.g.*, Bartel and Szostak, 1993, *Science* 261:1411-1418).

The invention also encompasses nucleic acid molecules which form triple helical structures. For example, expression of a marker of the invention can be inhibited
10 by targeting nucleotide sequences complementary to the regulatory region of the gene encoding the marker nucleic acid or protein (*e.g.*, the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. See generally Helene (1991) *Anticancer Drug Des.* 6(6):569-84; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14(12):807-15.

- 15 In various embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.*, 1996, *Bioorganic & Medicinal Chemistry* 4(1): 5-23). As used
20 herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be
25 performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996), *supra*; Perry-O'Keefe *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:14670-675.

PNAs can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific
30 modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup

(1996), *supra*; or as probes or primers for DNA sequence and hybridization (Hyrup, 1996, *supra*; Perry-O'Keefe *et al.*, 1996, *Proc. Natl. Acad. Sci. USA* 93:14670-675).

In another embodiment, PNAs can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated which can combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup, 1996, *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), *supra*, and Finn *et al.* (1996) *Nucleic Acids Res.* 24(17):3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a link between the PNA and the 5' end of DNA (Mag *et al.*, 1989, *Nucleic Acids Res.* 17:5973-88). PNA monomers are then coupled in a step-wise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*, 1996, *Nucleic Acids Res.* 24(17):3357-63). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Peterser *et al.*, 1975, *Bioorganic Med. Chem. Lett.* 5:1119-11124).

In other embodiments, the oligonucleotide can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, 1988, *Bio/Techniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide can be conjugated to another molecule, *e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The invention also includes molecular beacon nucleic acids having at least one region which is complementary to a nucleic acid of the invention, such that the molecular beacon is useful for quantitating the presence of the nucleic acid of the invention in a sample. A "molecular beacon" nucleic acid is a nucleic acid comprising a pair of complementary regions and having a fluorophore and a fluorescent quencher associated therewith. The fluorophore and quencher are associated with different portions of the nucleic acid in such an orientation that when the complementary regions are annealed with one another, fluorescence of the fluorophore is quenched by the quencher. When the complementary regions of the nucleic acid are not annealed with one another, fluorescence of the fluorophore is quenched to a lesser degree. Molecular beacon nucleic acids are described, for example, in U.S. Patent 5,876,930.

II. Isolated Proteins and Antibodies

One aspect of the invention pertains to isolated marker proteins and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a marker protein or a fragment thereof. In one embodiment, the native marker protein can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, a protein or peptide comprising the whole or a segment of the marker protein is produced by recombinant DNA techniques. Alternative to recombinant expression, such protein or peptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less

than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, *i.e.*, it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such
5 preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a marker protein include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the marker protein, which include fewer amino acids than the full
10 length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding full-length protein. A biologically active portion of a marker protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in
15 which other regions of the marker protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of the marker protein.

Preferred marker proteins are encoded by nucleotide sequences comprising the sequence of any of the sequences set forth in the Sequence Listing.
20 Other useful proteins are substantially identical (*e.g.*, at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to one of these sequences and retain the functional activity of the corresponding naturally-occurring marker protein yet differ in amino acid sequence due to natural allelic variation or mutagenesis.

To determine the percent identity of two amino acid sequences or of two
25 nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid
30 residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, %

identity = # of identical positions/total # of positions (e.g., overlapping positions) x100).
In one embodiment the two sequences are the same length.

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a
5 mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with
10 the BLASTN program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTP program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, a newer version of the BLAST algorithm called
15 Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402, which is able to perform gapped local alignments for the programs BLASTN, BLASTP and BLASTX. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the
20 respective programs (e.g., BLASTX and BLASTN) can be used. See <http://www.ncbi.nlm.nih.gov>. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software
25 package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Yet another useful algorithm for identifying regions of local sequence similarity and alignment is the FASTA algorithm as described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448. When using the FASTA algorithm for
30 comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a *k*-tuple value of 2.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

The invention also provides chimeric or fusion proteins comprising a
5 marker protein or a segment thereof. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably a biologically active part) of a marker protein operably linked to a heterologous polypeptide (*i.e.*, a polypeptide other than the marker protein). Within the fusion protein, the term "operably linked" is intended to indicate that the marker protein or segment thereof and the heterologous polypeptide are fused
10 in-frame to each other. The heterologous polypeptide can be fused to the amino-terminus or the carboxyl-terminus of the marker protein or segment.

One useful fusion protein is a GST fusion protein in which a marker protein or segment is fused to the carboxyl terminus of GST sequences. Such fusion proteins can facilitate the purification of a recombinant polypeptide of the invention.

15 In another embodiment, the fusion protein contains a heterologous signal sequence at its amino terminus. For example, the native signal sequence of a marker protein can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence of the baculovirus envelope protein can be used as a heterologous signal sequence (Ausubel *et al.*, ed., *Current Protocols in Molecular*
20 *Biology*, John Wiley & Sons, NY, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook *et al.*, *supra*) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New
25 Jersey).

In yet another embodiment, the fusion protein is an immunoglobulin fusion protein in which all or part of a marker protein is fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered
30 to a subject to inhibit an interaction between a ligand (soluble or membrane-bound) and a protein on the surface of a cell (receptor), to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion protein can be used to affect the bioavailability of a cognate ligand of a marker protein. Inhibition of ligand/receptor interaction can be

useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies directed against a marker protein in a subject, to purify ligands and in screening assays
5 to identify molecules which inhibit the interaction of the marker protein with ligands.

Chimeric and fusion proteins of the invention can be produced by standard recombinant DNA techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, *e.g.*, Ausubel *et al.*, *supra*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an
15 expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

A signal sequence can be used to facilitate secretion and isolation of marker proteins. Signal sequences are typically characterized by a core of hydrophobic amino acids which are generally cleaved from the mature protein during secretion in one
20 or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to marker proteins, fusion proteins or segments thereof having a signal sequence, as well as to such proteins from which the signal sequence has been proteolytically cleaved (*i.e.*, the cleavage products). In one
25 embodiment, a nucleic acid sequence encoding a signal sequence can be operably linked in an expression vector to a protein of interest, such as a marker protein or a segment thereof. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the
30 extracellular medium by art recognized methods. Alternatively, the signal sequence can be linked to the protein of interest using a sequence which facilitates purification, such as with a GST domain.

The present invention also pertains to variants of the marker proteins. Such variants have an altered amino acid sequence which can function as either agonists (mimetics) or as antagonists. Variants can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation. An agonist can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of the protein. An antagonist
5 of a protein can inhibit one or more of the activities of the naturally occurring form of the protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the protein of interest. Thus, specific biological effects can be elicited by treatment with a variant of limited function.

10 Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the protein.

Variants of a marker protein which function as either agonists (mimetics) or as antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*,
15 truncation mutants, of the protein of the invention for agonist or antagonist activity. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of
20 potential protein sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display). There are a variety of methods which can be used to produce libraries of potential variants of the marker proteins from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, 1983, *Tetrahedron* 39:3; Itakura
25 *et al.*, 1984, *Annu. Rev. Biochem.* 53:323; Itakura *et al.*, 1984, *Science* 198:1056; Ike *et al.*, 1983 *Nucleic Acid Res.* 11:477).

In addition, libraries of segments of a marker protein can be used to generate a variegated population of polypeptides for screening and subsequent selection of variant marker proteins or segments thereof. For example, a library of coding
30 sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different

nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes amino terminal and internal fragments of various sizes of the protein of interest.

5 Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,
10 transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify
15 variants of a protein of the invention (Arkin and Yourvan, 1992, *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.*, 1993, *Protein Engineering* 6(3):327- 331).

 Another aspect of the invention pertains to antibodies directed against a protein of the invention. In preferred embodiments, the antibodies specifically bind a marker protein or a fragment thereof. The terms "antibody" and "antibodies" as used
20 interchangeably herein refer to immunoglobulin molecules as well as fragments and derivatives thereof that comprise an immunologically active portion of an immunoglobulin molecule, (*i.e.*, such a portion contains an antigen binding site which specifically binds an antigen, such as a marker protein, *e.g.*, an epitope of a marker protein). An antibody which specifically binds to a protein of the invention is an
25 antibody which binds the protein, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the protein. Examples of an immunologically active portion of an immunoglobulin molecule include, but are not limited to, single-chain antibodies (scAb), F(ab) and F(ab')₂ fragments.

 An isolated protein of the invention or a fragment thereof can be used as
30 an immunogen to generate antibodies. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 8 (preferably 10, 15, 20, or 30 or more) amino acid residues of the amino acid sequence of one of the

proteins of the invention, and encompasses at least one epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with the protein. Preferred epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, *e.g.*, hydrophilic regions. Hydrophobicity sequence analysis, hydrophilicity sequence analysis, or similar analyses can be used to identify hydrophilic regions. In preferred embodiments, an isolated marker protein or fragment thereof is used as an immunogen.

An immunogen typically is used to prepare antibodies by immunizing a suitable (*i.e.* immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or vertebrate. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized protein or peptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or a similar immunostimulatory agent. Preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a protein of the invention. In such a manner, the resulting antibody compositions have reduced or no binding of human proteins other than a protein of the invention.

The invention provides polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope. Preferred polyclonal and monoclonal antibody compositions are ones that have been selected for antibodies directed against a protein of the invention. Particularly preferred polyclonal and monoclonal antibody preparations are ones that contain only antibodies directed against a marker protein or fragment thereof.

Polyclonal antibodies can be prepared by immunizing a suitable subject with a protein of the invention as an immunogen. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. At an appropriate time after immunization, *e.g.*, when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies (mAb) by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell

hybridoma technique (see Kozbor *et al.*, 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (see Cole *et al.*, pp. 77-96 In *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., 1985) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology*, Coligan *et al.* ed., John Wiley & Sons, New York, 1994). Hybridoma cells producing a
5 monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, *e.g.*, using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a
10 monoclonal antibody directed against a protein of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia
Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene
15 *SurfZAP Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT
20 Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275- 1281; Griffiths *et al.* (1993) *EMBO J.* 12:725-734.

The invention also provides recombinant antibodies that specifically bind
25 a protein of the invention. In preferred embodiments, the recombinant antibodies specifically binds a marker protein or fragment thereof. Recombinant antibodies include, but are not limited to, chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, single-chain antibodies and multi-specific antibodies. A chimeric antibody is a molecule in which different portions are
30 derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, *e.g.*, Cabilly *et al.*, U.S. Patent No. 4,816,567; and Boss *et al.*, U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Single-chain antibodies have an

antigen binding site and consist of a single polypeptide. They can be produced by techniques known in the art, for example using methods described in Ladner *et al.* U.S. Pat. No. 4,946,778 (which is incorporated herein by reference in its entirety); Bird *et al.*, (1988) *Science* 242:423-426; Whitlow *et al.*, (1991) *Methods in Enzymology* 2:1-9; 5 Whitlow *et al.*, (1991) *Methods in Enzymology* 2:97-105; and Huston *et al.*, (1991) *Methods in Enzymology Molecular Design and Modeling: Concepts and Applications* 203:46-88. Multi-specific antibodies are antibody molecules having at least two antigen-binding sites that specifically bind different antigens. Such molecules can be produced by techniques known in the art, for example using methods described in Segal, 10 U.S. Patent No. 4,676,980 (the disclosure of which is incorporated herein by reference in its entirety); Holliger *et al.*, (1993) *Proc. Natl. Acad. Sci. USA* 90:6444-6448; Whitlow *et al.*, (1994) *Protein Eng.* 7:1017-1026 and U.S. Pat. No. 6,121,424.

Humanized antibodies are antibody molecules from non-human species having one or more complementarity determining regions (CDRs) from the non-human 15 species and a framework region from a human immunoglobulin molecule. (See, *e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 20 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.* (1987) *J. Immunol.* 139:3521- 3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Cancer Res.* 47:999-1005; Wood *et al.* (1985) 25 *Nature* 314:446-449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559); Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.

More particularly, humanized antibodies can be produced, for example, 30 using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide corresponding to a marker of the invention. Monoclonal

antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995) *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, *e.g.*, U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, *e.g.*, a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers *et al.*, 1994, *Bio/technology* 12:899-903).

The antibodies of the invention can be isolated after production (*e.g.*, from the blood or serum of the subject) or synthesis and further purified by well-known techniques. For example, IgG antibodies can be purified using protein A chromatography. Antibodies specific for a protein of the invention can be selected or (*e.g.*, partially purified) or purified by, *e.g.*, affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, *i.e.*, one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those of the desired protein of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is

contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein of the invention.

In a preferred embodiment, the substantially purified antibodies of the invention may specifically bind to a signal peptide, a secreted sequence, an extracellular domain, a transmembrane or a cytoplasmic domain or cytoplasmic membrane of a protein of the invention. In a particularly preferred embodiment, the substantially purified antibodies of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of a protein of the invention. In a more preferred embodiment, the substantially purified antibodies of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of a marker protein.

An antibody directed against a protein of the invention can be used to isolate the protein by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the marker protein or fragment thereof (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the level and pattern of expression of the marker. The antibodies can also be used diagnostically to monitor protein levels in tissues or body fluids (*e.g.* in a cervical-associated body fluid) as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by the use of an antibody derivative, which comprises an antibody of the invention coupled to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Antibodies of the invention may also be used as therapeutic agents in treating cancers. In a preferred embodiment, completely human antibodies of the invention are used for therapeutic treatment of human cancer patients, particularly those having an cervical cancer. In another preferred embodiment, antibodies that bind
5 specifically to a marker protein or fragment thereof are used for therapeutic treatment. Further, such therapeutic antibody may be an antibody derivative or immunotoxin comprising an antibody conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D,
10 ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (*e.g.*, methotrexate,
15 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.*, mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.*, daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.*,
20 dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (*e.g.*, vincristine and vinblastine).

The conjugated antibodies of the invention can be used for modifying a given biological response, for the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or
25 polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as ribosome-inhibiting protein (see Better et al., U.S. Patent No. 6,146,631, the disclosure of which is incorporated herein in its entirety), abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor,
30 tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, *e.g.*, Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug
5 Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in
10 *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.*, 62:119-58 (1982).

Accordingly, in one aspect, the invention provides substantially purified antibodies, antibody fragments and derivatives, all of which specifically bind to a
15 protein of the invention and preferably, a marker protein. In various embodiments, the substantially purified antibodies of the invention, or fragments or derivatives thereof, can be human, non-human, chimeric and/or humanized antibodies. In another aspect, the invention provides non-human antibodies, antibody fragments and derivatives, all of which specifically bind to a protein of the invention and preferably, a marker protein.
20 Such non-human antibodies can be goat, mouse, sheep, horse, chicken, rabbit, or rat antibodies. Alternatively, the non-human antibodies of the invention can be chimeric and/or humanized antibodies. In addition, the non-human antibodies of the invention can be polyclonal antibodies or monoclonal antibodies. In still a further aspect, the invention provides monoclonal antibodies, antibody fragments and derivatives, all of
25 which specifically bind to a protein of the invention and preferably, a marker protein. The monoclonal antibodies can be human, humanized, chimeric and/or non-human antibodies.

The invention also provides a kit containing an antibody of the invention conjugated to a detectable substance, and instructions for use. Still another aspect of the
30 invention is a pharmaceutical composition comprising an antibody of the invention. In one embodiment, the pharmaceutical composition comprises an antibody of the invention and a pharmaceutically acceptable carrier.

III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a marker protein (or a portion of such a protein). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, namely expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, *Methods in Enzymology: Gene Expression Technology* vol.185, Academic Press, San Diego, CA (1991). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and

those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

The recombinant expression vectors of the invention can be designed for expression of a marker protein or a segment thereof in prokaryotic (*e.g.*, *E. coli*) or eukaryotic cells (*e.g.*, insect cells {using baculovirus expression vectors}, yeast cells or mammalian cells). Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988, *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, 1988, *Gene* 69:301-315) and pET 11d (Studier *et al.*, p. 60-89, In *Gene Expression Technology: Methods in Enzymology* vol.185, Academic Press, San Diego, CA, 1991). Target gene expression from the pTrc vector relies on host RNA

polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident prophage
5 harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, p. 119-128, In *Gene Expression Technology: Methods in Enzymology* vol. 185, Academic Press, San Diego, CA, 1990. Another
10 strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, 1992, *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

15 In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.*, 1987, *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, 1982, *Cell* 30:933-943), pJRY88 (Schultz *et al.*, 1987, *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

20 Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*, 1983, *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers, 1989, *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in
25 mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987, *Nature* 329:840) and pMT2PC (Kaufman *et al.*, 1987, *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2,
30 cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook *et al.*, *supra*.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable
5 tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.*, 1987, *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988, *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989, *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.*, 1983, *Cell* 33:729-740; Queen and Baltimore, 1983, *Cell* 33:741-748), neuron-specific promoters
10 (e.g., the neurofilament promoter; Byrne and Ruddle, 1989, *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund *et al.*, 1985, *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters
15 (Kessel and Gruss, 1990, *Science* 249:374-379) and the α -fetoprotein promoter (Camper and Tilghman, 1989, *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory
20 sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to the mRNA encoding a polypeptide of the invention. Regulatory sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or
25 enhancers, or regulatory sequences can be chosen which direct constitutive, tissue-specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the
30 vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, 1986, *Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential
5 progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic (*e.g.*, *E. coli*) or eukaryotic cell (*e.g.*,
10 insect cells, yeast or mammalian cells).

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid into a host cell, including calcium
15 phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells
20 may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid
25 can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce a marker protein or a segment thereof. Accordingly, the invention further provides methods for producing a marker protein or a segment
30 thereof using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of the invention (into which a recombinant expression vector encoding a marker protein or a segment thereof has been introduced) in a suitable medium such that the is produced. In another embodiment, the method further

comprises isolating the marker protein or a segment thereof from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a sequences encoding a marker protein or a segment thereof have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous sequences encoding a marker protein of the invention have been introduced into their genome or homologous recombinant animals in which endogenous gene(s) encoding a marker protein have been altered. Such animals are useful for studying the function and/or activity of the marker protein and for identifying and/or evaluating modulators of marker protein. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing a nucleic acid encoding a marker protein into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the polypeptide of the invention to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Patent No.

4,873,191 and in Hogan, *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of mRNA
5 encoding the transgene in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying the transgene can further be bred to other transgenic animals carrying other transgenes.

To create an homologous recombinant animal, a vector is prepared which
10 contains at least a portion of a gene encoding a marker protein into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the gene. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector
15 can be designed such that, upon homologous recombination, the endogenous gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous protein). In the homologous recombination vector, the altered portion of the gene is flanked at its 5' and 3' ends by additional nucleic acid of the gene to allow for
20 homologous recombination to occur between the exogenous gene carried by the vector and an endogenous gene in an embryonic stem cell. The additional flanking nucleic acid sequences are of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see, *e.g.*, Thomas and Capecchi, 1987, *Cell* 51:503 for a
25 description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced gene has homologously recombined with the endogenous gene are selected (see, *e.g.*, Li *et al.*, 1992, *Cell* 69:915). The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras (see, *e.g.*, Bradley,
30 *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, Ed., IRL, Oxford, 1987, pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed

animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in Bio/Technology* 2:823-829 and in PCT Publication
5 NOS. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, e.g., Lakso *et al.* (1992) *Proc.*
10 *Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991, *Science* 251:1351-1355). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be provided through the construction of
15 "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-
20 813 and PCT Publication NOS. WO 97/07668 and WO 97/07669.

IV. Pharmaceutical Compositions

The nucleic acid molecules, polypeptides, and antibodies (also referred to herein as "active compounds") of the invention can be incorporated into pharmaceutical
25 compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical
30 administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is

contemplated. Supplementary active compounds can also be incorporated into the compositions.

The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a marker nucleic acid or protein . Such methods comprise formulating a pharmaceutically acceptable carrier with
5 an agent which modulates expression or activity of a marker nucleic acid or protein. Such compositions can further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent which modulates expression or
10 activity of a marker nucleic acid or protein and one or more additional active compounds.

The invention also provides methods (also referred to herein as "screening assays") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, peptoids, small molecules or other drugs) which
15 (a) bind to the marker, or (b) have a modulatory (*e.g.*, stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (*e.g.*, peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker
20 and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker.

The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds.
25 Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, *e.g.*, Zuckermann *et al.*, 1994, *J. Med. Chem.*
30 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while

the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992, *Biotechniques* 13:412-421), or on beads (Lam, 1991, *Nature* 354:82-84), chips (Fodor, 1993, *Nature* 364:555-556), bacteria and/or spores, (Ladner, USP 5,223,409), plasmids (Cull *et al.*, 1992, *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith, 1990, *Science* 249:386-390; Devlin, 1990, *Science* 249:404-406; Cwirla *et al.*, 1990, *Proc. Natl. Acad. Sci.* 87:6378-6382; Felici, 1991, *J. Mol. Biol.* 222:301-310; Ladner, *supra.*).

In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a protein encoded by or corresponding to a marker or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to a protein encoded by or corresponding to a marker or biologically active portion thereof. Determining the ability of the test compound to directly bind to a protein can be accomplished, for example, by coupling the compound with a radioisotope or enzymatic label such that binding of the compound to the marker can be determined by detecting the labeled marker compound in a complex. For example, compounds (*e.g.*, marker substrates) can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, assay components can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

In another embodiment, the invention provides assays for screening candidate or test compounds which modulate the expression of a marker or the activity of a protein encoded by or corresponding to a marker, or a biologically active portion

thereof. In all likelihood, the protein encoded by or corresponding to the marker can, *in vivo*, interact with one or more molecules, such as but not limited to, peptides, proteins, hormones, cofactors and nucleic acids. For the purposes of this discussion, such cellular and extracellular molecules are referred to herein as "binding partners" or marker

5 "substrate".

One necessary embodiment of the invention in order to facilitate such screening is the use of a protein encoded by or corresponding to marker to identify the protein's natural *in vivo* binding partners. There are many ways to accomplish this which are known to one skilled in the art. One example is the use of the marker protein as "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.*, U.S. Patent No. 10 5,283,317; Zervos *et al*, 1993, *Cell* 72:223-232; Madura *et al*, 1993, *J. Biol. Chem.* 268:12046-12054; Bartel *et al*, 1993, *Biotechniques* 14:920-924; Iwabuchi *et al*, 1993 *Oncogene* 8:1693-1696; Brent WO94/10300) in order to identify other proteins which bind to or interact with the marker (binding partners) and, therefore, are possibly 15 involved in the natural function of the marker. Such marker binding partners are also likely to be involved in the propagation of signals by the marker protein or downstream elements of a marker protein-mediated signaling pathway. Alternatively, such marker protein binding partners may also be found to be inhibitors of the marker protein.

The two-hybrid system is based on the modular nature of most 20 transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that encodes a marker protein fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is 25 fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a marker-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) which is operably linked to a transcriptional regulatory site responsive to 30 the transcription factor. Expression of the reporter gene can be readily detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the marker protein.

In a further embodiment, assays may be devised through the use of the invention for the purpose of identifying compounds which modulate (*e.g.*, affect either positively or negatively) interactions between a marker protein and its substrates and/or binding partners. Such compounds can include, but are not limited to, molecules such as antibodies, peptides, hormones, oligonucleotides, nucleic acids, and analogs thereof. Such compounds may also be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. The preferred assay components for use in this embodiment is an cervical cancer marker protein identified herein, the known binding partner and/or substrate of same, and the test compound. Test compounds can be supplied from any source.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the marker protein and its binding partner involves preparing a reaction mixture containing the marker protein and its binding partner under conditions and for a time sufficient to allow the two products to interact and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the marker protein and its binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the marker protein and its binding partner is then detected. The formation of a complex in the control reaction, but less or no such formation in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the marker protein and its binding partner. Conversely, the formation of more complex in the presence of compound than in the control reaction indicates that the compound may enhance interaction of the marker protein and its binding partner.

The assay for compounds that interfere with the interaction of the marker protein with its binding partner may be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the marker protein or its binding partner onto a solid phase and detecting complexes anchored to the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds

that interfere with the interaction between the marker proteins and the binding partners (e.g., by competition) can be identified by conducting the reaction in the presence of the test substance, *i.e.*, by adding the test substance to the reaction mixture prior to or simultaneously with the marker and its interactive binding partner. Alternatively, test compounds that disrupt preformed complexes, *e.g.*, compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

In a heterogeneous assay system, either the marker protein or its binding partner is anchored onto a solid surface or matrix, while the other corresponding non-anchored component may be labeled, either directly or indirectly. In practice, microtitre plates are often utilized for this approach. The anchored species can be immobilized by a number of methods, either non-covalent or covalent, that are typically well known to one who practices the art. Non-covalent attachment can often be accomplished simply by coating the solid surface with a solution of the marker protein or its binding partner and drying. Alternatively, an immobilized antibody specific for the assay component to be anchored can be used for this purpose. Such surfaces can often be prepared in advance and stored.

In related embodiments, a fusion protein can be provided which adds a domain that allows one or both of the assay components to be anchored to a matrix. For example, glutathione-S-transferase/marker fusion proteins or glutathione-S-transferase/binding partner can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed marker or its binding partner, and the mixture incubated under conditions conducive to complex formation (*e.g.*, physiological conditions). Following incubation, the beads or microtiter plate wells are washed to remove any unbound assay components, the immobilized complex assessed either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of marker binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a marker protein or a marker protein binding partner can be immobilized utilizing conjugation of biotin and

streptavidin. Biotinylated marker protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the
5 protein-immobilized surfaces can be prepared in advance and stored.

In order to conduct the assay, the corresponding partner of the immobilized assay component is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted assay components are removed (*e.g.*, by washing) and any complexes formed will remain immobilized on the solid
10 surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; *e.g.*, using a labeled antibody specific for
15 the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, *e.g.*, a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which modulate (inhibit or enhance) complex formation or which disrupt preformed complexes can be detected.

In an alternate embodiment of the invention, a homogeneous assay may
20 be used. This is typically a reaction, analogous to those mentioned above, which is conducted in a liquid phase in the presence or absence of the test compound. The formed complexes are then separated from unreacted components, and the amount of complex formed is determined. As mentioned for heterogeneous assay systems, the order of addition of reactants to the liquid phase can yield information about which test
25 compounds modulate (inhibit or enhance) complex formation and which disrupt preformed complexes.

In such a homogeneous assay, the reaction products may be separated from unreacted assay components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and
30 immunoprecipitation. In differential centrifugation, complexes of molecules may be separated from uncomplexed molecules through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., *Trends Biochem Sci* 1993

Aug;18(8):284-7). Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger
5 complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the complex as compared to the uncomplexed molecules may be exploited to differentially separate the complex from the remaining individual reactants, for example through the use of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to
10 one skilled in the art (see, *e.g.*, Heegaard, 1998, *J Mol. Recognit.* 11:141-148; Hage and Tweed, 1997, *J. Chromatogr. B. Biomed. Sci. Appl.*, 699:499-525). Gel electrophoresis may also be employed to separate complexed molecules from unbound species (see, *e.g.*, Ausubel *et al* (eds.), In: *Current Protocols in Molecular Biology*, J. Wiley & Sons, New York. 1999). In this technique, protein or nucleic acid complexes are separated based on
15 size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, nondenaturing gels in the absence of reducing agent are typically preferred, but conditions appropriate to the particular interactants will be well known to one skilled in the art. Immunoprecipitation is another common technique utilized for the isolation of a protein-protein complex from solution (see, *e.g.*, Ausubel
20 *et al* (eds.), In: *Current Protocols in Molecular Biology*, J. Wiley & Sons, New York. 1999). In this technique, all proteins binding to an antibody specific to one of the binding molecules are precipitated from solution by conjugating the antibody to a polymer bead that may be readily collected by centrifugation. The bound assay components are released from the beads (through a specific proteolysis event or other
25 technique well known in the art which will not disturb the protein-protein interaction in the complex), and a second immunoprecipitation step is performed, this time utilizing antibodies specific for the correspondingly different interacting assay component. In this manner, only formed complexes should remain attached to the beads. Variations in complex formation in both the presence and the absence of a test compound can be
30 compared, thus offering information about the ability of the compound to modulate interactions between the marker protein and its binding partner.

Also within the scope of the present invention are methods for direct detection of interactions between the marker protein and its natural binding partner and/or a test compound in a homogeneous or heterogeneous assay system without further sample manipulation. For example, the technique of fluorescence energy transfer
5 may be utilized (see, *e.g.*, Lakowicz *et al*, U.S. Patent No. 5,631,169; Stavrianopoulos *et al*, U.S. Patent No. 4,868,103). Generally, this technique involves the addition of a fluorophore label on a first 'donor' molecule (*e.g.*, marker or test compound) such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule (*e.g.*, marker or test compound), which in turn is able to fluoresce
10 due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships
15 between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter). A test substance which either enhances or hinders participation of one of the species in
20 the preformed complex will result in the generation of a signal variant to that of background. In this way, test substances that modulate interactions between a marker and its binding partner can be identified in controlled assays.

In another embodiment, modulators of marker expression are identified in a method wherein a cell is contacted with a candidate compound and the expression
25 of marker mRNA or protein in the cell, is determined. The level of expression of marker mRNA or protein in the presence of the candidate compound is compared to the level of expression of marker mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of marker expression based on this comparison. For example, when expression of marker mRNA
30 or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of marker mRNA or protein expression. Conversely, when expression of marker mRNA or protein is less (statistically significantly less) in the presence of the candidate compound

than in its absence, the candidate compound is identified as an inhibitor of marker mRNA or protein expression. The level of marker mRNA or protein expression in the cells can be determined by methods described herein for detecting marker mRNA or protein.

5 In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a marker protein can be further confirmed *in vivo*, *e.g.*, in a whole animal model for cellular transformation and/or tumorigenesis.

10 This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a marker modulating agent, an antisense marker nucleic acid molecule, a marker-specific antibody, or a marker-binding
15 partner) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

20 It is understood that appropriate doses of small molecule agents and protein or polypeptide agents depends upon a number of factors within the knowledge of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of these agents will vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to
25 be administered, if applicable, and the effect which the practitioner desires the agent to have upon the nucleic acid or polypeptide of the invention. Exemplary doses of a small molecule include milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1
30 microgram per kilogram to about 50 micrograms per kilogram). Exemplary doses of a protein or polypeptide include gram, milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 5 grams per kilogram, about 100 micrograms per kilogram to about 500 milligrams per kilogram, or

about 1 milligram per kilogram to about 50 milligrams per kilogram). It is furthermore understood that appropriate doses of one of these agents depend upon the potency of the agent with respect to the expression or activity to be modulated. Such appropriate doses can be determined using the assays described herein. When one or more of these agents
5 is to be administered to an animal (*e.g.* a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher can, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend
10 upon a variety of factors including the activity of the specific agent employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

A pharmaceutical composition of the invention is formulated to be
15 compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline
20 solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with
25 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the
30 extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy

syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid
5 polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants.

Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid,
10 thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

15 Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium,
20 and then incorporating the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

25 Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid
30 carrier is applied orally and swished and expectorated or swallowed.

Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches, and the like can contain any of the following ingredients, or compounds of a similar nature: a

binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as
5 peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal
10 means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal
15 administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

20 In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid.
25 Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes having monoclonal antibodies incorporated therein or thereon) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled
30 in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the

subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

For antibodies, the preferred dosage is 0.1 mg/kg to 100 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (*e.g.*, into the cervical epithelium). A method for lipidation of antibodies is described by Cruikshank *et al.* (1997) *J. Acquired Immune Deficiency Syndromes and Human Retrovirology* 14:193.

The invention also provides vaccine compositions for the prevention and/or treatment of cervical cancer. The invention provides cervical cancer vaccine compositions in which a protein of a marker of Table 1, or a combination of proteins of the markers of Table 1, are introduced into a subject in order to stimulate an immune response against the cervical cancer. The invention also provides cervical cancer vaccine compositions in which a gene expression construct, which expresses a marker or fragment of a marker identified in Table 1, is introduced into the subject such that a protein or fragment of a protein encoded by a marker of Table 1 is produced by transfected cells in the subject at a higher than normal level and elicits an immune response.

In one embodiment, a cervical cancer vaccine is provided and employed as an immunotherapeutic agent for the prevention of cervical cancer. In another embodiment, a cervical cancer vaccine is provided and employed as an immunotherapeutic agent for the treatment of cervical cancer.

By way of example, a cervical cancer vaccine comprised of the proteins of the markers of Table 1, may be employed for the prevention and/or treatment of cervical cancer in a subject by administering the vaccine by a variety of routes, *e.g.*, intradermally, subcutaneously, or intramuscularly. In addition, the cervical cancer

vaccine can be administered together with adjuvants and/or immunomodulators to boost the activity of the vaccine and the subject's response. In one embodiment, devices and/or compositions containing the vaccine, suitable for sustained or intermittent release could be, implanted in the body or topically applied thereto for the relatively slow
5 release of such materials into the body. The cervical cancer vaccine can be introduced along with immunomodulatory compounds, which can alter the type of immune response produced in order to produce a response which will be more effective in eliminating the cancer.

In another embodiment, a cervical cancer vaccine comprised of an
10 expression construct of the markers of Table 1, may be introduced by injection into muscle or by coating onto microprojectiles and using a device designed for the purpose to fire the projectiles at high speed into the skin. The cells of the subject will then express the protein(s) or fragments of proteins of the markers of Table 1 and induce an immune
15 response. In addition, the cervical cancer vaccine may be introduced along with expression constructs for immunomodulatory molecules, such as cytokines, which may increase the immune response or modulate the type of immune response produced in order to produce a response which will be more effective in eliminating the cancer.

The marker nucleic acid molecules can be inserted into vectors and used
20 as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470), or by stereotactic injection (see, *e.g.*, Chen *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which
25 the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.* retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or
30 dispenser together with instructions for administration.

V. Predictive Medicine

The present invention pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trails are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining the level of expression of one or more marker proteins or nucleic acids, in order to determine whether an individual is at risk of developing cervical cancer. Such assays can be used for prognostic or predictive purposes to thereby prophylactically treat an individual prior to the onset of the cancer.

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs or other compounds administered either to inhibit cervical cancer or to treat or prevent any other disorder {*i.e.* in order to understand any cervical carcinogenic effects that such treatment may have}) on the expression or activity of a marker of the invention in clinical trials. These and other agents are described in further detail in the following sections.

A. Diagnostic Assays

An exemplary method for detecting the presence or absence of a marker protein or nucleic acid in a biological sample involves obtaining a biological sample (*e.g.* a cervical-associated body fluid) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (*e.g.*, mRNA, genomic DNA, or cDNA). The detection methods of the invention can thus be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of a marker protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of a marker protein include introducing into a subject a labeled antibody directed against the protein or fragment thereof. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

A general principle of such diagnostic and prognostic assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways.

For example, one method to conduct such an assay would involve anchoring the marker or probe onto a solid phase support, also referred to as a substrate, and detecting target marker/probe complexes anchored on the solid phase at the end of the reaction. In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of marker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay.

There are many established methods for anchoring assay components to a solid phase. These include, without limitation, marker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored.

Other suitable carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the marker or probe belongs. Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components may be removed (*e.g.*, by washing) under conditions such that any complexes formed will remain immobilized upon the solid phase. The detection of marker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein.

In a preferred embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known to one skilled in the art.

5 It is also possible to directly detect marker/probe complex formation without further manipulation or labeling of either component (marker or probe), for example by utilizing the technique of fluorescence energy transfer (see, for example, Lakowicz *et al.*, U.S. Patent No. 5,631,169; Stavrianopoulos, *et al.*, U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that, upon
10 excitation with incident light of appropriate wavelength, its emitted fluorescent energy will be absorbed by a fluorescent label on a second 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label
15 may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured
20 through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

 In another embodiment, determination of the ability of a probe to recognize a marker can be accomplished without labeling either assay component (probe or marker) by utilizing a technology such as real-time Biomolecular Interaction Analysis
25 (BIA) (see, *e.g.*, Sjolander, S. and Urbaniczky, C., 1991, *Anal. Chem.* 63:2338-2345 and Szabo *et al.*, 1995, *Curr. Opin. Struct. Biol.* 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index
30 of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with marker and probe as solutes in a liquid phase. In such an assay, the complexed marker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to:

5 differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, marker/probe complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., 1993, *Trends Biochem Sci.* 18(8):284-7).

10 Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively

15 different charge properties of the marker/probe complex as compared to the uncomplexed components may be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, e.g., Heegaard, N.H., 1998, *J. Mol. Recognit.* Winter 11(1-

20 6):141-8; Hage, D.S., and Tweed, S.A. *J Chromatogr B Biomed Sci Appl* 1997 Oct 10;699(1-2):499-525). Gel electrophoresis may also be employed to separate complexed assay components from unbound components (see, e.g., Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for

25 example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

In a particular embodiment, the level of marker mRNA can be

30 determined both by *in situ* and by *in vitro* formats in a biological sample using methods known in the art. The term "biological sample" is intended to include tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells and fluids present within a subject. Many expression detection methods use isolated RNA.

For *in vitro* methods, any RNA isolation technique that does not select against the isolation of mRNA can be utilized for the purification of RNA from cervical cells (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be
5 processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Patent No. 4,843,155).

The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain
10 reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and
15 sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a marker of the present invention. Other suitable probes for use in the diagnostic assays of the invention are described herein. Hybridization of an mRNA with the probe indicates that the marker in question is being expressed.

In one format, the mRNA is immobilized on a solid surface and contacted
20 with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level
25 of mRNA encoded by the markers of the present invention.

An alternative method for determining the level of mRNA marker in a sample involves the process of nucleic acid amplification, *e.g.*, by rtPCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA*, 88:189-193), self sustained
30 sequence replication (Guatelli *et al.*, 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *Bio/Technology* 6:1197), rolling circle replication (Lizardi *et al.*, U.S. Patent No. 5,854,033) or any other nucleic acid

amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being
5 a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid
10 molecule comprising the nucleotide sequence flanked by the primers.

For *in situ* methods, mRNA does not need to be isolated from the cervical cells prior to detection. In such methods, a cell or tissue sample is prepared/processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that
15 encodes the marker.

As an alternative to making determinations based on the absolute expression level of the marker, determinations may be based on the normalized expression level of the marker. Expression levels are normalized by correcting the absolute expression level of a marker by comparing its expression to the expression of a
20 gene that is not a marker, *e.g.*, a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the expression level in one sample, *e.g.*, a patient sample, to another sample, *e.g.*, a non-cervical cancer sample, or between samples from different sources.

Alternatively, the expression level can be provided as a relative
25 expression level. To determine a relative expression level of a marker, the level of expression of the marker is determined for 10 or more samples of normal versus cancer cell isolates, preferably 50 or more samples, prior to the determination of the expression level for the sample in question. The mean expression level of each of the genes assayed
30 in the larger number of samples is determined and this is used as a baseline expression level for the marker. The expression level of the marker determined for the test sample (absolute level of expression) is then divided by the mean expression value obtained for that marker. This provides a relative expression level.

Preferably, the samples used in the baseline determination will be from cervical cancer or from non-cervical cancer cells of cervical tissue. The choice of the cell source is dependent on the use of the relative expression level. Using expression found in normal tissues as a mean expression score aids in validating whether the marker
5 assayed is cervical specific (versus normal cells). In addition, as more data is accumulated, the mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from cervical cells provides a means for grading the severity of the cervical cancer state.

In another embodiment of the present invention, a marker protein is
10 detected. A preferred agent for detecting marker protein of the invention is an antibody capable of binding to such a protein or a fragment thereof, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment or derivative thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct
15 labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with
20 fluorescently labeled streptavidin.

Proteins from cervical cells can be isolated using techniques that are well known to those of skill in the art. The protein isolation methods employed can, for example, be such as those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring
25 Harbor, New York).

A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can
30 readily adapt known protein/antibody detection methods for use in determining whether cervical cells express a marker of the present invention.

In one format, antibodies, or antibody fragments or derivatives, can be used in methods such as Western blots or immunofluorescence techniques to detect the expressed proteins. In such uses, it is generally preferable to immobilize either the antibody or proteins on a solid support. Suitable solid phase supports or carriers include
5 any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present
10 invention. For example, protein isolated from cervical cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of
15 bound label on the solid support can then be detected by conventional means.

The invention also encompasses kits for detecting the presence of a marker protein or nucleic acid in a biological sample (*e.g.*, cervical smear). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing cervical cancer. For example, the kit can comprise a labeled compound or
20 agent capable of detecting a marker protein or nucleic acid in a biological sample and means for determining the amount of the protein or mRNA in the sample (*e.g.*, an antibody which binds the protein or a fragment thereof, or an oligonucleotide probe which binds to DNA or mRNA encoding the protein). Kits can also include instructions for interpreting the results obtained using the kit.

25 For antibody-based kits, the kit can comprise, for example: (1) a first antibody (*e.g.*, attached to a solid support) which binds to a marker protein; and, optionally, (2) a second, different antibody which binds to either the protein or the first antibody and is conjugated to a detectable label.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an
30 oligonucleotide, *e.g.*, a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a marker protein or (2) a pair of primers useful for amplifying a marker nucleic acid molecule. The kit can also comprise, *e.g.*, a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components

necessary for detecting the detectable label (*e.g.*, an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package,
5 along with instructions for interpreting the results of the assays performed using the kit.

B. Pharmacogenomics

The markers of the invention are also useful as pharmacogenomic markers. As used herein, a “pharmacogenomic marker” is an objective biochemical
10 marker whose expression level correlates with a specific clinical drug response or susceptibility in a patient (see, *e.g.*, McLeod *et al.* (1999) *Eur. J. Cancer* 35(12): 1650-1652). The presence or quantity of the pharmacogenomic marker expression is related to the predicted response of the patient and more particularly the patient’s tumor to therapy with a specific drug or class of drugs. By assessing the presence or quantity of
15 the expression of one or more pharmacogenomic markers in a patient, a drug therapy which is most appropriate for the patient, or which is predicted to have a greater degree of success, may be selected. For example, based on the presence or quantity of RNA or protein encoded by specific tumor markers in a patient, a drug or course of treatment may be selected that is optimized for the treatment of the specific tumor likely to be
20 present in the patient. The use of pharmacogenomic markers therefore permits selecting or designing the most appropriate treatment for each cancer patient without trying different drugs or regimes.

Another aspect of pharmacogenomics deals with genetic conditions that alters the way the body acts on drugs. These pharmacogenetic conditions can occur
25 either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes
30 is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show

exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of expression of a marker of the invention.

C. Monitoring Clinical Trials

Monitoring the influence of agents (*e.g.*, drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for cervical cancer. In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one or more selected markers of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the

level of expression of the marker(s) in the post-administration samples; (v) comparing the level of expression of the marker(s) in the pre-administration sample with the level of expression of the marker(s) in the post-administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example,

- 5 increased expression of the marker gene(s) during the course of treatment may indicate ineffective dosage and the desirability of increasing the dosage. Conversely, decreased expression of the marker gene(s) may indicate efficacious treatment and no need to change dosage.

10 D. Electronic Apparatus Readable Media and Arrays

Electronic apparatus readable media comprising a marker of the present invention is also provided. As used herein, "electronic apparatus readable media" refers to any suitable medium for storing, holding or containing data or information that can be read and accessed directly by an electronic apparatus. Such media can include, but are
15 not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as compact disc; electronic storage media such as RAM, ROM, EPROM, EEPROM and the like; general hard disks and hybrids of these categories such as magnetic/optical storage media. The medium is adapted or configured for having recorded thereon a marker of the present invention.

20 As used herein, the term "electronic apparatus" is intended to include any suitable computing or processing apparatus or other device configured or adapted for storing data or information. Examples of electronic apparatus suitable for use with the present invention include stand-alone computing apparatus; networks, including a local area network (LAN), a wide area network (WAN) Internet, Intranet, and Extranet;
25 electronic appliances such as a personal digital assistants (PDAs), cellular phone, pager and the like; and local and distributed processing systems.

As used herein, "recorded" refers to a process for storing or encoding information on the electronic apparatus readable medium. Those skilled in the art can readily adopt any of the presently known methods for recording information on known
30 media to generate manufactures comprising the markers of the present invention.

A variety of software programs and formats can be used to store the marker information of the present invention on the electronic apparatus readable medium. For example, the marker nucleic acid sequence can be represented in a word

processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like, as well as in other forms. Any number of data processor structuring formats (*e.g.*, text file or database) may be
5 employed in order to obtain or create a medium having recorded thereon the markers of the present invention.

By providing the markers of the invention in readable form, one can routinely access the marker sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the
10 present invention in readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequences of the invention which match a particular target sequence or target motif.

The present invention therefore provides a medium for holding
15 instructions for performing a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer, wherein the method comprises the steps of determining the presence or absence of a marker and based on the presence or absence of the marker, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer and/or recommending a particular treatment for cervical cancer or pre-
20 cervical cancer condition.

The present invention further provides in an electronic system and/or in a network, a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer associated with a marker wherein the method comprises the steps of determining the presence or absence of the marker, and based on the
25 presence or absence of the marker, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer, and/or recommending a particular treatment for the cervical cancer or pre-cervical cancer condition. The method may further comprise the step of receiving phenotypic information associated with the subject and/or acquiring from a network phenotypic information associated with the subject.

30 The present invention also provides in a network, a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer associated with a marker, said method comprising the steps of receiving information associated with the marker receiving phenotypic information associated with the subject,

acquiring information from the network corresponding to the marker and/or cervical cancer, and based on one or more of the phenotypic information, the marker, and the acquired information, determining whether the subject has a cervical cancer or a pre-disposition to cervical cancer. The method may further comprise the step of
5 recommending a particular treatment for the cervical cancer or pre-cervical cancer condition.

The present invention also provides a business method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer, said method comprising the steps of receiving information associated with the marker, receiving
10 phenotypic information associated with the subject, acquiring information from the network corresponding to the marker and/or cervical cancer, and based on one or more of the phenotypic information, the marker, and the acquired information, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer. The method may further comprise the step of recommending a particular treatment for the
15 cervical cancer or pre-cervical cancer condition.

The invention also includes an array comprising a marker of the present invention. The array can be used to assay expression of one or more genes in the array. In one embodiment, the array can be used to assay gene expression in a tissue to ascertain tissue specificity of genes in the array. In this manner, up to about 7600 genes
20 can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more tissues.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only tissue specificity, but also the level of expression of a battery of genes in the tissue is ascertainable. Thus, genes can be
25 grouped on the basis of their tissue expression *per se* and level of expression in that tissue. This is useful, for example, in ascertaining the relationship of gene expression between or among tissues. Thus, one tissue can be perturbed and the effect on gene expression in a second tissue can be determined. In this context, the effect of one cell type on another cell type in response to a biological stimulus can be determined. Such a
30 determination is useful, for example, to know the effect of cell-cell interaction at the level of gene expression. If an agent is administered therapeutically to treat one cell type but has an undesirable effect on another cell type, the invention provides an assay to determine the molecular basis of the undesirable effect and thus provides the

opportunity to co-administer a counteracting agent or otherwise treat the undesired effect. Similarly, even within a single cell type, undesirable biological effects can be determined at the molecular level. Thus, the effects of an agent on expression of other than the target gene can be ascertained and counteracted.

5 In another embodiment, the array can be used to monitor the time course of expression of one or more genes in the array. This can occur in various biological contexts, as disclosed herein, for example development of cervical cancer, progression of cervical cancer, and processes, such a cellular transformation associated with cervical cancer.

10 The array is also useful for ascertaining the effect of the expression of a gene on the expression of other genes in the same cell or in different cells. This provides, for example, for a selection of alternate molecular targets for therapeutic intervention if the ultimate or downstream target cannot be regulated.

The array is also useful for ascertaining differential expression patterns of
15 one or more genes in normal and abnormal cells. This provides a battery of genes that could serve as a molecular target for diagnosis or therapeutic intervention.

E. Surrogate Markers

The markers of the invention may serve as surrogate markers for one or
20 more disorders or disease states or for conditions leading up to disease states, and in particular, cervical cancer. As used herein, a "surrogate marker" is an objective biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (*e.g.*, with the presence or absence of a tumor). The presence or quantity of such markers is independent of the
25 disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (*e.g.*, early stage tumors), or when an assessment of disease progression is desired before a potentially dangerous clinical endpoint is
30 reached (*e.g.*, an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate

markers in the art include: Koomen *et al.* (2000) *J. Mass. Spectrom.* 35: 258-264; and James (1994) *AIDS Treatment News Archive* 209.

The markers of the invention are also useful as pharmacodynamic markers. As used herein, a "pharmacodynamic marker" is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the presence or activity of the drug in a subject. For example, a pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug *in vivo*. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected due to the nature of the marker itself; for example, using the methods described herein, antibodies may be employed in an immune-based detection system for a protein marker, or marker-specific radiolabeled probes may be used to detect a mRNA marker. Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda *et al.* US 6,033,862; Hattis *et al.* (1991) *Env. Health Perspect.* 90: 229-238; Schentag (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S21-S24; and Nicolau (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S16-S20.

VI. Experimental Protocol

A. Identification of clones

Cervical tumor specific cDNA clones were identified by transcription profiling using mRNA from 12 cervical tumors, 5 CIN III, 5 CIN I and 12 normal
5 cervical tissues. The subtracted libraries were constructed using mRNA from at least three independent normal ectocervix, B-lymphocytes, T-lymphocytes and other white blood cells (in activated and resting states) as drivers and four independent stage 1B cervical tumors or four independent CIN III cervical samples as testers. The top up-regulated clones in tumors or CIN III cervical tissues, as determined by proprietary
10 statistical analysis methods, were selected. The clusters in which the selected clones belong were blasted against both public and proprietary sequence databases in order to identify other EST sequences or clusters with significant overlap. Thus, contiguous EST sequences and/or clusters were assembled into full-length genes.

An identification of protein sequence corresponding to the clone was
15 accomplished by obtaining one of the following:

- a) a direct match between the protein sequence and at least one EST sequence in one of its 6 possible translations;
- b) a direct match between the nucleotide sequence for the mRNA corresponding to the protein sequence and at least one EST sequence;
- 20 c) a match between the protein sequence and a contiguous assembly (contig) of the EST sequences with other available EST sequences in the databases in one of its 6 possible translations; or
- d) a match between the nucleotide sequence for the mRNA corresponding to the protein sequence and a contiguous assembly of the EST sequences with other
25 available EST sequences in the databases in one of its 6 possible translations.

VII. Summary of the Data

Tables 1-3 list the markers obtained using the foregoing protocol. The tables provide the name of the gene corresponding to the marker ("Gene Name"), the
30 sequence listing identifier of the cDNA sequence of a nucleotide transcript encoded by or corresponding to the marker ("SEQ ID NO (nts)"), the sequence listing identifier of the amino acid sequence of a protein encoded by the nucleotide transcript ("SEQ ID NO

(AAs”), and the location of the protein coding sequence within the cDNA sequence (“CDS”).

Table 1 lists all of the markers of the invention which are over-expressed in cervical cancer cells compared to normal (*i.e.*, non-cancerous) cervical cells. Table 2
5 lists newly-identified nucleotide and amino acid sequences useful as cervical cancer markers. Table 3 lists newly-identified nucleotide sequences useful as cervical cancer markers.

Other Embodiments

10 Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims:

What is claimed:

1. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 143, 145, 147, 149, 151,
5 167, 203, 217, 231, 233, 51, 65, 67, 68, 100, and 153.
2. A vector which contains the nucleic acid molecule of claim 1.
3. A host cell which contains the nucleic acid molecule of claim 1.
- 10 4. A method of assessing whether a patient is afflicted with cervical cancer, the method comprising comparing:
 - a) the level of expression of a marker in a patient sample, wherein the marker is selected from Table 1; and
 - 15 b) the normal level of expression of the marker in a control non-cervical cancer sample,wherein a significant increase in the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer.
- 20 5. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 143, 145, 147, 149, 151, 167, 203, 217, 231, and 233.
- 25 6. An antibody which selectively binds to the polypeptide of claim 5.
7. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 144, 146, 148, 150, 152, 168, 204, 218, 232, and 234.
- 30 8. An antibody which selectively binds to the polypeptide of claim 7.

SEQUENCE LISTING

<110> Millennium Pharmaceuticals, Inc. et al.

<120> NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
OF CERVICAL CANCER

<130> MRI-035PC

<150> US 60/298,159

<151> 2001-06-13

<150> US 60/298,155

<151> 2001-06-13

<150> US 60/335,936

<151> 2001-11-14

<160> 238

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 12462

<212> DNA

<213> Homo sapiens

<400> 1

gaagatggcg	gcggcggcgg	cggtgacggc	gcttcccg	cggtgagga	cgatccgcca	60
gtgagcgcg	agactgcttc	cacttcgggc	gggggagccc	cggaccgaat	cggctctcta	120
ggcgtggag	cttgccgtcc	cacctccgtc	caaatcgacc	tttcctttct	atccccaacc	180
acccctcaac	ccctgttttc	ccctgccttc	cttgagaggg	ccatggagga	cgaggagaga	240
cagaagaagc	tggaggccgg	caaagccaag	cttgcccagt	ttcgacaaag	aaaagctcag	300
tcggatgggc	agagtccttc	caagaagcag	aaaaaaaaa	gaaaaacgct	aagcagtaaa	360
catgatgtgt	cagcacacca	tgatttgaat	attgatcaat	cacagtgtaa	tgaaatgtac	420
ataaatagtt	ctcagagagt	agaatcaact	gtgattcctg	aatctacaat	aatgagaact	480
ctacatagtg	gagaaataac	cagtcatgag	cagggtctct	ctgtggaact	ggaaagtga	540
atttcaacca	cagcagatga	ctgcagttca	gaggtaaatg	gttgagtttt	tgtgatgaga	600
acaggaaagc	ctacaaattt	attaagggaa	gaagaatttg	gtgttgatga	ttcttattct	660
gaacaaggag	cacaagacag	tccgactcat	ctagagatga	tggaaagtga	gttggctggg	720
aagcagcatg	agattgaaga	gctaaacaga	gagctggaag	aaatgagggg	tacctatggg	780
actgaaggac	tgcagcagtt	acaagaattt	gaagctgcca	ttaaacaagg	agatggcatt	840
ataaccagc	tactgctaa	tttacaacaa	gcaagaagag	aaaaggatga	gacaatgaga	900
gaatttttag	agttgacaga	acagagtcaa	aaattacaga	ttcaatttca	gcaattacag	960
gctagtga	ctctgagaaa	cagcactcat	agtagcacag	ctgcagactt	actacaagcc	1020
aaacaacaga	toctcactca	tcaacagcag	cttgaagaac	aagaccactt	attagaagat	1080
tatcagaaaa	agaaagaaga	cttcacaatg	caaattagtt	tcttgcaaga	gaaaattaaa	1140
gtatatgaaa	tggacaaga	taaaaaagta	gaaaactcaa	ataaagaaga	aatacaggaa	1200
aaggagacaa	tcattgaaga	attaaacaca	aaaataatag	aagaagaaaa	gaaaactctt	1260
gagctaaagg	ataaattaac	aactgctgat	aaattactag	gagaattaca	agaacagatt	1320
gtgcaaaa	accaagaaat	aaaaaacatg	aaattagagc	tgactaatto	taagcaaaaa	1380
gaaagacagt	cttctgaaga	aataaaacag	ttaatgggga	cagtcgaaga	acttcagaag	1440
agaaatcata	aagacagcca	gttcgaaact	gatatagtac	aacgaatgga	acaagaaaca	1500
caaagaaagt	tagaacaact	ccgggcagag	ctggatgaga	tgtatgggca	gcagatagtg	1560
caaatgaaac	aagaattaat	aagacaacac	atggcacaga	tggaggaaat	gaaaacacgg	1620
cataagggag	aaatggagaa	tgctttaagg	tcattattcaa	atattacagt	taatgaagat	1680
cagataaagt	taatgaatgt	ggcaataaat	gaactgaata	taaaattgca	agataactaac	1740
tctcaaaagg	aaaaactcaa	ggaagaacta	ggactaattt	tagaagaaaa	gtgtgctcta	1800

cagagacagc	ttgaagacct	tgttgaagaa	ttgagctttt	caagggaaca	gattcagaga	1860
gctagacaga	caatagctga	acaagaaagt	aaacttaatg	aagcacataa	gtcccttagt	1920
acagtggaa	atgttgaaagc	tgagattggt	tctgcatctg	aatccagaaa	ggaactagaa	1980
ttaaaacatg	aagcagaagt	tacaaattac	aagataaaac	ttgaaatggt	agaaaaagaa	2040
aagaatgctg	tgttagacag	aatggctgaa	tcacaagaag	ctgaattaga	gaggctgaga	2100
acacagcttc	tatttagtca	cgaagaagag	ctttccaaac	tgaaggaaga	tttagaaatt	2160
gaacatcgaa	taaatattga	aaaacttaaa	gataatttag	gcattcacta	taaacagcag	2220
atagatgggt	tacagaatga	aatgagtgaa	aagatagaaa	ccatgcaggt	tgaaaaggac	2280
aatttgataa	ctaagcagaa	tcaattaatt	ttggaaatgt	caaagctaaa	agattttacag	2340
cagtctcttg	taaatttcaa	gtcagaagaa	atgactcttc	aaatcaatga	acttcaaaaa	2400
gaaattgaaa	tactcagaca	agaagaaaaa	gaaaagggtg	cacttgaaca	agaagttcaa	2460
gaattacaa	ttaaaacaga	attggttagaa	aaacagatga	aggaaaaaga	gaatgatctt	2520
caagaaaaat	ttgcacaact	tgaagcagag	aatagcattc	ttaaagatga	aaagaaaacc	2580
cttgaagaca	tgttgaaaat	acatactcct	gttagccaag	aagaaaagatt	gatttttctta	2640
gactccatta	agtccaaatc	caaagactct	gtgtgggaaa	aagaaataga	aatacttata	2700
gagggaaatg	aggacctcaa	acaacaatgt	attcagctaa	atgaagagat	tgaaaagcaa	2760
aggaacactt	tttcattttgc	tgaaaaaaac	tttgaagtta	actatcaaga	gttacaagag	2820
gagtatgctt	gccttctcaa	agtaaaagat	gatttagaag	acagtaaaaa	taaacaggaa	2880
ttagagtata	aaagtaaact	taaagcactt	aatgaagagc	ttcattttgca	aagaataaat	2940
ccaactacag	tgaaaatgaa	aagttctgtc	tttgatgaag	acaaaacttt	tgtagcagaa	3000
acattgaaa	tgggtgaggt	tgttgaaaag	gatacaacag	aactcatgga	aaaacttgag	3060
gtaaccaagc	gagagaaatt	agagctgtca	cagagactgt	ctgatctttc	tgaacaattg	3120
aaacagaaac	atgggtgagat	tagttttcta	aatgaagaag	ttaaatcttt	aaagcaagag	3180
aaagaacaag	tttcatttgag	atgtagagag	ctagaaatca	ttattaacca	caacagggca	3240
gaaaatgtac	agtcattgtga	tactcaagta	agctctttat	tagatggagt	tgtgaccatg	3300
acaagcaggg	gtgctgaagg	atcagtttct	aaagtaataa	aaagtttttg	tgaagaatca	3360
aaaataatgg	tggaagataa	agtttctttt	gaaaatatga	ctggttgaga	agaaagtaag	3420
caagaacagt	tgatttttga	tcacttacca	tctgtaacaa	aggaatcatc	acttagagca	3480
actcaaccaa	gtgaaaatga	taaacttcag	aaagaactca	atgtacttaa	actagaacag	3540
aatgatttaa	ggctacagat	ggaagcccaa	cgcatttgcc	tctctctggg	ttattcaact	3600
catgtggatc	agggttcgtga	atatatggaa	aatgaaaaag	ataaagctct	ttgcagtctt	3660
aaagaagagc	ttattttttgc	tcaagaggaa	aagatcaagg	aacttcagaa	aatacaccag	3720
ttagaactac	agactatgaa	aacacaagaa	acaggtgatg	aaggaaagcc	tttcatctct	3780
ctcattggaa	aacttcaaaa	ggcagtgctc	gaagaatggt	cttatttttt	acagacttta	3840
tgcagtgtcc	ttgggtgaata	ttatactcct	gctttaaaat	gtgaagtaaa	tgcagaagac	3900
aaagagaatt	ctgggtgatta	cattttctgaa	aatgaagatc	cagaattaca	agattataga	3960
taagaagttc	aagactttca	agaaaatatg	cacactcttc	tcaacaaagt	aacagaagaa	4020
tacaacaac	tcttgggtact	tcaaacacga	ctaagcaaga	tctgggggaca	gcagacagat	4080
ggtatgaaac	ttgaattttgg	agaagaaaaac	cttccaaaag	aggaaacaga	gttttttatca	4140
atccattctc	agatgaccaa	tttggaagac	attgatgtca	atcataaaag	caagttatct	4200
tctctgcaag	atcttgaaaa	aactaaactt	gaagaacaag	ttcaagaatt	agaaagcctc	4260
atatcctctt	tgcagcaaca	gttgaaagaa	actgaacaaa	actatgaggc	agagatccac	4320
tgtttacaga	agaggcttca	agctgttagt	gagtcacagg	ttccgcgaag	cttacctgtt	4380
gattcgggtg	taattacaga	atctgatgca	cagagaacaa	tgtaccctgg	aagttgtgtg	4440
aaaaagaata	ttgatggtac	aatagagttt	tctgggtgaat	ttggagtga	agaggaaaca	4500
aatatcgttt	agttgcttga	aaaacaatac	caagaacaat	tagaagaaga	agtagctaag	4560
gttattgtgt	caatgagtat	agcattttgt	caacaaactg	aactgtctag	aatatctggg	4620
ggaaaagaaa	atactgcata	atcaaaagca	gcacatgctg	tgtgtcagca	agaacaacat	4680
tatttttaatg	aaatgaaatt	atcacaggat	caaattgggt	ttcagacttt	tgagacagtg	4740
gatgtgaaat	ttaaagaaga	atttaaacca	cttagtaaag	agttaggaga	acatggaaag	4800
gaaattttat	tatcaaatag	tgatcccat	gatataccag	aatcaaagga	ctgtgtgctg	4860
actatttcag	aagaaatggt	ctccaaagat	aaaacattta	tagttagaca	gtctattcat	4920
gatgagattt	cagtgtcaag	catggatgct	tctagacaac	taatgttgaa	tgaagaacag	4980
ttggaagata	tgagacagga	acttgtacga	caataccaag	aacatcaaca	ggcaacggaa	5040
ttgttaaggc	aagcacatat	gcggcaaatg	gagagacagc	gagaagacca	ggaacagcta	5100
caagaagaga	ttaaagagact	taatagacaa	ttagcccaga	gatcctccat	agataatgaa	5160
aacctgggtt	cagagagaga	gagggtgctt	ttagaggagc	tggaaagcact	aaagcagctg	5220
tcttttagctg	gaagagagaa	gctgtgttgt	gagctgcgca	acagcagtac	gcaaacacag	5280
aatggaaatg	aaaaccaagg	agaagttgaa	gaacaaacat	ttaaagaaaa	ggaattagac	5340

agaaaacctg	aagatgtgcc	tcctgagatt	ttgtctaatg	aaaggtatgc	actccagaaa	5400
gctaataata	gacttttgaa	gaccccttta	gaagttgtaa	agacaacagc	agctgttgaa	5460
gaaacaattg	gtcgccatgt	ccttgggatt	ctagatagat	ctagtaaaag	ccagtcattct	5520
gccagcctaa	tttggagggtc	agaagcagag	gcattctgtaa	agtcattgtgt	ccatgaggaa	5580
catacaagag	ttacagatga	atccattccc	tcttattctg	gaagtgatat	gccaagaaat	5640
gacattaaca	tgtggtcaaa	agtaactgag	gaaggaacag	agctgtcaca	acgacttgtg	5700
aggagtggtt	ttgctggaac	tgaatatagac	cctgaaaatg	aagaacttat	gctgaacatt	5760
agctctcgac	tacaagcagc	agttgaaaaa	ctcctagaag	ccataagtga	aactagcagt	5820
cagcttgaac	atgcgaaagt	gacacagaca	gagttgatgc	gtgagtcatt	tagacagaaa	5880
caagaagcaa	cagagtcctt	taagtgccaa	gaggaacttc	gagagcgcct	tcattgaggag	5940
tcaggggcca	gagaacagct	agctgtggag	ctcagtaagg	ctgagggcgt	cattgatggc	6000
tatgcagatg	aaaaaactct	ttttgaaagg	caaattcagg	aaaaaactga	tataatagat	6060
cgtcttgagc	aggagttggt	atgtgcaagt	aacagggttc	aagaattgga	ggcagagcaa	6120
cagcagatcc	aagaagaaaag	agaattactg	tccagacaaa	aggaagctat	gaaagcagag	6180
gcaggcccag	ttgaacaaca	attactacag	gagacagaaa	aattaatgaa	ggaaaaacta	6240
gaagtacaat	gtcaagctga	aaaagtacgt	gatgaccttc	aaaaacaagt	gaaagctcta	6300
gaaatagatg	tggaagaaca	agtcagtagg	tttatagagc	tggaacaaga	aaaaaatact	6360
gaactaatgg	attttaagaca	gcaaaaccaa	gcatttgaaa	agcagttaga	aaaaatgaga	6420
aaatttttag	atgagcaagc	cattgacaga	gaacatgaga	gagatgtatt	ccaacaggaa	6480
atacagaaac	tagaacagca	acttaagggtt	gttcctcgat	tccagcctat	cagtgaacat	6540
caactagag	agggttgaaca	gttagcaaat	catctgaaag	aaaaaacaga	caaatgcagt	6600
gagcttttgc	tctctaaaga	gcagcttcaa	agggatatac	aagaaaggaa	tgaagaaata	6660
gagaaactgg	agttcagagt	aagagaactg	gagcaggcgc	ttcttgtgag	tgcagatact	6720
tttcaaaagg	tagaggaccg	aaaacacttt	ggagctgtag	aagctaaacc	agaattgtcc	6780
ctagaagtac	aattgcaggc	tgaacgagat	gccatagaca	gaaaggaaaa	agagattaca	6840
aacttagaag	agcaattaga	acagttttaga	gaagaactgg	aaaataagaa	tgaagaagtt	6900
caacaattac	atatgcaatt	agaaatacag	aaaaagggaat	ctactacccg	cctacaagaa	6960
cttgaacagg	aaaacaaatt	atttaaggat	gacatggaga	aactgggact	tgccataaag	7020
gaatctgatg	ccatgtctac	tcaagaccaa	catgtgctat	ttgggaaatt	tgctcaaata	7080
atacaggaaa	aagaggtaga	aattgaccaa	ttaaatgaac	aagttacgaa	actccagcag	7140
caacttaaaa	ttacaacaga	taacaagggtt	attgaagaaa	aaaatgaact	gataagggat	7200
cttgaacccc	aaatagaatg	tttgatgagt	gatcaagaat	gtgtgaagag	aaatagagaa	7260
gaagaaatag	agcagctcaa	tgaagtgatt	gaaaaacttc	aacaggaatt	ggcaaattatt	7320
ggacagaaga	catcaatgaa	tgctcattcc	ctctcagaag	aagcagacag	tttaaaacat	7380
caattggatg	tggttatagc	tgaaaagctg	gccttggaa	agcaagtaga	aaccgcta	7440
gaagaaatga	ccttcattgaa	aaatgtactt	aaagaaacca	atttttaaaat	gaatcagcta	7500
acacagggaat	tattcagctt	aaagagagaa	cgtgaaagtg	tggaaaagat	tcaaagcata	7560
ccagagaata	gtgttaacgt	ggctatagat	catctgagca	aagacaaaacc	tgaactagaa	7620
gtagtccctta	cagaggatgc	tcttaaatcc	ctagaaaatc	agacatactt	caaatctttt	7680
gaagaaaatg	gcaaagggttc	cataattaat	ttggaaacaa	ggttgctaca	acttgagagc	7740
actgttagtg	caaaggactt	agaacttacc	cagtgttata	aacaaataaa	agacatgcaa	7800
gaacaaggcc	agtttgaaac	agaaatgctt	caaaagaaga	ttgtaaacct	acagaaaata	7860
gttgaagaaa	aagtggctgc	tgctcttgct	agtcaaatcc	aacttgaggc	agttcaggaa	7920
tatgcaaaat	tctgtcaaga	taatcaaaca	atttcatcag	aacctgaaag	aacaaatatt	7980
cagaatttaa	atcaactaag	agaagatgag	ttggggtcag	atatatcagc	attaaccttg	8040
agaatatcag	aattagaaaag	ccaggttggt	gaaatgcata	ctagtttgat	tttagaaaaa	8100
gaacaagtag	aaattgcaga	aaaaaatggt	ttagaaaaag	aaaagaagct	gctagaacta	8160
cagaagctat	tggagggcaa	tgagaaaaaa	cagagagaga	aagaaaaagaa	aagaagccct	8220
caagatgttg	aagttctcaa	gacaactact	gagctatttc	atagcaatga	agaaagtggg	8280
ttttttaatg	aactcgaggc	tcttagagct	gaatcagtg	ctaccaaaagc	agaacttgcc	8340
agttataaag	aaaaggctga	aaaacttcaa	gaagagcttt	tggtaaaaga	aacaaatatt	8400
acatctcttc	agaaagactt	aagccaagtt	agggatcacc	tcgcagaggc	aaaagagaaa	8460
ttgtccattt	tagaaaaaga	agatgagact	gaggtacaag	aaagcaaaaa	ggcctgcatg	8520
tttgagccac	ttcctataaa	actgagtaag	agcattgcac	cccagacaga	tgggactctg	8580
aagatcagta	gcagcaatca	gactccacaa	attcttgtaa	aaaatgcagg	aatacaaat	8640
aatttacaga	gtgaatgttc	ctcagaagaa	gttactgaaa	taatcagtca	gtttactgaa	8700
aaaattgaga	agatgcaaga	actacatgct	gctgaaat	tggacatgga	atccagacat	8760
atttcagaaa	ctgaaacctt	aaagagggaa	cactatgttg	cogttcagtt	actgaaagag	8820
gaatgtggtg	ccttgaaggc	agtgatacag	tgtctgagaa	gtaaagaggg	atcctcaatt	8880

cctgagctag	cacattctga	tgcttaccag	actagagaaa	tatgctccag	tgattctgga	8940
tcagactggg	gtcaggggaat	ttatcttaca	cacagtcagg	gatttgacat	agcatcagaa	9000
ggccgaggag	aagaaagtga	aagtgcaca	gattcctttc	caaagaaaat	aaagggatta	9060
ctgagagctg	tccataatga	aggcatgcag	gtgctttctc	tcactgagtc	tccctatagt	9120
gatggagagg	accattctat	tcagcaggtt	tcagaacctt	ggctagaaga	gagaaaagct	9180
tacatcaata	caatctcatc	tctaaaggat	ttaattacaa	agatgcaact	gcaaagagaa	9240
gccgaggttt	atgatagtct	tcaatctcat	gagagcttct	cagactggcg	aggtgaacta	9300
ctgcttgccc	ttcaacaagt	tttcttagaa	gagcgtagt	ttttactagc	agcatttcgg	9360
acggagctga	cagctctagg	tactacagat	gcagttgggt	tactaaaactg	tttggaaacag	9420
agaatacaag	aacagggtgt	tgaatatcaa	gcagctatgg	aatgcctcca	gaaagcagat	9480
agaaggagtt	tgttatctga	aattcaggca	ctgcatgcac	aatgaatgg	taggaaaatt	9540
actctgaaaa	gagaacaaga	gagtgcagaa	ccaagccaag	aactcttgga	atataatata	9600
cagcagaagc	agtctcaaat	gctggagatg	caagtggagc	tcagcagtat	gaaagacaga	9660
gcaacggaac	tgccaggagca	gctgagttct	gagaaaatgg	tggttgctga	actgaagagt	9720
gagcttgcac	aaactaaatt	ggaactagaa	acaacactca	aggcacagca	taaacaccta	9780
aaagaattgg	aggctttcag	gttggaagtt	aaagataaga	cagatgaagt	acatttgctt	9840
aatgacacat	tagcaagtga	acagaaaaaa	tcaagagagc	tccagtgggc	tttgaggaaa	9900
gagaaagcca	agttgggacg	cagtgaagaa	cgggataaag	agaacttga	ggatctgaag	9960
ttttcacttg	agagtcagaa	acaaaggaat	cttcagctaa	atctactttt	ggaacaacag	10020
aaacaactac	tgaacgaatc	ccagcaaaaa	atagaattcac	agagaatgct	atatgatgcc	10080
cagttgtcag	aagaacaagg	tcgaaactta	gagcttcagg	tacttcttga	atctgagaaa	10140
gttcgaattc	gggaaatgag	tagtacccta	gatagggagc	gggaattgca	cgcacagctg	10200
cagagcagtg	atggtactgg	acagtctcgg	ccacccttgc	cctcagagga	cctactgaaa	10260
gagctgcaga	aacagctaga	ggaaaaacac	agtcgcatag	tagaattggt	aatgagact	10320
gaaaaatata	aactggattc	tttgcaaaaca	cgacagcaaa	tggaaaaaga	taggcagggt	10380
cacaggaaaa	cactgcagac	agaacaggag	gccaacactg	agggacagaa	aaaaatgcat	10440
gagctccagt	ccaaagtggg	agatcttcag	cgccagctgg	aagagaaaaag	acaacaagtt	10500
tataagttag	accttgaagg	acagcgacta	caagggaatca	tgccagggaat	ccagaagcaa	10560
gaactagaac	gagagaataa	acgagaaagt	agaagaattc	tgtatcagaa	ccctaagtga	10620
ccaaccacgt	ggagcttaac	cagtgcagaa	actagaaatt	gggttcttca	acagaaaaata	10680
gaaggagaaa	caaaagaatc	aaactacgct	aaattgattg	aatgaatgg	aggagggaacc	10740
ggctgtaatc	atgaattaga	aatgatcaga	caaaagcttc	aatgtgtagc	ttcaaaacta	10800
caggttctac	cccagaaagc	ctctgagaga	ctacagtttg	aaacagcaga	tgatgaagat	10860
ttcatttggg	ttcaggaaaa	tattgatgaa	attattttac	aactacagaa	attaactggc	10920
cagcaagggtg	aagagccag	cttggtgtcc	ccaagtactt	cttgtggctc	attgactgaa	10980
agactactga	gacaaaatgc	tgagctgaca	gggcataatca	gtcaactgac	tgaagagaag	11040
aatgacttaa	ggaacatggt	tatgaagctg	gaagagcaga	tcaggtggta	tcgacagaca	11100
ggagctggta	gagataattc	ttccagggtt	tcattgaatg	gtggtgcca	cattgaagcc	11160
atcattgcct	ctgaaaaaga	agtatggaac	agagaaaaat	tgactctcca	gaaatctttg	11220
aaaagggcag	aggctgaagt	atacaaaactg	aaagctgaac	taagaaatga	ctcttttactt	11280
caaactctga	gccttgattc	tgaacatgct	acttttaaga	gaatttatgg	taaatacttg	11340
agggcagaaa	gttttcgaaa	ggctctcatt	taccagaaga	aatacctgct	gctgttactg	11400
ggtgggttcc	aggaatgtga	agatgccacc	ttggccctgc	ttgcccggt	ggggggggcag	11460
ccagctttca	cggatctaga	ggtgatcacc	aatcgcccaa	agggttcac	caggtttcgg	11520
tcggccgtca	gagtatccat	tgcaatttcc	agaatgaaat	ttttgggttcg	acggtggcat	11580
cgagtcacag	gttctgtttc	catcaatatt	aacagagatg	gctttggact	gaatcaaggt	11640
gcagaaaaga	ctgactcatt	ttatcattct	tctgggtggc	tgaggttata	tgagagaacca	11700
agacatacta	cgtatcgctc	aagatcagat	ctggactata	ttaggtcccc	tttaccattt	11760
cagaataggt	accaggcac	tccagctgat	ttcaatcctg	gttcttttagc	atgttctcag	11820
cttcagaatt	acgatcctga	cagagcccta	acagattata	tcactcggct	agaggcactg	11880
caaagacgac	ttggaactat	acagtccagt	tcaactactc	aatttcatgc	tggcagtgaga	11940
agataatcct	ttgaaacatc	attaattgaa	gtgatttttaa	atagattttcc	ttttgtaaat	12000
caatggttct	tttgtgcttt	tgtattgtga	atattcaatg	ggaccaatat	gaacacagct	12060
tatgatttga	tacaaatccc	ttgccagcac	atgaaaacaa	actggaattt	gtatatataa	12120
gcatttgtga	tgtattcatg	cacaataatt	attgaattac	ctgtatatatt	gtggaatgct	12180
aattttaaac	attaaattat	aaaccttgtg	tattttacaa	atgggtgaaa	agattaaact	12240
tttacgcatt	acaatactgc	tgaatgtgta	gctcgagggtg	tcctgcactt	ttcttataag	12300
gctactgaag	ttacatgttt	tgccctaatat	attctactgg	tgatgaagac	agataatatc	12360
acttgtagag	acctattttt	gtataatggt	agaagttttg	aatttttatgg	ggtatttttgt	12420

caagtactga aataaaaaatg acttcacccat tttcaccaca ct

12462

<210> 2

<211> 3907

<212> PRT

<213> Homo sapiens

<400> 2

Met	Glu	Asp	Glu	Glu	Arg	Gln	Lys	Lys	Leu	Glu	Ala	Gly	Lys	Ala	Lys
1				5					10					15	
Leu	Ala	Gln	Phe	Arg	Gln	Arg	Lys	Ala	Gln	Ser	Asp	Gly	Gln	Ser	Pro
		20						25					30		
Ser	Lys	Lys	Gln	Lys	Lys	Lys	Arg	Lys	Thr	Ser	Ser	Ser	Lys	His	Asp
		35					40					45			
Val	Ser	Ala	His	His	Asp	Leu	Asn	Ile	Asp	Gln	Ser	Gln	Cys	Asn	Glu
		50				55				60					
Met	Tyr	Ile	Asn	Ser	Ser	Gln	Arg	Val	Glu	Ser	Thr	Val	Ile	Pro	Glu
65					70				75					80	
Ser	Thr	Ile	Met	Arg	Thr	Leu	His	Ser	Gly	Glu	Ile	Thr	Ser	His	Glu
			85						90					95	
Gln	Gly	Phe	Ser	Val	Glu	Leu	Glu	Ser	Glu	Ile	Ser	Thr	Thr	Ala	Asp
			100					105					110		
Asp	Cys	Ser	Ser	Glu	Val	Asn	Gly	Cys	Ser	Phe	Val	Met	Arg	Thr	Gly
		115					120					125			
Lys	Pro	Thr	Asn	Leu	Leu	Arg	Glu	Glu	Glu	Phe	Gly	Val	Asp	Asp	Ser
	130					135						140			
Tyr	Ser	Glu	Gln	Gly	Ala	Gln	Asp	Ser	Pro	Thr	His	Leu	Glu	Met	Met
145					150				155						160
Glu	Ser	Glu	Leu	Ala	Gly	Lys	Gln	His	Glu	Ile	Glu	Glu	Leu	Asn	Arg
			165						170					175	
Glu	Leu	Glu	Glu	Met	Arg	Val	Thr	Tyr	Gly	Thr	Glu	Gly	Leu	Gln	Gln
			180					185					190		
Leu	Gln	Glu	Phe	Glu	Ala	Ala	Ile	Lys	Gln	Arg	Asp	Gly	Ile	Ile	Thr
		195					200					205			
Gln	Leu	Thr	Ala	Asn	Leu	Gln	Ala	Arg	Arg	Glu	Lys	Asp	Glu	Thr	
	210					215				220					
Met	Arg	Glu	Phe	Leu	Glu	Leu	Thr	Glu	Gln	Ser	Gln	Lys	Leu	Gln	Ile
225					230					235					240
Gln	Phe	Gln	Gln	Leu	Gln	Ala	Ser	Glu	Thr	Leu	Arg	Asn	Ser	Thr	His
			245						250					255	
Ser	Ser	Thr	Ala	Ala	Asp	Leu	Leu	Gln	Ala	Lys	Gln	Gln	Ile	Leu	Thr
		260						265					270		
His	Gln	Gln	Gln	Leu	Glu	Glu	Gln	Asp	His	Leu	Leu	Glu	Asp	Tyr	Gln
		275					280					285			
Lys	Lys	Lys	Glu	Asp	Phe	Thr	Met	Gln	Ile	Ser	Phe	Leu	Gln	Glu	Lys
	290					295					300				
Ile	Lys	Val	Tyr	Glu	Met	Glu	Gln	Asp	Lys	Lys	Val	Glu	Asn	Ser	Asn
305					310					315					320
Lys	Glu	Glu	Ile	Gln	Glu	Lys	Glu	Thr	Ile	Ile	Glu	Glu	Leu	Asn	Thr
			325						330					335	
Lys	Ile	Ile	Glu	Glu	Glu	Lys	Lys	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu
		340						345					350		
Thr	Thr	Ala	Asp	Lys	Leu	Leu	Gly	Glu	Leu	Gln	Glu	Gln	Ile	Val	Gln
		355					360						365		
Lys	Asn	Gln	Glu	Ile	Lys	Asn	Met	Lys	Leu	Glu	Leu	Thr	Asn	Ser	Lys
	370					375						380			
Gln	Lys	Glu	Arg	Gln	Ser	Ser	Glu	Glu	Ile	Lys	Gln	Leu	Met	Gly	Thr
385					390					395					400
Val	Glu	Glu	Leu	Gln	Lys	Arg	Asn	His	Lys	Asp	Ser	Gln	Phe	Glu	Thr

				405					410					415	
Asp	Ile	Val	Gln	Arg	Met	Glu	Gln	Glu	Thr	Gln	Arg	Lys	Leu	Glu	Gln
			420					425					430		
Leu	Arg	Ala	Glu	Leu	Asp	Glu	Met	Tyr	Gly	Gln	Gln	Ile	Val	Gln	Met
		435					440					445			
Lys	Gln	Glu	Leu	Ile	Arg	Gln	His	Met	Ala	Gln	Met	Glu	Glu	Met	Lys
		450				455					460				
Thr	Arg	His	Lys	Gly	Glu	Met	Glu	Asn	Ala	Leu	Arg	Ser	Tyr	Ser	Asn
465				470						475					480
Ile	Thr	Val	Asn	Glu	Asp	Gln	Ile	Lys	Leu	Met	Asn	Val	Ala	Ile	Asn
			485						490					495	
Glu	Leu	Asn	Ile	Lys	Leu	Gln	Asp	Thr	Asn	Ser	Gln	Lys	Glu	Lys	Leu
			500					505					510		
Lys	Glu	Glu	Leu	Gly	Leu	Ile	Leu	Glu	Glu	Lys	Cys	Ala	Leu	Gln	Arg
		515					520					525			
Gln	Leu	Glu	Asp	Leu	Val	Glu	Glu	Leu	Ser	Phe	Ser	Arg	Glu	Gln	Ile
		530				535					540				
Gln	Arg	Ala	Arg	Gln	Thr	Ile	Ala	Glu	Gln	Glu	Ser	Lys	Leu	Asn	Glu
545					550					555					560
Ala	His	Lys	Ser	Leu	Ser	Thr	Val	Glu	Asp	Leu	Lys	Ala	Glu	Ile	Val
			565						570					575	
Ser	Ala	Ser	Glu	Ser	Arg	Lys	Glu	Leu	Glu	Leu	Lys	His	Glu	Ala	Glu
			580					585					590		
Val	Thr	Asn	Tyr	Lys	Ile	Lys	Leu	Glu	Met	Leu	Glu	Lys	Glu	Lys	Asn
		595					600					605			
Ala	Val	Leu	Asp	Arg	Met	Ala	Glu	Ser	Gln	Glu	Ala	Glu	Leu	Glu	Arg
		610				615					620				
Leu	Arg	Thr	Gln	Leu	Leu	Phe	Ser	His	Glu	Glu	Glu	Leu	Ser	Lys	Leu
625					630					635					640
Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys
			645						650					655	
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn
			660					665					670		
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu
		675					680					685			
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp
		690				695					700				
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln
705					710					715					720
Ile	Asn	Glu	Leu	Gln	Lys	Glu	Ile	Glu	Ile	Leu	Arg	Gln	Glu	Glu	Lys
			725						730					735	
Glu	Lys	Gly	Thr	Leu	Glu	Gln	Glu	Val	Gln	Glu	Leu	Gln	Leu	Lys	Thr
		740						745					750		
Glu	Leu	Leu	Glu	Lys	Gln	Met	Lys	Glu	Lys	Glu	Asn	Asp	Leu	Gln	Glu
		755		</											

Ser	Lys	Asn	Lys	Gln	Glu	Leu	Glu	Tyr	Lys	Ser	Lys	Leu	Lys	Ala	Leu		
				885					890					895			
Asn	Glu	Glu	Leu	His	Leu	Gln	Arg	Ile	Asn	Pro	Thr	Thr	Val	Lys	Met		
			900					905					910				
Lys	Ser	Ser	Val	Phe	Asp	Glu	Asp	Lys	Thr	Phe	Val	Ala	Glu	Thr	Leu		
			915				920					925					
Glu	Met	Gly	Glu	Val	Val	Glu	Lys	Asp	Thr	Thr	Glu	Leu	Met	Glu	Lys		
			930				935					940					
Leu	Glu	Val	Thr	Lys	Arg	Glu	Lys	Leu	Glu	Leu	Ser	Gln	Arg	Leu	Ser		
945					950					955					960		
Asp	Leu	Ser	Glu	Gln	Leu	Lys	Gln	Lys	His	Gly	Glu	Ile	Ser	Phe	Leu		
				965					970					975			
Asn	Glu	Glu	Val	Lys	Ser	Leu	Lys	Gln	Glu	Lys	Glu	Gln	Val	Ser	Leu		
			980					985					990				
Arg	Cys	Arg	Glu	Leu	Glu	Ile	Ile	Ile	Asn	His	Asn	Arg	Ala	Glu	Asn		
			995				1000					1005					
Val	Gln	Ser	Cys	Asp	Thr	Gln	Val	Ser	Ser	Leu	Leu	Asp	Gly	Val	Val		
	1010					1015					1020						
Thr	Met	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Ser	Val	Ser	Lys	Val	Asn	Lys		
1025					1030					1035					1040		
Ser	Phe	Gly	Glu	Glu	Ser	Lys	Ile	Met	Val	Glu	Asp	Lys	Val	Ser	Phe		
				1045					1050					1055			
Glu	Asn	Met	Thr	Val	Gly	Glu	Glu	Ser	Lys	Gln	Glu	Gln	Leu	Ile	Leu		
			1060				1065						1070				
Asp	His	Leu	Pro	Ser	Val	Thr	Lys	Glu	Ser	Ser	Leu	Arg	Ala	Thr	Gln		
		1075					1080					1085					
Pro	Ser	Glu	Asn	Asp	Lys	Leu	Gln	Lys	Glu	Leu	Asn	Val	Leu	Lys	Ser		
		1090				1095					1100						
Glu	Gln	Asn	Asp	Leu	Arg	Leu	Gln	Met	Glu	Ala	Gln	Arg	Ile	Cys	Leu		
1105					1110					1115					1120		
Ser	Leu	Val	Tyr	Ser	Thr	His	Val	Asp	Gln	Val	Arg	Glu	Tyr	Met	Glu		
				1125					1130					1135			
Asn	Glu	Lys	Asp	Lys	Ala	Leu	Cys	Ser	Leu	Lys	Glu	Glu	Leu	Ile	Phe		
			1140					1145					1150				
Ala	Gln	Glu	Glu	Lys	Ile	Lys	Glu	Leu	Gln	Lys	Ile	His	Gln	Leu	Glu		
		1155					1160					1165					
Leu	Gln	Thr	Met	Lys	Thr	Gln	Glu	Thr	Gly	Asp	Glu	Gly	Lys	Pro	Leu		
		1170				1175					1180						
His	Leu	Leu	Ile	Gly	Lys	Leu	Gln	Lys	Ala	Val	Ser	Glu	Glu	Cys	Ser		
1185					1190					1195					1200		
Tyr	Phe	Leu	Gln	Thr	Leu	Cys	Ser	Val	Leu	Gly	Glu	Tyr	Tyr	Thr	Pro		
				1205					1210					1215			
Ala	Leu	Lys	Cys	Glu	Val	Asn	Ala	Glu	Asp	Lys	Glu	Asn	Ser	Gly	Asp		
			1220					1225					1230				
Tyr	Ile	Ser	Glu	Asn	Glu	Asp	Pro	Glu	Leu	Gln	Asp	Tyr	Arg	Tyr	Glu		
		1235					1240					1245					
Val	Gln	Asp	Phe	Gln	Glu	Asn	Met	His	Thr	Leu	Leu	Asn	Lys	Val	Thr		
						1255					1260						
Glu	Glu	Tyr	Asn	Lys	Leu	Leu	Val	Leu	Gln	Thr	Arg	Leu	Ser	Lys	Ile		
1265					1270					1275					1280		
Trp	Gly	Gln	Gln	Thr	Asp	Gly	Met	Lys	Leu	Glu	Phe	Gly	Glu	Glu	Asn		
				1285					1290					1295			
Leu	Pro	Lys	Glu	Glu	Thr	Glu	Phe	Leu	Ser	Ile	His	Ser	Gln	Met	Thr		
			1300					1305					1310				
Asn	Leu	Glu	Asp	Ile	Asp	Val	Asn	His	Lys	Ser	Lys	Leu	Ser	Ser	Leu		
		1315					1320					1325					
Gln	Asp	Leu	Glu	Lys	Thr	Lys	Leu	Glu	Glu	Gln	Val	Gln	Glu	Leu	Glu		
		1330				1335					1340						
Ser	Leu	Ile	Ser	Ser	Leu	Gln	Gln	Gln	Leu	Lys	Glu	Thr	Glu	Gln	Asn		

1345		1350		1355		1360
Tyr Glu Ala Glu Ile His Cys Leu Gln Lys Arg Leu Gln Ala Val Ser						
	1365		1370		1375	
Glu Ser Thr Val Pro Pro Ser Leu Pro Val Asp Ser Val Val Ile Thr						
	1380		1385		1390	
Glu Ser Asp Ala Gln Arg Thr Met Tyr Pro Gly Ser Cys Val Lys Lys						
	1395		1400		1405	
Asn Ile Asp Gly Thr Ile Glu Phe Ser Gly Glu Phe Gly Val Lys Glu						
	1410		1415		1420	
Glu Thr Asn Ile Val Lys Leu Leu Glu Lys Gln Tyr Gln Glu Gln Leu						
1425	1430		1435		1440	
Glu Glu Glu Val Ala Lys Val Ile Val Ser Met Ser Ile Ala Phe Ala						
	1445		1450		1455	
Gln Gln Thr Glu Leu Ser Arg Ile Ser Gly Gly Lys Glu Asn Thr Ala						
	1460		1465		1470	
Ser Ser Lys Gln Ala His Ala Val Cys Gln Gln Glu Gln His Tyr Phe						
	1475		1480		1485	
Asn Glu Met Lys Leu Ser Gln Asp Gln Ile Gly Phe Gln Thr Phe Glu						
	1490		1495		1500	
Thr Val Asp Val Lys Phe Lys Glu Glu Phe Lys Pro Leu Ser Lys Glu						
1505	1510		1515		1520	
Leu Gly Glu His Gly Lys Glu Ile Leu Leu Ser Asn Ser Asp Pro His						
	1525		1530		1535	
Asp Ile Pro Glu Ser Lys Asp Cys Val Leu Thr Ile Ser Glu Glu Met						
	1540		1545		1550	
Phe Ser Lys Asp Lys Thr Phe Ile Val Arg Gln Ser Ile His Asp Glu						
	1555		1560		1565	
Ile Ser Val Ser Ser Met Asp Ala Ser Arg Gln Leu Met Leu Asn Glu						
	1570		1575		1580	
Glu Gln Leu Glu Asp Met Arg Gln Glu Leu Val Arg Gln Tyr Gln Glu						
1585	1590		1595		1600	
His Gln Gln Ala Thr Glu Leu Leu Arg Gln Ala His Met Arg Gln Met						
	1605		1610		1615	
Glu Arg Gln Arg Glu Asp Gln Glu Gln Leu Gln Glu Glu Ile Lys Arg						
	1620		1625		1630	
Leu Asn Arg Gln Leu Ala Gln Arg Ser Ser Ile Asp Asn Glu Asn Leu						
	1635		1640		1645	
Val Ser Glu Arg Glu Arg Val Leu Leu Glu Glu Leu Glu Ala Leu Lys						
	1650		1655		1660	
Gln Leu Ser Leu Ala Gly Arg Glu Lys Leu Cys Cys Glu Leu Arg Asn						
1665	1670		1675		1680	
Ser Ser Thr Gln Thr Gln Asn Gly Asn Glu Asn Gln Gly Glu Val Glu						
	1685		1690		1695	
Glu Gln Thr Phe Lys Glu Lys Glu Leu Asp Arg Lys Pro Glu Asp Val						
	1700		1705		1710	
Pro Pro Glu Ile Leu Ser Asn Glu Arg Tyr Ala Leu Gln Lys Ala Asn						
	1715		1720		1725	
Asn Arg Leu Leu Lys Ile Leu Leu Glu Val Val Lys Thr Thr Ala Ala						
	1730		1735		1740	
Val Glu Glu Thr Ile Gly Arg His Val Leu Gly Ile Leu Asp Arg Ser						
1745	1750		1755		1760	
Ser Lys Ser Gln Ser Ser Ala Ser Leu Ile Trp Arg Ser Glu Ala Glu						
	1765		1770		1775	
Ala Ser Val Lys Ser Cys Val His Glu Glu His Thr Arg Val Thr Asp						
	1780		1785		1790	
Glu Ser Ile Pro Ser Tyr Ser Gly Ser Asp Met Pro Arg Asn Asp Ile						
	1795		1800		1805	
Asn Met Trp Ser Lys Val Thr Glu Glu Gly Thr Glu Leu Ser Gln Arg						
	1810		1815		1820	

Leu Val Arg Ser Gly Phe Ala Gly Thr Glu Ile Asp Pro Glu Asn Glu
 1825 1830 1835 1840
 Glu Leu Met Leu Asn Ile Ser Ser Arg Leu Gln Ala Ala Val Glu Lys
 1845 1850 1855
 Leu Leu Glu Ala Ile Ser Glu Thr Ser Ser Gln Leu Glu His Ala Lys
 1860 1865 1870
 Val Thr Gln Thr Glu Leu Met Arg Glu Ser Phe Arg Gln Lys Gln Glu
 1875 1880 1885
 Ala Thr Glu Ser Leu Lys Cys Gln Glu Glu Leu Arg Glu Arg Leu His
 1890 1895 1900
 Glu Glu Ser Arg Ala Arg Glu Gln Leu Ala Val Glu Leu Ser Lys Ala
 1905 1910 1915 1920
 Glu Gly Val Ile Asp Gly Tyr Ala Asp Glu Lys Thr Leu Phe Glu Arg
 1925 1930 1935
 Gln Ile Gln Glu Lys Thr Asp Ile Ile Asp Arg Leu Glu Gln Glu Leu
 1940 1945 1950
 Leu Cys Ala Ser Asn Arg Leu Gln Glu Leu Glu Ala Glu Gln Gln Gln
 1955 1960 1965
 Ile Gln Glu Glu Arg Glu Leu Leu Ser Arg Gln Lys Glu Ala Met Lys
 1970 1975 1980
 Ala Glu Ala Gly Pro Val Glu Gln Gln Leu Leu Gln Glu Thr Glu Lys
 1985 1990 1995 2000
 Leu Met Lys Glu Lys Leu Glu Val Gln Cys Gln Ala Glu Lys Val Arg
 2005 2010 2015
 Asp Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile Asp Val Glu Glu
 2020 2025 2030
 Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu Lys Asn Thr Glu Leu
 2035 2040 2045
 Met Asp Leu Arg Gln Gln Asn Gln Ala Leu Glu Lys Gln Leu Glu Lys
 2050 2055 2060
 Met Arg Lys Phe Leu Asp Glu Gln Ala Ile Asp Arg Glu His Glu Arg
 2065 2070 2075 2080
 Asp Val Phe Gln Gln Glu Ile Gln Lys Leu Glu Gln Gln Leu Lys Val
 2085 2090 2095
 Val Pro Arg Phe Gln Pro Ile Ser Glu His Gln Thr Arg Glu Val Glu
 2100 2105 2110
 Gln Leu Ala Asn His Leu Lys Glu Lys Thr Asp Lys Cys Ser Glu Leu
 2115 2120 2125
 Leu Leu Ser Lys Glu Gln Leu Gln Arg Asp Ile Gln Glu Arg Asn Glu
 2130 2135 2140
 Glu Ile Glu Lys Leu Glu Phe Arg Val Arg Glu Leu Glu Gln Ala Leu
 2145 2150 2155 2160
 Leu Val Ser Ala Asp Thr Phe Gln Lys Val Glu Asp Arg Lys His Phe
 2165 2170 2175
 Gly Ala Val Glu Ala Lys Pro Glu Leu Ser Leu Glu Val Gln Leu Gln
 2180 2185 2190
 Ala Glu Arg Asp Ala Ile Asp Arg Lys Glu Lys Glu Ile Thr Asn Leu
 2195 2200 2205
 Glu Glu Gln Leu Glu Gln Phe Arg Glu Glu Leu Glu Asn Lys Asn Glu
 2210 2215 2220
 Glu Val Gln Gln Leu His Met Gln Leu Glu Ile Gln Lys Lys Glu Ser
 2225 2230 2235 2240
 Thr Thr Arg Leu Gln Glu Leu Glu Gln Glu Asn Lys Leu Phe Lys Asp
 2245 2250 2255
 Asp Met Glu Lys Leu Gly Leu Ala Ile Lys Glu Ser Asp Ala Met Ser
 2260 2265 2270
 Thr Gln Asp Gln His Val Leu Phe Gly Lys Phe Ala Gln Ile Ile Gln
 2275 2280 2285
 Glu Lys Glu Val Glu Ile Asp Gln Leu Asn Glu Gln Val Thr Lys Leu

2290		2295		2300
Gln Gln Gln Leu Lys Ile Thr Thr Asp Asn Lys Val Ile Glu Glu Lys				
2305		2310		2320
Asn Glu Leu Ile Arg Asp Leu Glu Thr Gln Ile Glu Cys Leu Met Ser				
	2325		2330	2335
Asp Gln Glu Cys Val Lys Arg Asn Arg Glu Glu Glu Ile Glu Gln Leu				
	2340		2345	2350
Asn Glu Val Ile Glu Lys Leu Gln Gln Glu Leu Ala Asn Ile Gly Gln				
	2355		2360	2365
Lys Thr Ser Met Asn Ala His Ser Leu Ser Glu Glu Ala Asp Ser Leu				
	2370		2375	2380
Lys His Gln Leu Asp Val Val Ile Ala Glu Lys Leu Ala Leu Glu Gln				
2385		2390		2400
Gln Val Glu Thr Ala Asn Glu Glu Met Thr Phe Met Lys Asn Val Leu				
	2405		2410	2415
Lys Glu Thr Asn Phe Lys Met Asn Gln Leu Thr Gln Glu Leu Phe Ser				
	2420		2425	2430
Leu Lys Arg Glu Arg Glu Ser Val Glu Lys Ile Gln Ser Ile Pro Glu				
	2435		2440	2445
Asn Ser Val Asn Val Ala Ile Asp His Leu Ser Lys Asp Lys Pro Glu				
	2450		2455	2460
Leu Glu Val Val Leu Thr Glu Asp Ala Leu Lys Ser Leu Glu Asn Gln				
2465		2470		2480
Thr Tyr Phe Lys Ser Phe Glu Glu Asn Gly Lys Gly Ser Ile Ile Asn				
	2485		2490	2495
Leu Glu Thr Arg Leu Leu Gln Leu Glu Ser Thr Val Ser Ala Lys Asp				
	2500		2505	2510
Leu Glu Leu Thr Gln Cys Tyr Lys Gln Ile Lys Asp Met Gln Glu Gln				
	2515		2520	2525
Gly Gln Phe Glu Thr Glu Met Leu Gln Lys Lys Ile Val Asn Leu Gln				
	2530		2535	2540
Lys Ile Val Glu Glu Lys Val Ala Ala Ala Leu Val Ser Gln Ile Gln				
2545		2550		2560
Leu Glu Ala Val Gln Glu Tyr Ala Lys Phe Cys Gln Asp Asn Gln Thr				
	2565		2570	2575
Ile Ser Ser Glu Pro Glu Arg Thr Asn Ile Gln Asn Leu Asn Gln Leu				
	2580		2585	2590
Arg Glu Asp Glu Leu Gly Ser Asp Ile Ser Ala Leu Thr Leu Arg Ile				
	2595		2600	2605
Ser Glu Leu Glu Ser Gln Val Val Glu Met His Thr Ser Leu Ile Leu				
	2610		2615	2620
Glu Lys Glu Gln Val Glu Ile Ala Glu Lys Asn Val Leu Glu Lys Glu				
2625		2630		2640
Lys Lys Leu Leu Glu Leu Gln Lys Leu Leu Glu Gly Asn Glu Lys Lys				
	2645		2650	2655
Gln Arg Glu Lys Glu Lys Lys Arg Ser Pro Gln Asp Val Glu Val Leu				
	2660		2665	2670
Lys Thr Thr Thr Glu Leu Phe His Ser Asn Glu Glu Ser Gly Phe Phe				
	2675		2680	2685
Asn Glu Leu Glu Ala Leu Arg Ala Glu Ser Val Ala Thr Lys Ala Glu				
	2690		2695	2700
Leu Ala Ser Tyr Lys Glu Lys Ala Glu Lys Leu Gln Glu Glu Leu Leu				
2705		2710		2720
Val Lys Glu Thr Asn Met Thr Ser Leu Gln Lys Asp Leu Ser Gln Val				
	2725		2730	2735
Arg Asp His Leu Ala Glu Ala Lys Glu Lys Leu Ser Ile Leu Glu Lys				
	2740		2745	2750
Glu Asp Glu Thr Glu Val Gln Glu Ser Lys Lys Ala Cys Met Phe Glu				
	2755		2760	2765

Pro	Leu	Pro	Ile	Lys	Leu	Ser	Lys	Ser	Ile	Ala	Ser	Gln	Thr	Asp	Gly	2770	2775	2780
Thr	Leu	Lys	Ile	Ser	Ser	Ser	Asn	Gln	Thr	Pro	Gln	Ile	Leu	Val	Lys	2785	2790	2795
Asn	Ala	Gly	Ile	Gln	Ile	Asn	Leu	Gln	Ser	Glu	Cys	Ser	Ser	Glu	Glu	2805	2810	2815
Val	Thr	Glu	Ile	Ile	Ser	Gln	Phe	Thr	Glu	Lys	Ile	Glu	Lys	Met	Gln	2820	2825	2830
Glu	Leu	His	Ala	Ala	Glu	Ile	Leu	Asp	Met	Glu	Ser	Arg	His	Ile	Ser	2835	2840	2845
Glu	Thr	Glu	Thr	Leu	Lys	Arg	Glu	His	Tyr	Val	Ala	Val	Gln	Leu	Leu	2850	2855	2860
Lys	Glu	Glu	Cys	Gly	Thr	Leu	Lys	Ala	Val	Ile	Gln	Cys	Leu	Arg	Ser	2865	2870	2875
Lys	Glu	Gly	Ser	Ser	Ile	Pro	Glu	Leu	Ala	His	Ser	Asp	Ala	Tyr	Gln	2885	2890	2895
Thr	Arg	Glu	Ile	Cys	Ser	Ser	Asp	Ser	Gly	Ser	Asp	Trp	Gly	Gln	Gly	2900	2905	2910
Ile	Tyr	Leu	Thr	His	Ser	Gln	Gly	Phe	Asp	Ile	Ala	Ser	Glu	Gly	Arg	2915	2920	2925
Gly	Glu	Glu	Ser	Glu	Ser	Ala	Thr	Asp	Ser	Phe	Pro	Lys	Lys	Ile	Lys	2930	2935	2940
Gly	Leu	Leu	Arg	Ala	Val	His	Asn	Glu	Gly	Met	Gln	Val	Leu	Ser	Leu	2945	2950	2955
Thr	Glu	Ser	Pro	Tyr	Ser	Asp	Gly	Glu	Asp	His	Ser	Ile	Gln	Gln	Val	2965	2970	2975
Ser	Glu	Pro	Trp	Leu	Glu	Glu	Arg	Lys	Ala	Tyr	Ile	Asn	Thr	Ile	Ser	2980	2985	2990
Ser	Leu	Lys	Asp	Leu	Ile	Thr	Lys	Met	Gln	Leu	Gln	Arg	Glu	Ala	Glu	2995	3000	3005
Val	Tyr	Asp	Ser	Ser	Gln	Ser	His	Glu	Ser	Phe	Ser	Asp	Trp	Arg	Gly	3010	3015	3020
Glu	Leu	Leu	Leu	Ala	Leu	Gln	Gln	Val	Phe	Leu	Glu	Glu	Arg	Ser	Val	3025	3030	3035
Leu	Leu	Ala	Ala	Phe	Arg	Thr	Glu	Leu	Thr	Ala	Leu	Gly	Thr	Thr	Asp	3045	3050	3055
Ala	Val	Gly	Leu	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Gln	Glu	Gln	Gly		3060	3065	3070
Val	Glu	Tyr	Gln	Ala	Ala	Met	Glu	Cys	Leu	Gln	Lys	Ala	Asp	Arg	Arg	3075	3080	3085
Ser	Leu	Leu	Ser	Glu	Ile	Gln	Ala	Leu	His	Ala	Gln	Met	Asn	Gly	Arg	3090	3095	3100
Lys	Ile	Thr	Leu	Lys	Arg	Glu	Gln	Glu	Ser	Glu	Lys	Pro	Ser	Gln	Glu	3105	3110	3115
Leu	Leu	Glu	Tyr	Asn	Ile	Gln	Gln	Lys	Gln	Ser	Gln	Met	Leu	Glu	Met	3125	3130	3135
Gln	Val	Glu	Leu	Ser	Ser	Met	Lys	Asp	Arg	Ala	Thr	Glu	Leu	Gln	Glu	3140	3145	3150
Gln	Leu	Ser	Ser	Glu	Lys	Met	Val	Val	Ala	Glu	Leu	Lys	Ser	Glu	Leu	3155	3160	3165
Ala	Gln	Thr	Lys	Leu	Glu	Leu	Glu	Thr	Thr	Leu	Lys	Ala	Gln	His	Lys	3170	3175	3180
His	Leu	Lys	Glu	Leu	Glu	Ala	Phe	Arg	Leu	Glu	Val	Lys	Asp	Lys	Thr	3185	3190	3195
Asp	Glu	Val	His	Leu	Leu	Asn	Asp	Thr	Leu	Ala	Ser	Glu	Gln	Lys	Lys	3205	3210	3215
Ser	Arg	Glu	Leu	Gln	Trp	Ala	Leu	Glu	Lys	Glu	Lys	Ala	Lys	Leu	Gly	3220	3225	3230
Arg	Ser	Glu	Glu	Arg	Asp	Lys	Glu	Glu	Leu	Glu	Asp	Leu	Lys	Phe	Ser			

3235	3240	3245
Leu Glu Ser Gln Lys Gln Arg Asn Leu Gln Leu Asn Leu Leu Leu Glu		
3250	3255	3260
Gln Gln Lys Gln Leu Leu Asn Glu Ser Gln Gln Lys Ile Glu Ser Gln		
3265	3270	3275
Arg Met Leu Tyr Asp Ala Gln Leu Ser Glu Glu Gln Gly Arg Asn Leu		
3285	3290	3295
Glu Leu Gln Val Leu Leu Glu Ser Glu Lys Val Arg Ile Arg Glu Met		
3300	3305	3310
Ser Ser Thr Leu Asp Arg Glu Arg Glu Leu His Ala Gln Leu Gln Ser		
3315	3320	3325
Ser Asp Gly Thr Gly Gln Ser Arg Pro Pro Leu Pro Ser Glu Asp Leu		
3330	3335	3340
Leu Lys Glu Leu Gln Lys Gln Leu Glu Glu Lys His Ser Arg Ile Val		
3345	3350	3355
Glu Leu Leu Asn Glu Thr Glu Lys Tyr Lys Leu Asp Ser Leu Gln Thr		
3365	3370	3375
Arg Gln Gln Met Glu Lys Asp Arg Gln Val His Arg Lys Thr Leu Gln		
3380	3385	3390
Thr Glu Gln Glu Ala Asn Thr Glu Gly Gln Lys Lys Met His Glu Leu		
3395	3400	3405
Gln Ser Lys Val Glu Asp Leu Gln Arg Gln Leu Glu Glu Lys Arg Gln		
3410	3415	3420
Gln Val Tyr Lys Leu Asp Leu Glu Gly Gln Arg Leu Gln Gly Ile Met		
3425	3430	3435
Gln Glu Phe Gln Lys Gln Glu Leu Glu Arg Glu Glu Lys Arg Glu Ser		
3445	3450	3455
Arg Arg Ile Leu Tyr Gln Asn Leu Asn Glu Pro Thr Thr Trp Ser Leu		
3460	3465	3470
Thr Ser Asp Arg Thr Arg Asn Trp Val Leu Gln Gln Lys Ile Glu Gly		
3475	3480	3485
Glu Thr Lys Glu Ser Asn Tyr Ala Lys Leu Ile Glu Met Asn Gly Gly		
3490	3495	3500
Gly Thr Gly Cys Asn His Glu Leu Glu Met Ile Arg Gln Lys Leu Gln		
3505	3510	3515
Cys Val Ala Ser Lys Leu Gln Val Leu Pro Gln Lys Ala Ser Glu Arg		
3525	3530	3535
Leu Gln Phe Glu Thr Ala Asp Asp Glu Asp Phe Ile Trp Val Gln Glu		
3540	3545	3550
Asn Ile Asp Glu Ile Ile Leu Gln Leu Gln Lys Leu Thr Gly Gln Gln		
3555	3560	3565
Gly Glu Glu Pro Ser Leu Val Ser Pro Ser Thr Ser Cys Gly Ser Leu		
3570	3575	3580
Thr Glu Arg Leu Leu Arg Gln Asn Ala Glu Leu Thr Gly His Ile Ser		
3585	3590	3595
Gln Leu Thr Glu Glu Lys Asn Asp Leu Arg Asn Met Val Met Lys Leu		
3605	3610	3615
Glu Glu Gln Ile Arg Trp Tyr Arg Gln Thr Gly Ala Gly Arg Asp Asn		
3620	3625	3630
Ser Ser Arg Phe Ser Leu Asn Gly Gly Ala Asn Ile Glu Ala Ile Ile		
3635	3640	3645
Ala Ser Glu Lys Glu Val Trp Asn Arg Glu Lys Leu Thr Leu Gln Lys		
3650	3655	3660
Ser Leu Lys Arg Ala Glu Ala Glu Val Tyr Lys Leu Lys Ala Glu Leu		
3665	3670	3675
Arg Asn Asp Ser Leu Leu Gln Thr Leu Ser Pro Asp Ser Glu His Val		
3685	3690	3695
Thr Leu Lys Arg Ile Tyr Gly Lys Tyr Leu Arg Ala Glu Ser Phe Arg		
3700	3705	3710

Lys Ala Leu Ile Tyr Gln Lys Lys Tyr Leu Leu Leu Leu Gly Gly
 3715 3720 3725
 Phe Gln Glu Cys Glu Asp Ala Thr Leu Ala Leu Leu Ala Arg Met Gly
 3730 3735 3740
 Gly Gln Pro Ala Phe Thr Asp Leu Glu Val Ile Thr Asn Arg Pro Lys
 3745 3750 3755 3760
 Gly Phe Thr Arg Phe Arg Ser Ala Val Arg Val Ser Ile Ala Ile Ser
 3765 3770 3775
 Arg Met Lys Phe Leu Val Arg Arg Trp His Arg Val Thr Gly Ser Val
 3780 3785 3790
 Ser Ile Asn Ile Asn Arg Asp Gly Phe Gly Leu Asn Gln Gly Ala Glu
 3795 3800 3805
 Lys Thr Asp Ser Phe Tyr His Ser Ser Gly Gly Leu Glu Leu Tyr Gly
 3810 3815 3820
 Glu Pro Arg His Thr Thr Tyr Arg Ser Arg Ser Asp Leu Asp Tyr Ile
 3825 3830 3835 3840
 Arg Ser Pro Leu Pro Phe Gln Asn Arg Tyr Pro Gly Thr Pro Ala Asp
 3845 3850 3855
 Phe Asn Pro Gly Ser Leu Ala Cys Ser Gln Leu Gln Asn Tyr Asp Pro
 3860 3865 3870
 Asp Arg Ala Leu Thr Asp Tyr Ile Thr Arg Leu Glu Ala Leu Gln Arg
 3875 3880 3885
 Arg Leu Gly Thr Ile Gln Ser Gly Ser Thr Thr Gln Phe His Ala Gly
 3890 3895 3900
 Met Arg Arg
 3905

<210> 3

<211> 12438

<212> DNA

<213> Homo sapiens

<400> 3

gaagatggcg gcggcggcgg cggtgacggc gcttcccgtg cggctgagga cgatccgcc 60
 gtgagcgcg agactgcttc cacttcgggc gggggagccc cggaccgaat cggtctctta 120
 ggccgtggag cttgcgcgtcc cacctccgtc caaatcgacc ttctctttct atcccccaacc 180
 accctcaac cctgttttc ccctgccttc cttgcagagg ccatggagga cgaggagaga 240
 cagaagaagc tggaggccgg caaagccaag cttgccaggt ttcgacaaag aaaagctcag 300
 tcggatgggc agagtccctc caagaagcag aaaaaaaga gaaaaacgtc aagcagtaaa 360
 catgatgtgt cagcacacca tgatttgaat attgatcaat cacagtgtaa tgaaatgtac 420
 ataaatagtt ctacagagagt agaatacaact gtgattcctg aatctacaat aatgagaact 480
 ctacatagtg gagaaataac cagtcatgag cagggcttct ctgtggaact ggaaagtga 540
 atttcaacca cagcagatga ctgcagttca gaggtaaatg gttgcagttt tgtgatgaga 600
 acaggaaagc ctacaaattt attaagggaa gaagaatttg gtgttgatga ttcttattct 660
 gaacaaggag cacaagacag tccgactcat ctacagatga tggaaagtga gttggctggg 720
 aagcagcatg agattgaaga gctaaacaga gagctggaag aaatgagggg tacctatggg 780
 actgaaggac tgcagcagtt acaagaattht gaagctgcca ttaaacaag agatggcatt 840
 ataaccagc tcaactgctaa tttaacaaca gcaagaagag aaaaggatga gacaatgaga 900
 gaatttttag agttgacaga acagagtcaa aaattacaga ttcaatttca gcaattacag 960
 gctagtgaag ctctgagaaa cagcactcat agtagcacag ctgcagactt actacaagcc 1020
 aaacaacaga tcctcactca tcaacagcag cttgaagaac aagaccactt attagaagat 1080
 tatcagaaaa agaaagaaga cttcacaatg caaattagtt tcttgcaaga gaaaattaaa 1140
 gtatatgaaa tggaacaaga taaaaaagta gaaaactcaa ataaagaaga aatacaggaa 1200
 aaggagacaa tcattgaaga attaaacaca aaaataatag aagaagaaaa gaaaactctt 1260
 gagctaaagg ataaattaac aactgctgat aaattactag gagaattaca agaactatt 1320
 gtgcaaaaga accaagaaat aaaaaacatg aaattagagc tgactaattc taagcaaaaa 1380
 gaaagacagt cttctgaaga aataaaacag ttaattggga cagtcgaaga acttcagaag 1440
 agaaatcata aagacagcca gttcgaact gatatagtac aacgaatgga acaagaaaca 1500

caaagaaaagt	tagaacaact	cggggcagag	ctggatgaga	tgtatgggca	gcagatagtg	1560
caaatgaaac	aagaattaat	aagacaacac	atggcacaga	tggaggaaat	gaaaacacgg	1620
cataagggag	aaatggagaa	tgctttaagg	tcatattcaa	atattacagt	taatgaagat	1680
cagataaagt	taatgaatgt	ggcaataaat	gaactgaata	taaaattgca	agataactaac	1740
tctcaaaagg	aaaaactcaa	ggaagaacta	ggactaattt	tagaagaaaa	gtgtgctcta	1800
cagagacagc	ttgaagacct	tgttgaagaa	ttgagctttt	caagggaaaca	gattcagaga	1860
gctagacaga	caatagctga	acaagaaaagt	aaacttaatg	aagcacataa	gtcccttagt	1920
acagtggaa	atgttgaaagc	tgagattggt	tctgcatctg	aatccagaaa	ggaactagaa	1980
ttaaaacatg	aagcagaagt	tacaaattac	aagataaaaac	ttgaaatggt	agaaaaagaa	2040
aagaatgctg	tgtagacag	aatggctgaa	tcacaagaag	ctgaattaga	gaggctgaga	2100
acacagcttc	tatttagtca	cgaagaagag	ctttccaaac	tgaaggaaaga	tttagaaatt	2160
gaacatcgaa	taaattattga	aaaacttaaa	gataatttag	gcattcacta	taaacagcag	2220
atagatgggt	tacagaatga	aatgagtcac	aagatagaaa	ccatgcagtt	tgaaaaggac	2280
aatttgataa	ctaagcagaa	tcaatttaatt	ttggaaattt	caaagctaaa	agattttacag	2340
cagtctcttg	taaattcaaa	gtcagaagaa	atgactcttc	aaatcaatga	acttcaaaaa	2400
gaaattgaaa	tactcagaca	agaagaaaaa	gaaaagggtg	cacttgaaca	agaagttcaa	2460
gaattacaac	ttaaaacaga	attgtagtaa	aaacagatga	aggaaaaaga	gaatgatctt	2520
caagaaaaat	ttgcacaact	tgaagcagag	aatagcattc	ttaaagatga	aaagaaaacc	2580
cttgaagaca	tgtagaaaat	acatactcct	gttagccaag	aagaaaagatt	gatttttctta	2640
gactccatta	agtcocaaatc	caaagactct	gtgtgggaaa	aagaaataga	aatacttata	2700
gaggaaaatg	aggacctcaa	acaacaatgt	attcagctaa	atgaagagat	tgaaaagcaa	2760
aggaaactct	tttcatattg	tgaaaaaaac	tttgaagtta	actatcaaga	gttacaagag	2820
gagtatgctt	gccttctcaa	agtaaaagat	gatttagaag	acagtaaaaa	taaacaggaa	2880
ttagagtata	aaagtaaact	taaagcactt	aatgaagagc	ttcatttgca	agaataaat	2940
ccaactacag	tgaaaatgaa	aagtctctgtc	tttgatgaag	acaaaacttt	tgtagcagaa	3000
acattggaaa	tggttgagggt	tgtagaaaag	gatacaacag	aactcatgga	aaaacttgag	3060
gtaaccaagc	gagagaaaat	agagctgtca	cagagactgt	ctgatctttc	tgaacaattg	3120
aaacagaaaac	atggttgagat	tagttttcta	aatgaagaag	ttaaatcttt	aaagcaagag	3180
aaagaacaag	tttcatttag	atgtagagag	ctagaaatca	ttattaacca	caacagggca	3240
gaaaatgtac	agtcattgtga	tactcaagtta	agctctttat	tagatggagt	tgtgacctag	3300
acaagcaggg	gtgctgaagg	atcagtttct	aaagtaataa	aaagtttttg	tgaagaatca	3360
aaaataatgg	tggaagataa	agtttctttt	gaaaatatga	ctgttgagaa	agaaagtaag	3420
caagaacagt	tgatttttga	tcacttacca	tctgtaacaa	aggaatcatc	acttagagca	3480
actcaaccaa	gtgaaaatga	taaacttcag	aaagaactca	atgtacttaa	atcagaacag	3540
aatgatttaa	ggctacagat	ggaagcccaa	cgcattttgc	tctctctggt	ttattcaact	3600
catgtggatc	aggttcgtga	atatatggaa	aatgaaaaag	ataaagctct	ttgcagctct	3660
aaagaagagc	ttatttttgc	tcaagaggaa	aagatcaagg	aacttcagaa	aatacaccag	3720
ttagaactac	agacttgaa	aacacaagaa	acaggtgatg	aaggaaaagc	tttacatctg	3780
ctcattggaa	aacttcaaaa	ggcagtgctc	gaagaatggt	cttatttttt	acagacttta	3840
tgtagtgctc	ttggtgaata	ttatactcct	gcttttaaaat	gtgaagttaa	tgtagaagac	3900
aaagagaatt	ctggtgatta	cattttctgaa	aatgaagatc	cagaattaca	agattataga	3960
tatgaagtgc	aagactttca	agaaaatatg	cacactcttc	tcaacaaagt	aacagaagaa	4020
tacaacaaac	tcttggtact	tcaaacacga	ctaagcaaga	tctggggaca	gcagacagat	4080
ggtatgaaac	ttgaattttg	agaagaaaaac	cttccaaaag	aggaaacaga	gttttttatca	4140
atccattctc	agatgaccaa	tttggaagac	attgatgtca	atcataaaag	caagttatct	4200
tctctgcaag	atcttgaaaa	aactaaactt	gaagaacaag	ttcaagaatt	agaaagcctc	4260
atatcctctt	tgtagcaaca	gttgaaagaa	actgaacaaa	actatgaggc	agagatccac	4320
tgtagacaga	agaggcttca	agctgttagt	gagtcacagg	ttccgccaag	cttacctggt	4380
gattcggtgg	taattacaga	atctgatgca	cagagaacaa	tgtaccctgg	aagttgtgtg	4440
aaaaagaata	ttgatggtac	aatagagttt	tctggtgaat	ttggagtga	agaggaaaca	4500
aatatcggtt	agttgcttga	aaaacaatac	caagaacaat	tagaagaaga	agtagctaag	4560
gttattgtgt	caatgagtat	agcattttgct	caacaaactg	aactgtctag	aatatctggg	4620
ggaaaagaaa	atactgcata	atcaaagcaa	gcacatgctg	tgtgtcagca	agaacaacat	4680
tatttttaatt	aaatgaaatt	atcacaggat	caaattgggt	ttcagacttt	tgagacagtg	4740
gatgtgaaat	ttaaagaaga	atttaaacca	cttagtaaag	agttaggaga	acatggaaag	4800
gaaattttat	tatcaaatag	tgatcccat	gatataccag	aatcaaagga	ctgtgtgctg	4860
actattttcag	aagaaatggt	ctccaaagat	aaaacattta	tagttagaca	gtctatttcat	4920
gatgagattt	cagtgtcaag	catggatgct	tctagacaac	taatgttgaa	tgaagaacag	4980
ttggaagata	tgagacagga	acttgtagca	caataccaag	aacatcaaca	ggcaacggaa	5040

ttgttaaggc	aagcacatat	gcggcaaatg	gagagacagc	gagaagacca	ggaacagcta	5100
caagaagaga	ttaagagact	taatagacaa	ttagcccaga	gatcctccat	agataaatgaa	5160
aacctggttt	cagagagaga	gagggtgctt	ttagaggagc	tggaagcact	aaagcagctg	5220
tcttttagctg	gaagagagaa	gctgtgttgt	gagctgcgca	acagcagtac	gcaaacacag	5280
aatggaaatg	aaaaccaagg	agaagttgaa	gaacaaacat	ttaaagaaaa	ggaattagac	5340
agaaaacctg	aagatgtgcc	tcctgagatt	ttgtctaattg	aaaggatatgc	actccagaaa	5400
gctaataata	gactttttgaa	gatcctctta	gaagttgtaa	agacaacagc	agctgttgaa	5460
gaaacaattg	gtcgccatgt	ccttgggatt	ctagatagat	ctagtaaaag	ccagtcattct	5520
gccagcctaa	tttggagggtc	agaagcagag	gcatctgtaa	agtcattgtgt	ccatgaggaa	5580
catacaagag	ttacagatga	atccattccc	tcttattctg	gaagtgatat	gccaagaaa	5640
gacattaaca	tgtggtcaaaa	agtaactgag	gaaggaacag	agctgtcaca	acgacttgtg	5700
aggagtgggt	ttgctggaac	tgaaatagac	cctgaaaatg	aagaacttat	gctgaacatt	5760
agctctcgac	tacaagcagc	agttgaaaaa	ctcctagaag	ccataagtga	aactagcagt	5820
cagcttgaac	atgcgaaagt	gacacagaca	gagttgatgc	gtgagtcatt	tagacagaaa	5880
caagaagcaa	cagagtccct	taagtgccaa	gaggaacttc	gagagcgcct	tcatgaggag	5940
tccagggccca	gagaacagct	agctgtggag	ctcagtaagg	ctgagggcgt	cattgatggc	6000
tatgcagatg	aaaaaactct	ttttgaaagg	caaatttcagg	aaaaaactga	tataatagat	6060
cgctttgagc	aggagttgtt	atgtgcaagt	aacaggttgc	aagaattgga	ggcagagcaa	6120
cagcagatcc	aagaagaaag	agaattactg	tccagacaaa	aggaagctat	gaaagcagag	6180
gcaggcccag	ttgaacaaca	attactacag	gagacagaaa	aattaatgaa	ggaaaaacta	6240
gaagtacaat	gtcaagctga	aaaagtacgt	gatgaccttc	aaaaacaagt	gaaagctcta	6300
gaaatagatg	tggaagaaca	agtcagtagg	tttatagagc	tggaacaaga	aaaaaatact	6360
gaactaatgg	attttaagaca	gcaaaaacaa	gcatttgaaa	agcagttaga	aaaaatgaga	6420
aaatttttag	atgagcaagc	cattgacaga	gaacatgaga	gagatgtatt	ccaacaggaa	6480
atacagaaac	tagaacagca	acttaagggt	gttcctcgat	tccagcctat	cagtgaacat	6540
caaactagag	aggttgaaca	gttagcaaat	catctgaaag	aaaaaacaga	caaatgcagt	6600
gagcttttgc	tctctaaaga	gcagcttcaa	agggatatac	aagaaaggaa	tgaagaaata	6660
gagaaactgg	agttcagagt	aagagaactg	gagcaggcgc	ttcttgtaga	ggaccgaaaa	6720
cacttttgag	ctgtagaagc	taaaccagaa	ttgtccctag	aagtacaatt	gcaggctgaa	6780
cgagatgcca	tagacagaaa	ggaaaaagag	attacaaact	tagaagagca	attagaacag	6840
tttagagaag	aactggaaaa	taagaatgaa	gaagttcaac	aattacatat	gcaattagaa	6900
atacagaaaa	aggaatctac	taccgcgcta	caagaacttg	aacaggaaaa	caaattattt	6960
aaggatgaca	tggagaaaact	gggacttgcc	ataaaggaat	ctgatgccat	gtctactcaa	7020
gaccaacatg	tgctattttg	gaaatttgct	caaataatac	aggaaaaaga	ggtagaaaatt	7080
gaccaattaa	atgaacaagt	tacgaaactc	cagcagcaac	ttaaaattac	aacagataac	7140
aaggttattg	aagaaaaaaa	tgaactgata	agggatcttg	aaacccaaat	agaatgtttg	7200
atgagtgatc	aagaatgtgt	gaagagaat	agagaagaag	aaatagagca	gctcaatgaa	7260
gtgattgaaa	aacttcaaca	ggaattggca	aatattggac	agaagacatc	aatgaatgct	7320
cattccctct	cagaagaagc	agacagttta	aaacatcaat	tggatgtggg	tatagctgaa	7380
aagctggcct	tggaacagca	agtagaaacc	gctaattgaag	aatgacctt	catgaaaaat	7440
gtacttaaaag	aaaccaattt	taaaatgaat	cagctaacac	aggaattatt	cagcttaaaag	7500
agagaacgtg	aaagtgtgga	aaagattcaa	agcataccag	agaatagtgt	taacgtggct	7560
atagatcatc	tgagcaaaga	caaacctgaa	ctagaagtag	tccttacaga	ggatgctctt	7620
aaatccctag	aaaatcagac	atacttcaaa	tcttttgaag	aaaatggcaa	aggttccata	7680
attaattttgg	aaacaagggt	gctacaactt	gagagcactg	ttagtgcaaa	ggacttagaa	7740
cttaccaggt	gttataaaaca	aataaaagac	atgcaagaac	aaggccagtt	tgaaacagaa	7800
atgcttcaaa	agaagattgt	aaacctacag	aaaatagttg	aagaaaaagt	ggctgctgct	7860
cttgtcagtc	aaatccaact	tgaggcagtt	caggaatatg	caaaattctg	tcaagataat	7920
caaacaattt	catcagaacc	tgaaagaaca	aatattcaga	atttaaataca	actaagagaa	7980
gatgagttgg	ggtcagatat	atcagcatta	accttgagaa	tatcagaatt	agaaagccag	8040
gttggtgaaa	tgcatactag	tttgatttta	gaaaaagaac	aagtagaaat	tgcaaaaaaa	8100
aatgttttag	aaaaagaaaa	gaagctgcta	gaactacaga	agctattgga	gggcaatgag	8160
aaaaaacaga	gagagaaaga	aaagaaaaga	agccctcaag	atggtgaagt	tctcaagaca	8220
actactgagc	tatttcatag	caatgaagaa	agtggaatgt	ttaatgaact	cgaggctctt	8280
agagctgaat	cagtggctac	caaagcagaa	cttgccagtt	ataaagaaaa	ggctgaaaaa	8340
cttcaagaag	agctttttggt	aaaagaaaca	aatatgacat	ctotttcagaa	agacttaagc	8400
caagttaggg	atcacctcgc	agaggcaaaa	gagaaattgt	ccatttttaga	aaaagaagat	8460
gagactgagg	tacaagaaag	caaaaaggcc	tgcatgtttg	agccacttcc	tataaaactg	8520
agtaagagca	ttgcatccca	gacagatggg	actctgaaga	tcagtagcag	caatcagact	8580

ccacaaattc	ttgttaaaaa	tgcaggaata	caaattaatt	tacagagtga	atgttcctca	8640
gaagaagtta	ctgaaataat	cagtcagttt	actgaaaaaa	ttgagaagat	gcaagaacta	8700
catgctgctg	aaattttga	catggaatcc	agacatat	cagaaactga	aaccttaag	8760
agggaaact	atgttgccgt	tcagttactg	aaagaggaat	gtggtacctt	gaaggcagtg	8820
atacagtgtc	tgagaagtaa	agagggatcc	tcaattcctg	agctagcaca	ttctgatgct	8880
taccagacta	gagaaatatg	ctccagtgat	tctggatcag	actggggtca	gggaatttat	8940
cttacacaca	gtcagggatt	tgacatagca	tcagaaggcc	gaggagaaga	aagtgaaggt	9000
gcaacagatt	cctttccaaa	gaaaataaag	ggattactga	gagctgtcca	taatgaaggc	9060
atgcaggtgc	tttctctcac	tgagtctccc	tatagtgtatg	gagaggacca	ttctattcag	9120
caggtttcag	aaccttggtc	agaagagaga	aaagcttaca	tcaatacaat	ctcatctcta	9180
aaggatttaa	ttacaaagat	gcaactgcaa	agagaagccg	aggtttatga	tagttctcaa	9240
tctcatgaga	gcttctcaga	ctggcgaggt	gaactactgc	ttgcccttca	acaagttttc	9300
ttagaagagc	gtagtgtttt	actagcagca	tttcggacgg	agctgacagc	tctaggtact	9360
acagatgcag	ttggtttact	aaactgtttg	gaacagagaa	tacaagaaca	gggtgttgaa	9420
tatcaagcag	ctatggaatg	cctccagaaa	gcagatagaa	ggagtttgtt	atctgaaatt	9480
caggcactgc	atgcacaaat	gaatggtagg	aaaattactc	tgaaaagaga	acaagagagt	9540
gagaaacca	gccaaagaact	cctggaatat	aatatacagc	agaagcagtc	tcaaagctg	9600
gagatgcaag	tggagctcag	cagtatgaaa	gacagagcaa	cggaaactgca	ggagcagctg	9660
agttctgaga	aaatgggtgt	tgctgaactg	aagagttagc	ttgcacaaac	taaattggaa	9720
ctagaacaaa	cactcaaggc	acagcataaa	cacctaaaag	aattggaggc	tttcaggttg	9780
gaagttaaa	ataagacaga	tgaagtacat	ttgcttaatg	acacattagc	aagtgaacag	9840
aaaaaatcaa	gagagctcca	gtgggctttg	gagaaagaga	aagccaagtt	gggacgcagt	9900
gaagaacggg	ataaagaaga	acttgaggat	ctgaagtttt	cacttgagag	tcagaaacaa	9960
aggaatcttc	agctaaatct	acttttggaa	caacagaaac	aactactgaa	cgaatccag	10020
caaaaaatag	aatcacagag	aatgctatat	gatgccaggt	tgtcagaaga	acaaggctga	10080
aacttagagc	ttcaggtact	tcttgaatct	gagaaagttc	gaattcggga	aatgagtagt	10140
accctagata	gggagcggga	attgcacgca	cagctgcaga	gcagtgtatg	tactggacag	10200
tctcgccac	ccttgccctc	agaggaccta	ctgaaagagc	tgcaaaaaca	gctagaggaa	10260
aaacacagtc	gcatagtaga	attgttaaat	gagactgaaa	aataataaact	ggattctttg	10320
caaacacgac	agcaaatgga	aaaagatagg	caggttcaca	ggaaaacact	gcagacagaa	10380
caggaggcca	acactgaggg	acagaaaaaa	atgcatgagc	tccagtccaa	agtggaagat	10440
cttcagcgcc	agctggaaga	gaaaagacaa	caagtttata	agtttagacct	tgaaggacag	10500
cgactacaag	gaatcatgca	ggaattccag	aagcaagaac	tagaacgaga	agaaaaacga	10560
gaaagtagaa	gaattctgta	tcagaacctt	aatgagccaa	ccacgtggag	cttaaccagt	10620
gatagaacta	gaaattgggt	tcttcaacag	aaaatagaag	gagaaacaaa	agaatcaaac	10680
tacgctaaat	tgattgaaat	gaatggagga	ggaaccgggt	gtaatcatga	attagaaatg	10740
atcagacaaa	agcttcaatg	tgtagcttca	aaactacagg	ttctacccca	gaaagcctct	10800
gagagactac	agtttgaaac	agcagatgat	gaagatttca	tttgggttca	ggaaaatatt	10860
gatgaaatta	ttttacaact	acagaaatta	actggccagc	aagggtgaaga	gccagcttg	10920
gtgtcccaa	gtacttcttg	tggctcattg	actgaaagac	tactgagaca	aaatgctgag	10980
ctgacagggc	atatcagtca	actgactgaa	gagaagaatg	acttaaggaa	catggttatg	11040
aagctggaag	agcagatcag	gtggtatcga	cagacaggag	ctggtagaga	taattcttcc	11100
aggttttcat	tgaatggtgg	tgccaacatt	gaagccatca	ttgcctctga	aaaagaagta	11160
tggaaacagag	aaaaattgac	tctccagaaa	tctttgaaaa	gggcagaggc	tgaagtatac	11220
aaactgaaag	ctgaactaag	aaatgactct	ttacttcaaa	ctctgagccc	tgattctgaa	11280
catgtcactt	taaagagaat	ttatggtaaa	tacttgaggg	cagaaagt	tcgaaaggct	11340
ctcatttacc	agaagaaata	cctgctgctg	ttactgggtg	ggttccagga	atgtgaagat	11400
gccaccttgg	ccctgcttgc	ccggatgggg	gggcagccag	ctttcacgga	tctagagggtg	11460
atcaccaatc	gccc aaagg	cttcaccagg	tttcggctcg	ccgtcagagt	atccattgca	11520
atttccagaa	tgaaattttt	ggttcgacgg	tggcatcgag	tcacagggtc	tgtttccatc	11580
aatattaaca	gagatggctt	tggactgaat	caagggtgcag	aaaagactga	ctcattttat	11640
cattcttctg	gtgggctgga	gttatatgga	gaaccaagac	atactacgta	tcgctcaaga	11700
tcagatctgg	actatattag	gtccccttta	ccatttcaga	ataggtaccc	aggcactcca	11760
gctgatttca	atcctgggtc	tttagcatgt	tctcagcttc	agaattacga	tcctgacaga	11820
gccataacag	attatctcac	tcggctagag	gcactgcaaa	gacgacttgg	aactatacag	11880
tcagggtcaa	ctactcaatt	tcagtctggc	atgagaagat	aatcctttga	aacatcatta	11940
attgaagtga	ttttaaatag	atttcctttt	gtaaatcaat	ggttcttttg	tgcttttgta	12000
ttgtgaatat	tcaatgggac	caatatgaac	acagcttatg	attgtatata	aatcccttgc	12060
cagcacatga	aaacaaactg	gaatttgtat	atataagcat	tgtgtatgta	ttcatgcaca	12120


```

ataattattg aattacctgt atatttgtgg aatgctaatt taaaacatta aattataaac 12180
cttgtgtatt tatcaaattg gtgaaaagat taaactttta cgcattacaa tactgctgaa 12240
tgtgtagctc gaggtgtcct gcacttttct tataaggcta ctgaagttac atgttttgcc 12300
taatatatcc taactggtgat gaagacagat aatatcactt gtagagacct atttttgtat 12360
aatggtagaa gttttgaatt ttatggggta ttttgtcaag tactgaaata aaaatgactt 12420
caccattttc accacact                                     12438

```

<210> 4

<211> 3899

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
 1          5          10          15
Leu Ala Gln Phe Arg Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro
 20          25          30
Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
 35          40          45
Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
 50          55          60
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
 65          70          75          80
Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
 85          90          95
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100          105          110
Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115          120          125
Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
130          135          140
Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145          150          155          160
Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
165          170          175
Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
180          185          190
Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
195          200          205
Gln Leu Thr Ala Asn Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr
210          215          220
Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225          230          235          240
Gln Phe Gln Gln Leu Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His
245          250          255
Ser Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr
260          265          270
His Gln Gln Gln Leu Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln
275          280          285
Lys Lys Lys Glu Asp Phe Thr Met Gln Ile Ser Phe Leu Gln Glu Lys
290          295          300
Ile Lys Val Tyr Glu Met Glu Gln Asp Lys Lys Val Glu Asn Ser Asn
305          310          315          320
Lys Glu Glu Ile Gln Glu Lys Glu Thr Ile Ile Glu Glu Leu Asn Thr
325          330          335
Lys Ile Ile Glu Glu Glu Lys Lys Thr Leu Glu Leu Lys Asp Lys Leu
340          345          350
Thr Thr Ala Asp Lys Leu Leu Gly Glu Leu Gln Glu Gln Ile Val Gln
355          360          365

```

Lys	Asn	Gln	Glu	Ile	Lys	Asn	Met	Lys	Leu	Glu	Leu	Thr	Asn	Ser	Lys
370					375					380					
Gln	Lys	Glu	Arg	Gln	Ser	Ser	Glu	Glu	Ile	Lys	Gln	Leu	Met	Gly	Thr
385					390					395					400
Val	Glu	Glu	Leu	Gln	Lys	Arg	Asn	His	Lys	Asp	Ser	Gln	Phe	Glu	Thr
				405					410					415	
Asp	Ile	Val	Gln	Arg	Met	Glu	Gln	Glu	Thr	Gln	Arg	Lys	Leu	Glu	Gln
			420					425					430		
Leu	Arg	Ala	Glu	Leu	Asp	Glu	Met	Tyr	Gly	Gln	Gln	Ile	Val	Gln	Met
		435					440					445			
Lys	Gln	Glu	Leu	Ile	Arg	Gln	His	Met	Ala	Gln	Met	Glu	Glu	Met	Lys
450						455					460				
Thr	Arg	His	Lys	Gly	Glu	Met	Glu	Asn	Ala	Leu	Arg	Ser	Tyr	Ser	Asn
465					470					475					480
Ile	Thr	Val	Asn	Glu	Asp	Gln	Ile	Lys	Leu	Met	Asn	Val	Ala	Ile	Asn
				485					490					495	
Glu	Leu	Asn	Ile	Lys	Leu	Gln	Asp	Thr	Asn	Ser	Gln	Lys	Glu	Lys	Leu
			500					505					510		
Lys	Glu	Glu	Leu	Gly	Leu	Ile	Leu	Glu	Glu	Lys	Cys	Ala	Leu	Gln	Arg
		515					520					525			
Gln	Leu	Glu	Asp	Leu	Val	Glu	Glu	Leu	Ser	Phe	Ser	Arg	Glu	Gln	Ile
530						535					540				
Gln	Arg	Ala	Arg	Gln	Thr	Ile	Ala	Glu	Gln	Glu	Ser	Lys	Leu	Asn	Glu
545					550					555					560
Ala	His	Lys	Ser	Leu	Ser	Thr	Val	Glu	Asp	Leu	Lys	Ala	Glu	Ile	Val
				565					570					575	
Ser	Ala	Ser	Glu	Ser	Arg	Lys	Glu	Leu	Glu	Leu	Lys	His	Glu	Ala	Glu
			580					585					590		
Val	Thr	Asn	Tyr	Lys	Ile	Lys	Leu	Glu	Met	Leu	Glu	Lys	Glu	Lys	Asn
		595					600					605			
Ala	Val	Leu	Asp	Arg	Met	Ala	Glu	Ser	Gln	Glu	Ala	Glu	Leu	Glu	Arg
610						615					620				
Leu	Arg	Thr	Gln	Leu	Leu	Phe	Ser	His	Glu	Glu	Glu	Leu	Ser	Lys	Leu
625					630					635					640
Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys
			645						650					655	
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn
		660						665					670		
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu
		675					680					685			
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp
690						695					700				
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln
705					710					715					720
Ile	Asn	Glu	Leu	Gln	Lys	Glu	Ile	Glu	Ile	Leu	Arg	Gln	Glu	Glu	Lys
			725						730					735	
Glu	Lys	Gly	Thr	Leu	Glu	Gln	Glu	Val	Gln	Glu	Leu	Gln	Leu	Lys	Thr
			740					745					750		
Glu	Leu	Leu	Glu	Lys	Gln	Met	Lys	Glu	Lys	Glu	Asn	Asp	Leu	Gln	Glu
		755					760					765			
Lys	Phe	Ala	Gln	Leu	Glu	Ala	Glu	Asn	Ser	Ile	Leu	Lys	Asp	Glu	Lys
770						775					780				
Lys	Thr	Leu	Glu	Asp	Met	Leu	Lys	Ile	His	Thr	Pro	Val	Ser	Gln	Glu
785					790					795					800
Glu	Arg	Leu	Ile	Phe	Leu	Asp	Ser	Ile	Lys	Ser	Lys	Ser	Lys	Asp	Ser
			805						810					815	
Val	Trp	Glu	Lys	Glu	Ile	Glu	Ile	Leu	Ile	Glu	Glu	Asn	Glu	Asp	Leu
			820					825					830		
Lys	Gln	Gln	Cys	Ile	Gln	Leu	Asn	Glu	Glu	Ile	Glu	Lys	Gln	Arg	Asn

Asn Leu Glu Asp Ile Asp Val Asn His Lys Ser Lys Leu Ser Ser Leu
 1315 1320 1325
 Gln Asp Leu Glu Lys Thr Lys Leu Glu Glu Gln Val Gln Glu Leu Glu
 1330 1335 1340
 Ser Leu Ile Ser Ser Leu Gln Gln Gln Leu Lys Glu Thr Glu Gln Asn
 1345 1350 1355 1360
 Tyr Glu Ala Glu Ile His Cys Leu Gln Lys Arg Leu Gln Ala Val Ser
 1365 1370 1375
 Glu Ser Thr Val Pro Pro Ser Leu Pro Val Asp Ser Val Val Ile Thr
 1380 1385 1390
 Glu Ser Asp Ala Gln Arg Thr Met Tyr Pro Gly Ser Cys Val Lys Lys
 1395 1400 1405
 Asn Ile Asp Gly Thr Ile Glu Phe Ser Gly Glu Phe Gly Val Lys Glu
 1410 1415 1420
 Glu Thr Asn Ile Val Lys Leu Leu Glu Lys Gln Tyr Gln Glu Gln Leu
 1425 1430 1435 1440
 Glu Glu Glu Val Ala Lys Val Ile Val Ser Met Ser Ile Ala Phe Ala
 1445 1450 1455
 Gln Gln Thr Glu Leu Ser Arg Ile Ser Gly Gly Lys Glu Asn Thr Ala
 1460 1465 1470
 Ser Ser Lys Gln Ala His Ala Val Cys Gln Gln Glu Gln His Tyr Phe
 1475 1480 1485
 Asn Glu Met Lys Leu Ser Gln Asp Gln Ile Gly Phe Gln Thr Phe Glu
 1490 1495 1500
 Thr Val Asp Val Lys Phe Lys Glu Glu Phe Lys Pro Leu Ser Lys Glu
 1505 1510 1515 1520
 Leu Gly Glu His Gly Lys Glu Ile Leu Leu Ser Asn Ser Asp Pro His
 1525 1530 1535
 Asp Ile Pro Glu Ser Lys Asp Cys Val Leu Thr Ile Ser Glu Glu Met
 1540 1545 1550
 Phe Ser Lys Asp Lys Thr Phe Ile Val Arg Gln Ser Ile His Asp Glu
 1555 1560 1565
 Ile Ser Val Ser Ser Met Asp Ala Ser Arg Gln Leu Met Leu Asn Glu
 1570 1575 1580
 Glu Gln Leu Glu Asp Met Arg Gln Glu Leu Val Arg Gln Tyr Gln Glu
 1585 1590 1595 1600
 His Gln Gln Ala Thr Glu Leu Leu Arg Gln Ala His Met Arg Gln Met
 1605 1610 1615
 Glu Arg Gln Arg Glu Asp Gln Glu Gln Leu Gln Glu Glu Ile Lys Arg
 1620 1625 1630
 Leu Asn Arg Gln Leu Ala Gln Arg Ser Ser Ile Asp Asn Glu Asn Leu
 1635 1640 1645
 Val Ser Glu Arg Glu Arg Val Leu Leu Glu Glu Leu Glu Ala Leu Lys
 1650 1655 1660
 Gln Leu Ser Leu Ala Gly Arg Glu Lys Leu Cys Cys Glu Leu Arg Asn
 1665 1670 1675 1680
 Ser Ser Thr Gln Thr Gln Asn Gly Asn Glu Asn Gln Gly Glu Val Glu
 1685 1690 1695
 Glu Gln Thr Phe Lys Glu Lys Glu Leu Asp Arg Lys Pro Glu Asp Val
 1700 1705 1710
 Pro Pro Glu Ile Leu Ser Asn Glu Arg Tyr Ala Leu Gln Lys Ala Asn
 1715 1720 1725
 Asn Arg Leu Leu Lys Ile Leu Leu Glu Val Val Lys Thr Thr Ala Ala
 1730 1735 1740
 Val Glu Glu Thr Ile Gly Arg His Val Leu Gly Ile Leu Asp Arg Ser
 1745 1750 1755 1760
 Ser Lys Ser Gln Ser Ser Ala Ser Leu Ile Trp Arg Ser Glu Ala Glu
 1765 1770 1775
 Ala Ser Val Lys Ser Cys Val His Glu Glu His Thr Arg Val Thr Asp

1780	1785	1790
Glu Ser Ile Pro Ser Tyr Ser	Gly Ser Asp Met Pro Arg Asn Asp Ile	
1795	1800	1805
Asn Met Trp Ser Lys Val Thr	Glu Glu Gly Thr Glu Leu Ser Gln Arg	
1810	1815	1820
Leu Val Arg Ser Gly Phe Ala	Gly Thr Glu Ile Asp Pro Glu Asn Glu	
1825	1830	1835
Glu Leu Met Leu Asn Ile Ser	Ser Arg Leu Gln Ala Ala Val Glu Lys	
1845	1850	1855
Leu Leu Glu Ala Ile Ser Glu	Thr Ser Ser Gln Leu Glu His Ala Lys	
1860	1865	1870
Val Thr Gln Thr Glu Leu Met	Arg Glu Ser Phe Arg Gln Lys Gln Glu	
1875	1880	1885
Ala Thr Glu Ser Leu Lys Cys	Gln Glu Glu Leu Arg Glu Arg Leu His	
1890	1895	1900
Glu Glu Ser Arg Ala Arg Glu	Gln Leu Ala Val Glu Leu Ser Lys Ala	
1905	1910	1915
Glu Gly Val Ile Asp Gly Tyr	Ala Asp Glu Lys Thr Leu Phe Glu Arg	
1925	1930	1935
Gln Ile Gln Glu Lys Thr Asp	Ile Ile Asp Arg Leu Glu Gln Glu Leu	
1940	1945	1950
Leu Cys Ala Ser Asn Arg Leu	Gln Glu Leu Glu Ala Glu Gln Gln Gln	
1955	1960	1965
Ile Gln Glu Glu Arg Glu Leu	Leu Ser Arg Gln Lys Glu Ala Met Lys	
1970	1975	1980
Ala Glu Ala Gly Pro Val Glu	Gln Gln Leu Leu Gln Glu Thr Glu Lys	
1985	1990	1995
Leu Met Lys Glu Lys Leu Glu	Val Gln Cys Gln Ala Glu Lys Val Arg	
2005	2010	2015
Asp Asp Leu Gln Lys Gln Val	Lys Ala Leu Glu Ile Asp Val Glu Glu	
2020	2025	2030
Gln Val Ser Arg Phe Ile Glu	Leu Glu Gln Glu Lys Asn Thr Glu Leu	
2035	2040	2045
Met Asp Leu Arg Gln Gln Asn	Gln Ala Leu Glu Lys Gln Leu Glu Lys	
2050	2055	2060
Met Arg Lys Phe Leu Asp Glu	Gln Ala Ile Asp Arg Glu His Glu Arg	
2065	2070	2075
Asp Val Phe Gln Gln Glu Ile	Gln Lys Leu Glu Gln Gln Leu Lys Val	
2085	2090	2095
Val Pro Arg Phe Gln Pro Ile	Ser Glu His Gln Thr Arg Glu Val Glu	
2100	2105	2110
Gln Leu Ala Asn His Leu Lys	Glu Lys Thr Asp Lys Cys Ser Glu Leu	
2115	2120	2125
Leu Leu Ser Lys Glu Gln Leu	Gln Arg Asp Ile Gln Glu Arg Asn Glu	
2130	2135	2140
Glu Ile Glu Lys Leu Glu Phe	Arg Val Arg Glu Leu Glu Gln Ala Leu	
2145	2150	2155
Leu Val Glu Asp Arg Lys His	Phe Gly Ala Val Glu Ala Lys Pro Glu	
2165	2170	2175
Leu Ser Leu Glu Val Gln Leu	Gln Ala Glu Arg Asp Ala Ile Asp Arg	
2180	2185	2190
Lys Glu Lys Glu Ile Thr Asn	Leu Glu Glu Gln Leu Glu Gln Phe Arg	
2195	2200	2205
Glu Glu Leu Glu Asn Lys Asn	Glu Glu Val Gln Gln Leu His Met Gln	
2210	2215	2220
Leu Glu Ile Gln Lys Lys Glu	Ser Thr Thr Arg Leu Gln Glu Leu Glu	
2225	2230	2235
Gln Glu Asn Lys Leu Phe Lys	Asp Asp Met Glu Lys Leu Gly Leu Ala	
2245	2250	2255

Ile	Lys	Glu	Ser	Asp	Ala	Met	Ser	Thr	Gln	Asp	Gln	His	Val	Leu	Phe	2260	2265	2270
Gly	Lys	Phe	Ala	Gln	Ile	Ile	Gln	Glu	Lys	Glu	Val	Glu	Ile	Asp	Gln	2275	2280	2285
Leu	Asn	Glu	Gln	Val	Thr	Lys	Leu	Gln	Gln	Gln	Leu	Lys	Ile	Thr	Thr	2290	2295	2300
Asp	Asn	Lys	Val	Ile	Glu	Glu	Lys	Asn	Glu	Leu	Ile	Arg	Asp	Leu	Glu	2305	2310	2315
Thr	Gln	Ile	Glu	Cys	Leu	Met	Ser	Asp	Gln	Glu	Cys	Val	Lys	Arg	Asn	2325	2330	2335
Arg	Glu	Glu	Glu	Ile	Glu	Gln	Leu	Asn	Glu	Val	Ile	Glu	Lys	Leu	Gln	2340	2345	2350
Gln	Glu	Leu	Ala	Asn	Ile	Gly	Gln	Lys	Thr	Ser	Met	Asn	Ala	His	Ser	2355	2360	2365
Leu	Ser	Glu	Glu	Ala	Asp	Ser	Leu	Lys	His	Gln	Leu	Asp	Val	Val	Ile	2370	2375	2380
Ala	Glu	Lys	Leu	Ala	Leu	Glu	Gln	Gln	Val	Glu	Thr	Ala	Asn	Glu	Glu	2385	2390	2395
Met	Thr	Phe	Met	Lys	Asn	Val	Leu	Lys	Glu	Thr	Asn	Phe	Lys	Met	Asn	2405	2410	2415
Gln	Leu	Thr	Gln	Glu	Leu	Phe	Ser	Leu	Lys	Arg	Glu	Arg	Glu	Ser	Val	2420	2425	2430
Glu	Lys	Ile	Gln	Ser	Ile	Pro	Glu	Asn	Ser	Val	Asn	Val	Ala	Ile	Asp	2435	2440	2445
His	Leu	Ser	Lys	Asp	Lys	Pro	Glu	Leu	Glu	Val	Val	Leu	Thr	Glu	Asp	2450	2455	2460
Ala	Leu	Lys	Ser	Leu	Glu	Asn	Gln	Thr	Tyr	Phe	Lys	Ser	Phe	Glu	Glu	2465	2470	2475
Asn	Gly	Lys	Gly	Ser	Ile	Ile	Asn	Leu	Glu	Thr	Arg	Leu	Leu	Gln	Leu	2485	2490	2495
Glu	Ser	Thr	Val	Ser	Ala	Lys	Asp	Leu	Glu	Leu	Thr	Gln	Cys	Tyr	Lys	2500	2505	2510
Gln	Ile	Lys	Asp	Met	Gln	Glu	Gln	Gly	Gln	Phe	Glu	Thr	Glu	Met	Leu	2515	2520	2525
Gln	Lys	Lys	Ile	Val	Asn	Leu	Gln	Lys	Ile	Val	Glu	Glu	Lys	Val	Ala	2530	2535	2540
Ala	Ala	Leu	Val	Ser	Gln	Ile	Gln	Leu	Glu	Ala	Val	Gln	Glu	Tyr	Ala	2545	2550	2555
Lys	Phe	Cys	Gln	Asp	Asn	Gln	Thr	Ile	Ser	Ser	Glu	Pro	Glu	Arg	Thr	2565	2570	2575
Asn	Ile	Gln	Asn	Leu	Asn	Gln	Leu	Arg	Glu	Asp	Glu	Leu	Gly	Ser	Asp	2580	2585	2590
Ile	Ser	Ala	Leu	Thr	Leu	Arg	Ile	Ser	Glu	Leu	Glu	Ser	Gln	Val	Val	2595	2600	2605
Glu	Met	His	Thr	Ser	Leu	Ile	Leu	Glu	Lys	Glu	Gln	Val	Glu	Ile	Ala	2610	2615	2620
Glu	Lys	Asn	Val	Leu	Glu	Lys	Glu	Lys	Lys	Leu	Leu	Glu	Leu	Gln	Lys	2625	2630	2635
Leu	Leu	Glu	Gly	Asn	Glu	Lys	Lys	Gln	Arg	Glu	Lys	Glu	Lys	Lys	Arg	2645	2650	2655
Ser	Pro	Gln	Asp	Val	Glu	Val	Leu	Lys	Thr	Thr	Thr	Glu	Leu	Phe	His	2660	2665	2670
Ser	Asn	Glu	Glu	Ser	Gly	Phe	Phe	Asn	Glu	Leu	Glu	Ala	Leu	Arg	Ala	2675	2680	2685
Glu	Ser	Val	Ala	Thr	Lys	Ala	Glu	Leu	Ala	Ser	Tyr	Lys	Glu	Lys	Ala	2690	2695	2700
Glu	Lys	Leu	Gln	Glu	Glu	Leu	Leu	Val	Lys	Glu	Thr	Asn	Met	Thr	Ser	2705	2710	2715
Leu	Gln	Lys	Asp	Leu	Ser	Gln	Val	Arg	Asp	His	Leu	Ala	Glu	Ala	Lys	2720		

				2725					2730					2735	
Glu	Lys	Leu	Ser	Ile	Leu	Glu	Lys	Glu	Asp	Glu	Thr	Glu	Val	Gln	Glu
				2740					2745					2750	
Ser	Lys	Lys	Ala	Cys	Met	Phe	Glu	Pro	Leu	Pro	Ile	Lys	Leu	Ser	Lys
				2755					2760					2765	
Ser	Ile	Ala	Ser	Gln	Thr	Asp	Gly	Thr	Leu	Lys	Ile	Ser	Ser	Ser	Asn
				2770					2775					2780	
Gln	Thr	Pro	Gln	Ile	Leu	Val	Lys	Asn	Ala	Gly	Ile	Gln	Ile	Asn	Leu
				2785					2790					2800	
Gln	Ser	Glu	Cys	Ser	Ser	Glu	Glu	Val	Thr	Glu	Ile	Ile	Ser	Gln	Phe
				2805					2810					2815	
Thr	Glu	Lys	Ile	Glu	Lys	Met	Gln	Glu	Leu	His	Ala	Ala	Glu	Ile	Leu
				2820					2825					2830	
Asp	Met	Glu	Ser	Arg	His	Ile	Ser	Glu	Thr	Glu	Thr	Leu	Lys	Arg	Glu
				2835					2840					2845	
His	Tyr	Val	Ala	Val	Gln	Leu	Leu	Lys	Glu	Glu	Cys	Gly	Thr	Leu	Lys
				2850					2855					2860	
Ala	Val	Ile	Gln	Cys	Leu	Arg	Ser	Lys	Glu	Gly	Ser	Ser	Ile	Pro	Glu
				2865					2870					2880	
Leu	Ala	His	Ser	Asp	Ala	Tyr	Gln	Thr	Arg	Glu	Ile	Cys	Ser	Ser	Asp
				2885					2890					2895	
Ser	Gly	Ser	Asp	Trp	Gly	Gln	Gly	Ile	Tyr	Leu	Thr	His	Ser	Gln	Gly
				2900					2905					2910	
Phe	Asp	Ile	Ala	Ser	Glu	Gly	Arg	Gly	Glu	Glu	Ser	Glu	Ser	Ala	Thr
				2915					2920					2925	
Asp	Ser	Phe	Pro	Lys	Lys	Ile	Lys	Gly	Leu	Leu	Arg	Ala	Val	His	Asn
				2930					2935					2940	
Glu	Gly	Met	Gln	Val	Leu	Ser	Leu	Thr	Glu	Ser	Pro	Tyr	Ser	Asp	Gly
				2945					2950					2960	
Glu	Asp	His	Ser	Ile	Gln	Gln	Val	Ser	Glu	Pro	Trp	Leu	Glu	Glu	Arg
				2965					2970					2975	
Lys	Ala	Tyr	Ile	Asn	Thr	Ile	Ser	Ser	Leu	Lys	Asp	Leu	Ile	Thr	Lys
				2980					2985					2990	
Met	Gln	Leu	Gln	Arg	Glu	Ala	Glu	Val	Tyr	Asp	Ser	Ser	Gln	Ser	His
				2995					3000					3005	
Glu	Ser	Phe	Ser	Asp	Trp	Arg	Gly	Glu	Leu	Leu	Leu	Ala	Leu	Gln	Gln
				3010					3015					3020	
Val	Phe	Leu	Glu	Glu	Arg	Ser	Val	Leu	Leu	Ala	Ala	Phe	Arg	Thr	Glu
				3025					3030					3040	
Leu	Thr	Ala	Leu	Gly	Thr	Thr	Asp	Ala	Val	Gly	Leu	Leu	Asn	Cys	Leu
				3045					3050					3055	
Glu	Gln	Arg	Ile	Gln	Glu	Gln	Gly	Val	Glu	Tyr	Gln	Ala	Ala	Met	Glu
				3060					3065					3070	
Cys	Leu	Gln	Lys	Ala	Asp	Arg	Arg	Ser	Leu	Leu	Ser	Glu	Ile	Gln	Ala
				3075					3080					3085	
Leu	His	Ala	Gln	Met	Asn	Gly	Arg	Lys	Ile	Thr	Leu	Lys	Arg	Glu	Gln
				3090					3095					3100	
Glu	Ser	Glu	Lys	Pro	Ser	Gln	Glu	Leu	Leu	Glu	Tyr	Asn	Ile	Gln	Gln
				3105					3110					3120	
Lys	Gln	Ser	Gln	Met	Leu	Glu	Met	Gln	Val	Glu	Leu	Ser	Ser	Met	Lys
				3125					3130					3135	
Asp	Arg	Ala	Thr	Glu	Leu	Gln	Glu	Gln	Leu	Ser	Ser	Glu	Lys	Met	Val
				3140					3145					3150	
Val	Ala	Glu	Leu	Lys	Ser	Glu	Leu	Ala	Gln	Thr	Lys	Leu	Glu	Leu	Glu
				3155					3160					3165	
Thr	Thr	Leu	Lys	Ala	Gln	His	Lys	His	Leu	Lys	Glu	Leu	Glu	Ala	Phe
				3170					3175					3180	
Arg	Leu	Glu	Val	Lys	Asp	Lys	Thr	Asp	Glu	Val	His	Leu	Leu	Asn	Asp
				3185					3190					3200	

Thr Leu Ala Ser Glu Gln Lys Lys Ser Arg Glu Leu Gln Trp Ala Leu
 3205 3210 3215
 Glu Lys Glu Lys Ala Lys Leu Gly Arg Ser Glu Glu Arg Asp Lys Glu
 3220 3225 3230
 Glu Leu Glu Asp Leu Lys Phe Ser Leu Glu Ser Gln Lys Gln Arg Asn
 3235 3240 3245
 Leu Gln Leu Asn Leu Leu Leu Glu Gln Gln Lys Gln Leu Leu Asn Glu
 3250 3255 3260
 Ser Gln Gln Lys Ile Glu Ser Gln Arg Met Leu Tyr Asp Ala Gln Leu
 3265 3270 3275 3280
 Ser Glu Glu Gln Gly Arg Asn Leu Glu Leu Gln Val Leu Leu Glu Ser
 3285 3290 3295
 Glu Lys Val Arg Ile Arg Glu Met Ser Ser Thr Leu Asp Arg Glu Arg
 3300 3305 3310
 Glu Leu His Ala Gln Leu Gln Ser Ser Asp Gly Thr Gly Gln Ser Arg
 3315 3320 3325
 Pro Pro Leu Pro Ser Glu Asp Leu Leu Lys Glu Leu Gln Lys Gln Leu
 3330 3335 3340
 Glu Glu Lys His Ser Arg Ile Val Glu Leu Leu Asn Glu Thr Glu Lys
 3345 3350 3355 3360
 Tyr Lys Leu Asp Ser Leu Gln Thr Arg Gln Gln Met Glu Lys Asp Arg
 3365 3370 3375
 Gln Val His Arg Lys Thr Leu Gln Thr Glu Gln Glu Ala Asn Thr Glu
 3380 3385 3390
 Gly Gln Lys Lys Met His Glu Leu Gln Ser Lys Val Glu Asp Leu Gln
 3395 3400 3405
 Arg Gln Leu Glu Glu Lys Arg Gln Gln Val Tyr Lys Leu Asp Leu Glu
 3410 3415 3420
 Gly Gln Arg Leu Gln Gly Ile Met Gln Glu Phe Gln Lys Gln Glu Leu
 3425 3430 3435 3440
 Glu Arg Glu Glu Lys Arg Glu Ser Arg Arg Ile Leu Tyr Gln Asn Leu
 3445 3450 3455
 Asn Glu Pro Thr Thr Trp Ser Leu Thr Ser Asp Arg Thr Arg Asn Trp
 3460 3465 3470
 Val Leu Gln Gln Lys Ile Glu Gly Glu Thr Lys Glu Ser Asn Tyr Ala
 3475 3480 3485
 Lys Leu Ile Glu Met Asn Gly Gly Gly Thr Gly Cys Asn His Glu Leu
 3490 3495 3500
 Glu Met Ile Arg Gln Lys Leu Gln Cys Val Ala Ser Lys Leu Gln Val
 3505 3510 3515 3520
 Leu Pro Gln Lys Ala Ser Glu Arg Leu Gln Phe Glu Thr Ala Asp Asp
 3525 3530 3535
 Glu Asp Phe Ile Trp Val Gln Glu Asn Ile Asp Glu Ile Ile Leu Gln
 3540 3545 3550
 Leu Gln Lys Leu Thr Gly Gln Gln Gly Glu Glu Pro Ser Leu Val Ser
 3555 3560 3565
 Pro Ser Thr Ser Cys Gly Ser Leu Thr Glu Arg Leu Leu Arg Gln Asn
 3570 3575 3580
 Ala Glu Leu Thr Gly His Ile Ser Gln Leu Thr Glu Glu Lys Asn Asp
 3585 3590 3595 3600
 Leu Arg Asn Met Val Met Lys Leu Glu Glu Gln Ile Arg Trp Tyr Arg
 3605 3610 3615
 Gln Thr Gly Ala Gly Arg Asp Asn Ser Ser Arg Phe Ser Leu Asn Gly
 3620 3625 3630
 Gly Ala Asn Ile Glu Ala Ile Ile Ala Ser Glu Lys Glu Val Trp Asn
 3635 3640 3645
 Arg Glu Lys Leu Thr Leu Gln Lys Ser Leu Lys Arg Ala Glu Ala Glu
 3650 3655 3660
 Val Tyr Lys Leu Lys Ala Glu Leu Arg Asn Asp Ser Leu Leu Gln Thr

3665		3670		3675		3680
Leu Ser Pro Asp	Ser Glu His Val Thr	Leu Lys Arg Ile Tyr Gly Lys				
	3685	3690		3695		
Tyr Leu Arg Ala Glu Ser Phe Arg Lys Ala Leu Ile Tyr Gln Lys Lys						
	3700	3705		3710		
Tyr Leu Leu Leu Leu Leu Gly Gly Phe Gln Glu Cys Glu Asp Ala Thr						
	3715	3720		3725		
Leu Ala Leu Leu Ala Arg Met Gly Gly Gln Pro Ala Phe Thr Asp Leu						
	3730	3735		3740		
Glu Val Ile Thr Asn Arg Pro Lys Gly Phe Thr Arg Phe Arg Ser Ala						
3745	3750	3755		3760		
Val Arg Val Ser Ile Ala Ile Ser Arg Met Lys Phe Leu Val Arg Arg						
	3765	3770		3775		
Trp His Arg Val Thr Gly Ser Val Ser Ile Asn Ile Asn Arg Asp Gly						
	3780	3785		3790		
Phe Gly Leu Asn Gln Gly Ala Glu Lys Thr Asp Ser Phe Tyr His Ser						
	3795	3800		3805		
Ser Gly Gly Leu Glu Leu Tyr Gly Glu Pro Arg His Thr Thr Tyr Arg						
	3810	3815		3820		
Ser Arg Ser Asp Leu Asp Tyr Ile Arg Ser Pro Leu Pro Phe Gln Asn						
3825	3830	3835		3840		
Arg Tyr Pro Gly Thr Pro Ala Asp Phe Asn Pro Gly Ser Leu Ala Cys						
	3845	3850		3855		
Ser Gln Leu Gln Asn Tyr Asp Pro Asp Arg Ala Leu Thr Asp Tyr Ile						
	3860	3865		3870		
Thr Arg Leu Glu Ala Leu Gln Arg Arg Leu Gly Thr Ile Gln Ser Gly						
	3875	3880		3885		
Ser Thr Thr Thr Gln Phe His Ala Gly Met Arg Arg						
	3890	3895				

<210> 5

<211> 12337

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 12055, 12126, 12288

<223> n = A,T,C or G

<400> 5

gaagatggcg	gcggcgggcg	cggtgacggc	gcttcccgtg	cggctgagga	cgatccgcca	60
gtgagcgcg	agactgcttc	cacttcgggc	gggggagccc	cggaccgaat	cggtctctta	120
ggcgtggag	cttgccgtcc	cacctccgtc	caaatcgacc	tttcctttct	atccccaacc	180
acccctcaac	ccctgttttc	ccctgccttc	cttgagagag	ccatggagga	cgaggagaga	240
cagaagaagc	tggaggccgg	caaagccaag	cttgcccagt	ttcgacaaag	aaaagctcag	300
tcggatgggc	agagtccttc	caagaagcag	aaaaaaaaa	gaaaaacgtc	aagcagtaaa	360
catgatgtgt	cagcacacca	tgatttgaat	attgatcaat	cacagtgtaa	tgaaatgtac	420
ataaatagtt	ctcagagagt	agaatcaact	gtgattcctg	aatctacaat	aatgagaact	480
ctacatagtg	gagaaataac	cagtcattgag	cagggcttct	ctgtggaact	ggaaagtga	540
atttcaacca	cagcagatga	ctgcagttca	gaggtaaatg	gttgacagttt	tgtgatgaga	600
acaggaaagc	ctacaaattt	attaagggaa	gaagaatttg	gtgttgatga	ttcttattct	660
gaacaaggag	cacaagacag	tccgactcat	ctagagatga	tggaaagtga	gttggtggg	720
aagcagcatg	agattgaaga	gctaaacaga	gagctggaag	aaatgagggt	tacctatggg	780
actgaaggac	tgcagcagtt	acaagaattt	gaagctgcca	ttaaacaaag	agatggcatt	840
ataaccacgc	tcaactgctaa	tttacaacaa	gcaagaagag	aaaaggatga	gacaatgaga	900
gaatttttag	agttgacaga	acagagtcaa	aaattacaga	ttcaatttca	gcaattacag	960
gctagtga	ctctgagaaa	cagcactcat	agtagcacag	ctgcagaett	actacaagcc	1020

aaacaacaga	tcctcactca	tcaacagcag	cttgaagaac	aagaccactt	attagaagat	1080
tatcagaaaa	agaaagaaga	cttcacaatg	caaattagtt	tcttgcaaga	gaaaattaaa	1140
gtatatgaaa	tggaacaaga	taaaaaagta	gaaaactcaa	ataaagaaga	aatacaggaa	1200
aaggagacaa	tcattgaaga	attaaacaca	aaaataatag	aagaagaaaa	gaaaactctt	1260
gagctaaagg	ataaattaac	aactgctgat	aaattactag	gagaattaca	agaacagatt	1320
gtgcaaaaaga	accaagaaat	aaaaaacatg	aaattagagc	tgactaattc	taagcaaaaa	1380
gaaagacagt	cttctgaaga	aataaaacag	ttaatgggga	cagtcgaaga	acttcagaag	1440
agaaatcata	aagacagcca	gttcgaaact	gatatagtac	aacgaatgga	acaagaaaca	1500
caaagaaagt	tagaacaact	ccgggcagag	ctggatgaga	tgtatgggca	gcagatagt	1560
c aaatgaaac	aagaattaat	aagacaacac	atggcacaga	tggaggaaat	gaaaacacgg	1620
cataagggag	aaatggagaa	tgctttaagg	tcataattcaa	atattacagt	taatgaagat	1680
cagataaagt	taatgaatgt	ggcaataaat	gaactgaata	taaaattgca	agataactaac	1740
tctcaaaagg	aaaaactcaa	ggaagaacta	ggactaattt	tagaagaaaa	gtgtgctcta	1800
cagagacagc	ttgaagacct	tggtgaagaa	ttgagctttt	caagggaaaca	gattcagaga	1860
gctagacaga	caatagctga	acaagaaagt	aaacttaatg	aagcacataa	gtcccttagt	1920
acagtggaa	atttgaaagc	tgagattgtt	tctgcatctg	aatccagaaa	ggaactagaa	1980
ttaaaacatg	aagcagaagt	tacaaattac	aagataaaac	ttgaaatggt	agaaaaagaa	2040
aagaatgctg	tggtagacag	aatggctgaa	tcacaagaag	ctgaattaga	gaggctgaga	2100
acacagcttc	tatttagtca	cgaagaagag	ctttccaaac	tgaaggaa	tttagaaatt	2160
gaacatcgaa	taaatattga	aaaacttaaa	gataatttag	gcattcacta	taaacagcag	2220
atagatggtt	tacagaatga	aatgagtcaa	aagatagaaa	ccatgcagtt	tgaaaaggac	2280
aatttgataa	ctaagcagaa	tcaattaatt	ttggaaattt	caaagctaaa	agatttacag	2340
cagtctcttg	taaattcaaa	gtcagaagaa	atgactcttc	aatcaatga	acttcaaaaa	2400
gaaattgaaa	tactcagaca	agaagaaaaa	gaaaagggtg	cacttgaaca	agaagttcaa	2460
gaattacaac	ttaaaacaga	attgttagaa	aaacagatga	aggaaaaaga	gaatgatctt	2520
caagaaaaat	ttgcacaact	tgaagcagag	aatagcattc	ttaaagatga	aaagaaaacc	2580
cttgaagaca	tggtgaaaat	acatactcct	gttagccaa	aagaaagatt	gattttctta	2640
gactccatta	agtccaaatc	caaagactct	gtgtgggaaa	aagaaataga	aatacttata	2700
gaggaaaatg	aggacctcaa	acaacaatgt	attcagctaa	atgaagagat	tgaaaagcaa	2760
aggaacactt	tttcattttgc	tgaaaaaaac	tttgaagtta	actatcaaga	gttacaagag	2820
gagtatgctt	gcctttctcaa	agtaaaagat	gatttagaag	acagtaaaaa	taaacaggaa	2880
ttagagtata	aaagtaaact	taaagcactt	aatgaagagc	ttcattttgca	aagaataaat	2940
ccaactacag	tgaaaatgaa	aagttctgtc	tttgatgaag	acaaaacttt	tgtagcagaa	3000
acattggaaa	tgggtgaggt	tggtgaaaag	gatacaacag	aactcatgga	aaaacttgag	3060
gtaaccaagc	gagagaaatt	agagctgtca	cagagactgt	ctgatctttc	tgaacaattg	3120
aaacagaaac	atggtgagat	tagttttcta	aatgaagaag	ttaaatcttt	aaagcaagag	3180
aaagaacaag	tttcatttgag	atgtagagag	ctagaaatca	ttattaacca	caacagggga	3240
gaaaatgtac	agtcattgtga	tactcaagta	agctctttat	tagatggagt	tgtgaccatg	3300
acaagcagg	gtgctgaagg	atcagtttct	aaagtaaata	aaagtttttg	tgaagaatca	3360
aaaataatgg	tggaagataa	agtttctttt	gaaaatatga	ctggttgaga	agaaagtaag	3420
caagaacagt	tgatttttga	tcacttacca	tctgtaacaa	aggaatcatc	acttagagca	3480
actcaaccaa	gtgaaaatga	taaacttcag	aaagaactca	atgtacttaa	atcagaacag	3540
aatgatttaa	ggctacagat	ggaagcccaa	cgcattttgcc	tctctctggt	ttattcaact	3600
catgtggatc	aggttcgtga	atatatggaa	aatgaaaaag	ataaagctct	ttgcagctct	3660
aaagaagagc	ttattttttgc	tcaagaggaa	aagatcaagg	aacttcagaa	aatacaccag	3720
ttagaactac	agactatgaa	aacacaagaa	acagggtgat	aaggaaaagg	tttacatctg	3780
ctcattggaa	aacttcaaaa	ggcagtgctc	gaagaatgtt	cttatttttt	acagacttta	3840
tgcagtgctc	ttggtgaata	ttatactcct	gctttaaaat	gtgaagtaaa	tgcagaagac	3900
aaagagaatt	ctggtgatta	catttctgaa	aatgaagatc	cagaattaca	agattataga	3960
tatgaagttc	aagactttca	agaaaatatg	cacactcttc	tcaacaaagt	aacagaagaa	4020
tacaacaaac	tcttggtact	tcaaacacga	ctaagcaaga	tctggggaca	gcagacagat	4080
ggtatgaaac	ttgaattttg	agaagaaaaac	cttccaaaag	aggaaaacaga	gtttttatca	4140
atccattctc	agatgaccaa	tttgggaagc	attgatgtca	atcataaaag	caagttatct	4200
tctctgcaag	atcttgaaaa	aactaaactt	gaagaacaag	ttcaagaatt	agaaagcctc	4260
atatactctt	tgcagcaaca	gttgaaagaa	actgaacaaa	actatgaggc	agagatccac	4320
tgtttacaga	agaggcttca	agctgttagt	gagtccacgg	ttccgccaag	cttacctgtt	4380
gattcggtgg	taattacaga	atctgatgca	cagagaacaa	tgtaccctgg	aagtttgtgtg	4440
aaaaagaata	ttgatggtac	aatagagttt	tctggtgaat	ttggagtga	agaggaaaca	4500
aatatcgtta	agttgcttga	aaaacaatac	caagaacaat	tagaagaaga	agtagctaag	4560

gttattgtgt	caatgagtat	agcattttgct	caacaaactg	aactgtctag	aatatctggg	4620
ggaaaagaaa	atactgcata	atcaaagcaa	gcacatgctg	tgtgtcagca	agaacaacat	4680
tatttttaag	aaatgaaatt	atcacaggat	caaattgggt	ttcagacttt	tgagacagtg	4740
gatgtgaaat	ttaaagaaga	atttaaacca	cttagtaaag	agttaggaga	acatggaaag	4800
gaaattttat	tatcaaatag	tgatcccat	gatataccag	aatcaaagga	ctgtgtgctg	4860
actatttcag	aagaaatggt	ctccaaagat	aaaacattta	tagttagaca	gtctattcat	4920
gatgagattt	cagtgtcaag	catggatgct	tctagacaac	taatgttgaa	tgaagaacag	4980
ttggaagata	tgagacagga	acttgtaacg	caataccaag	aacatcaaca	ggcaacggaa	5040
ttgttaaggc	aagcacatat	gcggcacaa	gagagacagc	gagaagacca	ggaacagcta	5100
caagaagaga	ttaagagact	taatagacaa	ttagcccaga	gacccctccat	agataatgaa	5160
aacctgggtt	cagagagaga	gaggggtgct	ttagaggagc	tggaagcact	aaagcagctg	5220
tctttagctg	gaagagagaa	gctgtgttgt	gagctgagca	acagcagtac	gcaaacacag	5280
aatggaaatg	aaaaccaagg	agaagttgaa	gaacaaacat	ttaaagaaaa	ggaattagac	5340
agaaaacctg	aagatgtgcc	tcctgagatt	ttgtctaatg	aaaggtatgc	actccagaaa	5400
gctaataata	gacttttgaa	gacccctcta	gaagttgtaa	agacaacagc	agctgttgaa	5460
gaaacaattg	gtcgccatgt	ccttgggatt	ctagatagat	ctagtataag	ccagtcattc	5520
gccagcctaa	tttgagggtc	agaagcagag	gcattctgta	agtcattgtg	ccatgaggaa	5580
catacaagag	ttacagatga	atccattccc	tcttattctg	gaagtgtatg	gccaagaaat	5640
gacattaaca	tgtggtcaaa	agtaactgag	gaaggaacag	agctgtcaca	acgacttgtg	5700
aggagtgggt	ttgctggaac	tgaaaatagc	cctgaaaatg	aagaacttat	gctgaacatt	5760
agctctcgac	tacaagcagc	agttgaaaaa	ctcctagaag	ccataagtga	aactagcagt	5820
cagcttgaac	atgcgaaagt	gacacagaca	gagttgatgc	gtgagtcatt	tagacagaaa	5880
caagaagcaa	cagagtccct	taagtgccaa	gaggaacttc	gagagcgcct	tcattgaggag	5940
tccagggcca	gagaacagct	agctgtggag	ctcagtaagg	ctgagggcgt	cattgatggc	6000
tatgcagatg	aaaaaactct	ttttgaaagg	caaattcagg	aaaaaactga	tataatagat	6060
cgtcttgagc	aggagtgtgt	atgtgcaagt	aacagggtgc	aagaattgga	ggcagagcaa	6120
cagcagatcc	aagaagaaa	agaattactg	tccagacaaa	aggaagctat	gaaagcagag	6180
gcaggcccag	ttgaacaaca	attactacag	gagacagaaa	aattaatgaa	ggaaaaacta	6240
gaagtacaat	gtcaagctga	aaaagtacgt	gatgaccttc	aaaaacaagt	gaaagctcta	6300
gaaatagatg	tggaagaaca	agtcagtagg	tttatagagc	tggaacaaga	aaaaataact	6360
gaactaatgg	atttaagaca	gcaaaaccaa	gcattggaaa	agcagttaga	aaaaatgaga	6420
aaattttttag	atgagcaagc	cattgacaga	gaacatgaga	gagatgtatt	ccaacaggaa	6480
atacagaaac	tagaacagca	acttaagggt	gttcctcgat	tccagcctat	cagtgaacat	6540
caaactagag	aggttgaaca	gttagcaaat	catctgaaag	aaaaaacaga	caaatgcagt	6600
gagcttttgc	tctctaaaga	gcagcttcaa	agggatatac	aagaaaggaa	tgaagaaata	6660
gagaaactgg	agttcagagt	aagagaactg	gagcaggcgc	ttcttgtgag	tgcatagata	6720
tttcaaaagg	tagaggaccg	aaaacacttt	ggagctgtag	aagctaacc	agaattgttc	6780
ctagaagtac	aattgcaggc	tgaaacagat	gccatagaca	gaaaggaaaa	agagattaca	6840
aacttagaag	agcaattaga	acagtttaga	gaagaactgg	aaaataagaa	tgaagaagtt	6900
caacaattac	atatgcaatt	agaaatacag	aaaaaggaa	ctactaccgc	cctacaagaa	6960
cttgaacagg	aaaacaaatt	atttaaggat	gacatggaga	aactgggact	tgccataaag	7020
gaatctgatg	ccatgtctac	tcaagaccaa	catgtgctat	ttgggaaatt	tgctcaataa	7080
atacaggaaa	aagaggtaga	aattgaccaa	ttaaatgaac	aagttaacgaa	actccagcag	7140
caacttaaaa	ttacaacaga	taacaagggt	attgaagaaa	aaaatgaact	gataagggat	7200
cttgaaaccc	aaatagaatg	tttgatgagt	gatcaagaat	gtgtgaagag	aaatagagaa	7260
gaagaaatag	agcagctcaa	tgaagtgatt	gaaaaacttc	aacagggaatt	ggcaaatatt	7320
ggacagaaga	catcaatgaa	tgctcattcc	ctctcagaag	aagcagacag	tttaaaacat	7380
caattggatg	tggttatagc	tgaaaagctg	gccttggaa	agcaagtaga	aaccgcta	7440
gaagaaatga	ccttcattgaa	aaatgtactt	aaagaaacca	attttaaaat	gaatcagcta	7500
acacaggaat	tattcagctt	aaagagagaa	cgtgaaagtg	tggaagagat	tcaaagcata	7560
ccagagaata	gtgttaacgt	ggctatagat	catctgagca	aagacaaacc	tgaactagaa	7620
gtagtcctta	cagaggatgc	tcttaaatcc	ctagaaaatc	agacataact	caaatctttt	7680
gaagaaaatg	gcaaagggtc	cataattaat	ttggaacaaa	ggttgctaca	acttgagagc	7740
actgttagtg	caaaggactt	agaacttacc	cagtgttata	aacaaataaa	agacatgcaa	7800
gaacaaggcc	agtttgaaac	agaaatgctt	caaaagagaa	ttgtaaacct	acagaaaaat	7860
gttgaagaaa	aagtggctgc	tgctcttgct	agtcaaatcc	aacttgaggc	agttcaggaa	7920
tatgcaaaat	tctgtcaaga	taatcaaaca	atttcattcag	aacctgaaag	aacaaatatt	7980
cagaatttaa	atcaactaag	agaagatgag	ttgggggtcag	atatatcagc	attaaccttg	8040
agaatatcag	aattagaaag	ccagggttgt	gaaatgcata	ctagtttgat	tttagaaaaa	8100

gaacaagtag	aaattgcaga	aaaaaatggt	ttagaaaaag	aaaagaagct	gctagaacta	8160
cagaagctat	tggagggcaa	tgagaaaaaa	cagagagaga	aagaaaagaa	aagaagccct	8220
caagatggtg	aagttctcaa	gacaactact	gagctatttc	atagcaatga	agaaagtgga	8280
ttttttaatg	aactcgaggc	tcttagagct	gaatcagtg	ctaccaaagc	agaacttgcc	8340
agttataaag	aaaaggctga	aaaacttcaa	gaagagcttt	tggtaaaaga	aacaaatatg	8400
acatctcttc	agaaagactt	aagccaagtt	agggatcacc	tcgcagaggc	aaaagagaaa	8460
ttgtccattt	tagaaaaaga	agatgagact	gaggtacaag	aaagcaaaaa	ggcctgcatg	8520
tttgagccac	ttcctataaa	actgagtaag	agcattgcat	cccagacaga	tgggactctg	8580
aagatcagta	gcagcaatca	gactccacaa	attcttggtt	aaaatgcagg	aatacaaat	8640
aatttacaga	gtgaatgttc	ctcagaagaa	gttactgaaa	taatcagtca	gtttactgaa	8700
aaaattgaga	agatgcaaga	actacatgct	gctgaaattt	tggacatgga	atccagacat	8760
atttcagaaa	ctgaaacctt	aaagagggaa	cactatgttg	ccgttcagtt	actgaaagag	8820
gaatgtggta	ccttgaaggc	agtgatacag	tgtctgagaa	gtaaagaggg	atcctcaatt	8880
cctgagctag	cacattctga	tgttaccag	actagagaaa	tatgctccag	tgattctgga	8940
tcagactggg	gtcagggaat	ttatcttaca	cacagtcagg	gatttgacat	agcatcagaa	9000
ggccgaggag	aagaaagtga	aagtgcaaca	gattcccttc	caaagaaaat	aaagggatta	9060
ctgagagctg	tccataatga	aggcatgcag	gtgctttctc	tcaactgagtc	tccctatagt	9120
gatggagagg	accattctat	tcagcagggt	tcagaacctt	ggctagaaga	gagaaaagct	9180
tacatcaata	caatctcatc	tctaaaggat	ttaattacaa	agatgcaact	gcaaagagaa	9240
gccgaggttt	atgatgttc	tcaatctcat	gagagcttct	cagactggcg	aggtgaacta	9300
ctgcttgccc	ttcaacaagt	tttcttagaa	gagcgtagt	ttttactagc	agcatttcgg	9360
acggagctga	cagctctagg	tactacagat	gcagttgggt	tactaaaactg	tttggaacag	9420
agaatacaag	aacaggggtg	tgaatatcaa	gcagctatgg	aatgcctcca	gaaagcagat	9480
agaaggagtt	tgttatctga	aattcaggca	ctgcatgcac	aaatgaatgg	taggaaaatt	9540
actctgaaaa	gagaacaaga	gagtgagaaa	ccaagccaag	aactcttgga	atataatata	9600
cagcagaagc	agtctcaaat	gctggagatg	caagtggagc	tcagcagtat	gaaagacaga	9660
gcaacggaac	tgcaaggagca	gctgagttct	gagaaaatgg	tggttgctga	actgaagagt	9720
gagcttgcc	aaactaaatt	ggaactagaa	acaacactca	aggcacagca	taaacacct	9780
aaagaattgg	aggctttcag	gttggaagtt	aaagataaga	cagatgaagt	acatttgctt	9840
aatgacacat	tagcaagtga	acagaaaaaa	tcaagagagc	tccagtgggc	tttgagagaa	9900
gagaaagcca	agttgggacg	cagtgaagaa	cgggataaag	aagaacttga	ggatctgaag	9960
ttttcacttg	agagtcagaa	acaaaggaat	cttcagctaa	atctactttt	ggaacaacag	10020
aaacaactac	tgaacgaatc	ccagcaaaaa	atagaatcac	agagaatgct	atatgatgcc	10080
cagttgtcag	aagaacaagg	tcgaaaactta	gagcttcagg	tacttcttga	atctgagaaa	10140
gttcgaattc	gggaaatgag	tagtacccta	gatagggagc	gggaattgca	cgcacagctg	10200
cagagcagtg	atggtactgg	acagtctcgg	ccacccttgc	cctcagagga	cctactgaaa	10260
gagctgcaga	aacagctaga	ggaaaaaac	agtcgcatag	tagaattggt	aaatgagact	10320
gaaaaatata	aactggattc	tttgcaaaaa	cgacagcaaa	tggaaaaaga	taggcaggtt	10380
cacaggaaaa	cactgcagac	agaacaggag	gccaacactg	agggacagaa	aaaaatgcat	10440
gagctccagt	ccaaagtgga	agatcttcag	cgccagctgg	aagagaaaag	acaacaagtt	10500
tataagttag	accttgaagg	acagcgacta	caaggaaatca	tgcagggaatt	ccagaagcaa	10560
gaactagaac	gagaagaaaa	acgagaaaag	agaagaattc	tgtatcagaa	ccttaatgag	10620
ccaaccacgt	ggagcttaac	cagtgataga	actagaaatt	gggttcttca	acagaaaata	10680
gaaggagaaa	caaaagaatc	aaactacgct	aaattgattg	aatgaatgg	aggaggaacc	10740
ggctgtaatc	atgaattaga	aatgatcaga	caaaagcttc	aatgtgtagc	ttcaaaaact	10800
caggttctac	cccagaaaag	ctctgagaga	ctacagtttg	aaacagcaga	tgatgaagat	10860
ttcatttggg	ttcaggaaaa	tattgatgaa	attatttttac	aactacagaa	attaactggc	10920
cagcaagggtg	aagagcccag	cttggtgtcc	ccaagtactt	cttggtggctc	attgactgaa	10980
agactactga	gacaaaatgc	tgagctgaca	gggcataatca	gtcaactgac	tgaagagaag	11040
aatgacttaa	ggaacatgg	tatgaagctg	gaagagcaga	tcaggtggta	tcgacagaca	11100
ggagctggta	gagataaatt	ttocaggttt	tcattgaatg	gtggtgccaa	cattgaagcc	11160
atcattgcct	ctgaaaaaga	agtatggaac	agagaaaaat	tgactctcca	gaaatctttg	11220
aaaagggcag	aggctgaagt	atacaaaactg	aaagctgaac	taagaaatga	ctctttactt	11280
caaactctga	gccctgattc	tgaacatgtc	actttaaaga	gaatttatgg	taaatacttg	11340
agggcagaaa	ggttctgaaa	ggctctcatt	taccagaaga	aatacctgct	gctgttactg	11400
ggtgggttcc	aggaatgtga	agatgccacc	ttggccctgc	ttgcccggat	gggggggag	11460
ccagctttca	cggatctaga	ggtgatcacc	aatcgcccaa	agggcttcac	cagggttccg	11520
tcggccgtca	gagtatccat	tgcaatttcc	agaatgaaat	ttttggttcg	acggtggcat	11580
cgagtcacag	gttctgtttc	catcaatatt	aacagagatg	gctttggact	gaatcaaggt	11640

```

gcagaaaaga ctgactcatt ttatcattct tctgggtgggc tggagttata tggagaacca 11700
agacatacta cgtatcgctc aagatcagat ctggactata ttaggtcccc ttaccatttt 11760
cagaataggt acccaggcac tccagctgat ttcaatcctg gttctttagc atgttctcag 11820
cttcagaatt acgatcctga cagagcccta acagattata tcaactcggct agaggcactg 11880
caaagacgac ttggaactat acagtcaggt gctctgagtt taaccacatc ttggcagcac 11940
cacagtgcga gacccacagc tccccttttc tttgaaattc tttcacactc attaggataa 12000
tcaaagcttc cagtttagtg catgagctaa ttattaagtt agccaaagct taaanttttg 12060
taaccagcag agaaactgac tttaaataat ttaagtgaat atatgattta tcaccccaga 12120
tcccantcct cccaaaaatg atttcctact atgttcattc agcggactga tgacacaaaa 12180
tgcacaatga gcaccagtgt gcaaggtact ctgagtttac agagcctaac tggagaacgt 12240
attcctaagt agcgcattggc agaaagtggg aaggccgtgc cgcagcantc cagcctgggc 12300
agcagagcga gaccctgtct caaagaaaaa aaaaaaaa 12337

```

<210> 6

<211> 3925

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
 1           5           10           15
Leu Ala Gln Phe Arg Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro
 20           25           30
Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
 35           40           45
Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
 50           55           60
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
 65           70           75           80
Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
 85           90           95
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100           105           110
Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115           120           125
Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
130           135           140
Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145           150           155           160
Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
165           170           175
Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
180           185           190
Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
195           200           205
Gln Leu Thr Ala Asn Leu Gln Ala Arg Arg Glu Lys Asp Glu Thr
210           215           220
Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225           230           235           240
Gln Phe Gln Gln Leu Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His
245           250           255
Ser Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr
260           265           270
His Gln Gln Gln Leu Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln
275           280           285
Lys Lys Lys Glu Asp Phe Thr Met Gln Ile Ser Phe Leu Gln Glu Lys
290           295           300
Ile Lys Val Tyr Glu Met Glu Gln Asp Lys Lys Val Glu Asn Ser Asn
305           310           315           320

```

Lys Glu Glu Ile Gln Glu Lys Glu Thr Ile Ile Glu Glu Leu Asn Thr
 325 330 335
 Lys Ile Ile Glu Glu Glu Lys Lys Thr Leu Glu Leu Lys Asp Lys Leu
 340 345 350
 Thr Thr Ala Asp Lys Leu Leu Gly Glu Leu Gln Glu Gln Ile Val Gln
 355 360 365
 Lys Asn Gln Glu Ile Lys Asn Met Lys Leu Glu Leu Thr Asn Ser Lys
 370 375 380
 Gln Lys Glu Arg Gln Ser Ser Glu Glu Ile Lys Gln Leu Met Gly Thr
 385 390 395 400
 Val Glu Glu Leu Gln Lys Arg Asn His Lys Asp Ser Gln Phe Glu Thr
 405 410 415
 Asp Ile Val Gln Arg Met Glu Gln Glu Thr Gln Arg Lys Leu Glu Gln
 420 425 430
 Leu Arg Ala Glu Leu Asp Glu Met Tyr Gly Gln Gln Ile Val Gln Met
 435 440 445
 Lys Gln Glu Leu Ile Arg Gln His Met Ala Gln Met Glu Glu Met Lys
 450 455 460
 Thr Arg His Lys Gly Glu Met Glu Asn Ala Leu Arg Ser Tyr Ser Asn
 465 470 475 480
 Ile Thr Val Asn Glu Asp Gln Ile Lys Leu Met Asn Val Ala Ile Asn
 485 490 495
 Glu Leu Asn Ile Lys Leu Gln Asp Thr Asn Ser Gln Lys Glu Lys Leu
 500 505 510
 Lys Glu Glu Leu Gly Leu Ile Leu Glu Glu Lys Cys Ala Leu Gln Arg
 515 520 525
 Gln Leu Glu Asp Leu Val Glu Glu Leu Ser Phe Ser Arg Glu Gln Ile
 530 535 540
 Gln Arg Ala Arg Gln Thr Ile Ala Glu Gln Glu Ser Lys Leu Asn Glu
 545 550 555 560
 Ala His Lys Ser Leu Ser Thr Val Glu Asp Leu Lys Ala Glu Ile Val
 565 570 575
 Ser Ala Ser Glu Ser Arg Lys Glu Leu Glu Leu Lys His Glu Ala Glu
 580 585 590
 Val Thr Asn Tyr Lys Ile Lys Leu Glu Met Leu Glu Lys Glu Lys Asn
 595 600 605
 Ala Val Leu Asp Arg Met Ala Glu Ser Gln Glu Ala Glu Leu Glu Arg
 610 615 620
 Leu Arg Thr Gln Leu Leu Phe Ser His Glu Glu Glu Leu Ser Lys Leu
 625 630 635 640
 Lys Glu Asp Leu Glu Ile Glu His Arg Ile Asn Ile Glu Lys Leu Lys
 645 650 655
 Asp Asn Leu Gly Ile His Tyr Lys Gln Gln Ile Asp Gly Leu Gln Asn
 660 665 670
 Glu Met Ser Gln Lys Ile Glu Thr Met Gln Phe Glu Lys Asp Asn Leu
 675 680 685
 Ile Thr Lys Gln Asn Gln Leu Ile Leu Glu Ile Ser Lys Leu Lys Asp
 690 695 700
 Leu Gln Gln Ser Leu Val Asn Ser Lys Ser Glu Glu Met Thr Leu Gln
 705 710 715 720
 Ile Asn Glu Leu Gln Lys Glu Ile Glu Ile Leu Arg Gln Glu Glu Lys
 725 730 735
 Glu Lys Gly Thr Leu Glu Gln Glu Val Gln Glu Leu Gln Leu Lys Thr
 740 745 750
 Glu Leu Leu Glu Lys Gln Met Lys Glu Lys Glu Asn Asp Leu Gln Glu
 755 760 765
 Lys Phe Ala Gln Leu Glu Ala Glu Asn Ser Ile Leu Lys Asp Glu Lys
 770 775 780
 Lys Thr Leu Glu Asp Met Leu Lys Ile His Thr Pro Val Ser Gln Glu

785		790		795		800
Glu Arg Leu Ile	Phe Leu Asp Ser Ile	Lys Ser Lys Ser Lys Asp Ser				
	805	810			815	
Val Trp Glu Lys	Glu Ile Glu Ile Leu Ile Glu Glu Asn Glu Asp Leu					
	820	825			830	
Lys Gln Gln Cys	Ile Gln Leu Asn Glu Glu Ile Glu Lys Gln Arg Asn					
	835	840			845	
Thr Phe Ser Phe	Ala Glu Lys Asn Phe Glu Val Asn Tyr Gln Glu Leu					
	850	855			860	
Gln Glu Glu Tyr	Ala Cys Leu Leu Lys Val Lys Asp Asp Leu Glu Asp					
	865	870			875	880
Ser Lys Asn Lys	Gln Glu Leu Glu Tyr Lys Ser Lys Leu Lys Ala Leu					
	885	890			895	
Asn Glu Glu Leu	His Leu Gln Arg Ile Asn Pro Thr Thr Val Lys Met					
	900	905			910	
Lys Ser Ser Val	Phe Asp Glu Asp Lys Thr Phe Val Ala Glu Thr Leu					
	915	920			925	
Glu Met Gly Glu	Val Val Glu Lys Asp Thr Thr Glu Leu Met Glu Lys					
	930	935			940	
Leu Glu Val Thr	Lys Arg Glu Lys Leu Glu Leu Ser Gln Arg Leu Ser					
	945	950			955	960
Asp Leu Ser Glu	Gln Leu Lys Gln Lys His Gly Glu Ile Ser Phe Leu					
	965	970			975	
Asn Glu Glu Val	Lys Ser Leu Lys Gln Glu Lys Glu Gln Val Ser Leu					
	980	985			990	
Arg Cys Arg Glu	Leu Glu Ile Ile Ile Asn His Asn Arg Ala Glu Asn					
	995	1000			1005	
Val Gln Ser Cys	Asp Thr Gln Val Ser Ser Leu Leu Asp Gly Val Val					
	1010	1015			1020	
Thr Met Thr Ser	Arg Gly Ala Glu Gly Ser Val Ser Lys Val Asn Lys					
	1025	1030			1035	1040
Ser Phe Gly Glu	Glu Ser Lys Ile Met Val Glu Asp Lys Val Ser Phe					
	1045	1050			1055	
Glu Asn Met Thr	Val Gly Glu Glu Ser Lys Gln Glu Gln Leu Ile Leu					
	1060	1065			1070	
Asp His Leu Pro	Ser Val Thr Lys Glu Ser Ser Leu Arg Ala Thr Gln					
	1075	1080			1085	
Pro Ser Glu Asn	Asp Lys Leu Gln Lys Glu Leu Asn Val Leu Lys Ser					
	1090	1095			1100	
Glu Gln Asn Asp	Leu Arg Leu Gln Met Glu Ala Gln Arg Ile Cys Leu					
	1105	1110			1115	1120
Ser Leu Val Tyr	Ser Thr His Val Asp Gln Val Arg Glu Tyr Met Glu					
	1125	1130			1135	
Asn Glu Lys Asp	Lys Ala Leu Cys Ser Leu Lys Glu Glu Leu Ile Phe					
	1140	1145			1150	
Ala Gln Glu Lys	Ile Lys Glu Leu Gln Lys Ile His Gln Leu Glu					
	1155	1160			1165	
Leu Gln Thr Met	Lys Thr Gln Glu Thr Gly Asp Glu Gly Lys Pro Leu					
	1170	1175			1180	
His Leu Leu Ile	Gly Lys Leu Gln Lys Ala Val Ser Glu Glu Cys Ser					
	1185	1190			1195	1200
Tyr Phe Leu Gln	Thr Leu Cys Ser Val Leu Gly Glu Tyr Tyr Thr Pro					
	1205	1210			1215	
Ala Leu Lys Cys	Glu Val Asn Ala Glu Asp Lys Glu Asn Ser Gly Asp					
	1220	1225			1230	
Tyr Ile Ser Glu	Asn Glu Asp Pro Glu Leu Gln Asp Tyr Arg Tyr Glu					
	1235	1240			1245	
Val Gln Asp Phe	Gln Glu Asn Met His Thr Leu Leu Asn Lys Val Thr					
	1250	1255			1260	

Glu Glu Tyr Asn Lys Leu Leu Val Leu Gln Thr Arg Leu Ser Lys Ile
 1265 1270 1275 1280
 Trp Gly Gln Gln Thr Asp Gly Met Lys Leu Glu Phe Gly Glu Glu Asn
 1285 1290 1295
 Leu Pro Lys Glu Glu Thr Glu Phe Leu Ser Ile His Ser Gln Met Thr
 1300 1305 1310
 Asn Leu Glu Asp Ile Asp Val Asn His Lys Ser Lys Leu Ser Ser Leu
 1315 1320 1325
 Gln Asp Leu Glu Lys Thr Lys Leu Glu Glu Gln Val Gln Glu Leu Glu
 1330 1335 1340
 Ser Leu Ile Ser Ser Leu Gln Gln Gln Leu Lys Glu Thr Glu Gln Asn
 1345 1350 1355 1360
 Tyr Glu Ala Glu Ile His Cys Leu Gln Lys Arg Leu Gln Ala Val Ser
 1365 1370 1375
 Glu Ser Thr Val Pro Pro Ser Leu Pro Val Asp Ser Val Val Ile Thr
 1380 1385 1390
 Glu Ser Asp Ala Gln Arg Thr Met Tyr Pro Gly Ser Cys Val Lys Lys
 1395 1400 1405
 Asn Ile Asp Gly Thr Ile Glu Phe Ser Gly Glu Phe Gly Val Lys Glu
 1410 1415 1420
 Glu Thr Asn Ile Val Lys Leu Leu Glu Lys Gln Tyr Gln Glu Gln Leu
 1425 1430 1435 1440
 Glu Glu Glu Val Ala Lys Val Ile Val Ser Met Ser Ile Ala Phe Ala
 1445 1450 1455
 Gln Gln Thr Glu Leu Ser Arg Ile Ser Gly Gly Lys Glu Asn Thr Ala
 1460 1465 1470
 Ser Ser Lys Gln Ala His Ala Val Cys Gln Gln Glu Gln His Tyr Phe
 1475 1480 1485
 Asn Glu Met Lys Leu Ser Gln Asp Gln Ile Gly Phe Gln Thr Phe Glu
 1490 1495 1500
 Thr Val Asp Val Lys Phe Lys Glu Glu Phe Lys Pro Leu Ser Lys Glu
 1505 1510 1515 1520
 Leu Gly Glu His Gly Lys Glu Ile Leu Leu Ser Asn Ser Asp Pro His
 1525 1530 1535
 Asp Ile Pro Glu Ser Lys Asp Cys Val Leu Thr Ile Ser Glu Glu Met
 1540 1545 1550
 Phe Ser Lys Asp Lys Thr Phe Ile Val Arg Gln Ser Ile His Asp Glu
 1555 1560 1565
 Ile Ser Val Ser Ser Met Asp Ala Ser Arg Gln Leu Met Leu Asn Glu
 1570 1575 1580
 Glu Gln Leu Glu Asp Met Arg Gln Glu Leu Val Arg Gln Tyr Gln Glu
 1585 1590 1595 1600
 His Gln Gln Ala Thr Glu Leu Leu Arg Gln Ala His Met Arg Gln Met
 1605 1610 1615
 Glu Arg Gln Arg Glu Asp Gln Glu Gln Leu Gln Glu Glu Ile Lys Arg
 1620 1625 1630
 Leu Asn Arg Gln Leu Ala Gln Arg Ser Ser Ile Asp Asn Glu Asn Leu
 1635 1640 1645
 Val Ser Glu Arg Glu Arg Val Leu Leu Glu Glu Leu Glu Ala Leu Lys
 1650 1655 1660
 Gln Leu Ser Leu Ala Gly Arg Glu Lys Leu Cys Cys Glu Leu Arg Asn
 1665 1670 1675 1680
 Ser Ser Thr Gln Thr Gln Asn Gly Asn Glu Asn Gln Gly Glu Val Glu
 1685 1690 1695
 Glu Gln Thr Phe Lys Glu Lys Glu Leu Asp Arg Lys Pro Glu Asp Val
 1700 1705 1710
 Pro Pro Glu Ile Leu Ser Asn Glu Arg Tyr Ala Leu Gln Lys Ala Asn
 1715 1720 1725
 Asn Arg Leu Leu Lys Ile Leu Leu Glu Val Val Lys Thr Thr Ala Ala

1730	1735	1740
Val Glu Glu Thr Ile Gly Arg His Val Leu Gly Ile Leu Asp Arg Ser		
1745	1750	1755
Ser Lys Ser Gln Ser Ser Ala Ser Leu Ile Trp Arg Ser Glu Ala Glu		1760
	1765	1770
Ala Ser Val Lys Ser Cys Val His Glu Glu His Thr Arg Val Thr Asp		1775
	1780	1785
Glu Ser Ile Pro Ser Tyr Ser Gly Ser Asp Met Pro Arg Asn Asp Ile		1790
	1795	1800
Asn Met Trp Ser Lys Val Thr Glu Glu Gly Thr Glu Leu Ser Gln Arg		1805
	1810	1815
Leu Val Arg Ser Gly Phe Ala Gly Thr Glu Ile Asp Pro Glu Asn Glu		1820
1825	1830	1835
Glu Leu Met Leu Asn Ile Ser Ser Arg Leu Gln Ala Ala Val Glu Lys		1840
	1845	1850
Leu Leu Glu Ala Ile Ser Glu Thr Ser Ser Gln Leu Glu His Ala Lys		1855
	1860	1865
Val Thr Gln Thr Glu Leu Met Arg Glu Ser Phe Arg Gln Lys Gln Glu		1870
	1875	1880
Ala Thr Glu Ser Leu Lys Cys Gln Glu Glu Leu Arg Glu Arg Leu His		1885
	1890	1895
Glu Glu Ser Arg Ala Arg Glu Gln Leu Ala Val Glu Leu Ser Lys Ala		1900
1905	1910	1915
Glu Gly Val Ile Asp Gly Tyr Ala Asp Glu Lys Thr Leu Phe Glu Arg		1920
	1925	1930
Gln Ile Gln Glu Lys Thr Asp Ile Ile Asp Arg Leu Glu Gln Glu Leu		1935
	1940	1945
Leu Cys Ala Ser Asn Arg Leu Gln Glu Leu Glu Ala Glu Gln Gln Gln		1950
	1955	1960
Ile Gln Glu Glu Arg Glu Leu Leu Ser Arg Gln Lys Glu Ala Met Lys		1965
	1970	1975
Ala Glu Ala Gly Pro Val Glu Gln Gln Leu Leu Gln Glu Thr Glu Lys		1980
1985	1990	1995
Leu Met Lys Glu Lys Leu Glu Val Gln Cys Gln Ala Glu Lys Val Arg		2000
	2005	2010
Asp Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile Asp Val Glu Glu		2015
	2020	2025
Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu Lys Asn Thr Glu Leu		2030
	2035	2040
Met Asp Leu Arg Gln Gln Asn Gln Ala Leu Glu Lys Gln Leu Glu Lys		2045
	2050	2055
Met Arg Lys Phe Leu Asp Glu Gln Ala Ile Asp Arg Glu His Glu Arg		2060
2065	2070	2075
Asp Val Phe Gln Gln Glu Ile Gln Lys Leu Glu Gln Gln Leu Lys Val		2080
	2085	2090
Val Pro Arg Phe Gln Pro Ile Ser Glu His Gln Thr Arg Glu Val Glu		2095
	2100	2105
Gln Leu Ala Asn His Leu Lys Glu Lys Thr Asp Lys Cys Ser Glu Leu		2110
	2115	2120
Leu Leu Ser Lys Glu Gln Leu Gln Arg Asp Ile Gln Glu Arg Asn Glu		2125
	2130	2135
Glu Ile Glu Lys Leu Glu Phe Arg Val Arg Glu Leu Glu Gln Ala Leu		2140
2145	2150	2155
Leu Val Ser Ala Asp Thr Phe Gln Lys Val Glu Asp Arg Lys His Phe		2160
	2165	2170
Gly Ala Val Glu Ala Lys Pro Glu Leu Ser Leu Glu Val Gln Leu Gln		2175
	2180	2185
Ala Glu Arg Asp Ala Ile Asp Arg Lys Glu Lys Glu Ile Thr Asn Leu		2190
2195	2200	2205

Glu Glu Gln Leu Glu Gln Phe Arg Glu Glu Leu Glu Asn Lys Asn Glu
 2210 2215 2220
 Glu Val Gln Gln Leu His Met Gln Leu Glu Ile Gln Lys Lys Glu Ser
 2225 2230 2235 2240
 Thr Thr Arg Leu Gln Glu Leu Glu Gln Glu Asn Lys Leu Phe Lys Asp
 2245 2250 2255
 Asp Met Glu Lys Leu Gly Leu Ala Ile Lys Glu Ser Asp Ala Met Ser
 2260 2265 2270
 Thr Gln Asp Gln His Val Leu Phe Gly Lys Phe Ala Gln Ile Ile Gln
 2275 2280 2285
 Glu Lys Glu Val Glu Ile Asp Gln Leu Asn Glu Gln Val Thr Lys Leu
 2290 2295 2300
 Gln Gln Gln Leu Lys Ile Thr Thr Asp Asn Lys Val Ile Glu Glu Lys
 2305 2310 2315 2320
 Asn Glu Leu Ile Arg Asp Leu Glu Thr Gln Ile Glu Cys Leu Met Ser
 2325 2330 2335
 Asp Gln Glu Cys Val Lys Arg Asn Arg Glu Glu Glu Ile Glu Gln Leu
 2340 2345 2350
 Asn Glu Val Ile Glu Lys Leu Gln Gln Glu Leu Ala Asn Ile Gly Gln
 2355 2360 2365
 Lys Thr Ser Met Asn Ala His Ser Leu Ser Glu Glu Ala Asp Ser Leu
 2370 2375 2380
 Lys His Gln Leu Asp Val Val Ile Ala Glu Lys Leu Ala Leu Glu Gln
 2385 2390 2395 2400
 Gln Val Glu Thr Ala Asn Glu Glu Met Thr Phe Met Lys Asn Val Leu
 2405 2410 2415
 Lys Glu Thr Asn Phe Lys Met Asn Gln Leu Thr Gln Glu Leu Phe Ser
 2420 2425 2430
 Leu Lys Arg Glu Arg Glu Ser Val Glu Lys Ile Gln Ser Ile Pro Glu
 2435 2440 2445
 Asn Ser Val Asn Val Ala Ile Asp His Leu Ser Lys Asp Lys Pro Glu
 2450 2455 2460
 Leu Glu Val Val Leu Thr Glu Asp Ala Leu Lys Ser Leu Glu Asn Gln
 2465 2470 2475 2480
 Thr Tyr Phe Lys Ser Phe Glu Glu Asn Gly Lys Gly Ser Ile Ile Asn
 2485 2490 2495
 Leu Glu Thr Arg Leu Leu Gln Leu Glu Ser Thr Val Ser Ala Lys Asp
 2500 2505 2510
 Leu Glu Leu Thr Gln Cys Tyr Lys Gln Ile Lys Asp Met Gln Glu Gln
 2515 2520 2525
 Gly Gln Phe Glu Thr Glu Met Leu Gln Lys Lys Ile Val Asn Leu Gln
 2530 2535 2540
 Lys Ile Val Glu Glu Lys Val Ala Ala Ala Leu Val Ser Gln Ile Gln
 2545 2550 2555 2560
 Leu Glu Ala Val Gln Glu Tyr Ala Lys Phe Cys Gln Asp Asn Gln Thr
 2565 2570 2575
 Ile Ser Ser Glu Pro Glu Arg Thr Asn Ile Gln Asn Leu Asn Gln Leu
 2580 2585 2590
 Arg Glu Asp Glu Leu Gly Ser Asp Ile Ser Ala Leu Thr Leu Arg Ile
 2595 2600 2605
 Ser Glu Leu Glu Ser Gln Val Val Glu Met His Thr Ser Leu Ile Leu
 2610 2615 2620
 Glu Lys Glu Gln Val Glu Ile Ala Glu Lys Asn Val Leu Glu Lys Glu
 2625 2630 2635 2640
 Lys Lys Leu Leu Glu Leu Gln Lys Leu Leu Glu Gly Asn Glu Lys Lys
 2645 2650 2655
 Gln Arg Glu Lys Glu Lys Lys Arg Ser Pro Gln Asp Val Glu Val Leu
 2660 2665 2670
 Lys Thr Thr Thr Glu Leu Phe His Ser Asn Glu Glu Ser Gly Phe Phe

2675	2680	2685
Asn Glu Leu Glu Ala Leu Arg Ala Glu Ser Val Ala Thr Lys Ala Glu		
2690	2695	2700
Leu Ala Ser Tyr Lys Glu Lys Ala Glu Lys Leu Gln Glu Glu Leu Leu		
2705	2710	2715
Val Lys Glu Thr Asn Met Thr Ser Leu Gln Lys Asp Leu Ser Gln Val		
2725	2730	2735
Arg Asp His Leu Ala Glu Ala Lys Glu Lys Leu Ser Ile Leu Glu Lys		
2740	2745	2750
Glu Asp Glu Thr Glu Val Gln Glu Ser Lys Lys Ala Cys Met Phe Glu		
2755	2760	2765
Pro Leu Pro Ile Lys Leu Ser Lys Ser Ile Ala Ser Gln Thr Asp Gly		
2770	2775	2780
Thr Leu Lys Ile Ser Ser Ser Asn Gln Thr Pro Gln Ile Leu Val Lys		
2785	2790	2795
Asn Ala Gly Ile Gln Ile Asn Leu Gln Ser Glu Cys Ser Ser Glu Glu		
2805	2810	2815
Val Thr Glu Ile Ile Ser Gln Phe Thr Glu Lys Ile Glu Lys Met Gln		
2820	2825	2830
Glu Leu His Ala Ala Glu Ile Leu Asp Met Glu Ser Arg His Ile Ser		
2835	2840	2845
Glu Thr Glu Thr Leu Lys Arg Glu His Tyr Val Ala Val Gln Leu Leu		
2850	2855	2860
Lys Glu Glu Cys Gly Thr Leu Lys Ala Val Ile Gln Cys Leu Arg Ser		
2865	2870	2875
Lys Glu Gly Ser Ser Ile Pro Glu Leu Ala His Ser Asp Ala Tyr Gln		
2885	2890	2895
Thr Arg Glu Ile Cys Ser Ser Asp Ser Gly Ser Asp Trp Gly Gln Gly		
2900	2905	2910
Ile Tyr Leu Thr His Ser Gln Gly Phe Asp Ile Ala Ser Glu Gly Arg		
2915	2920	2925
Gly Glu Glu Ser Glu Ser Ala Thr Asp Ser Phe Pro Lys Lys Ile Lys		
2930	2935	2940
Gly Leu Leu Arg Ala Val His Asn Glu Gly Met Gln Val Leu Ser Leu		
2945	2950	2955
Thr Glu Ser Pro Tyr Ser Asp Gly Glu Asp His Ser Ile Gln Gln Val		
2965	2970	2975
Ser Glu Pro Trp Leu Glu Glu Arg Lys Ala Tyr Ile Asn Thr Ile Ser		
2980	2985	2990
Ser Leu Lys Asp Leu Ile Thr Lys Met Gln Leu Gln Arg Glu Ala Glu		
2995	3000	3005
Val Tyr Asp Ser Ser Gln Ser His Glu Ser Phe Ser Asp Trp Arg Gly		
3010	3015	3020
Glu Leu Leu Leu Ala Leu Gln Gln Val Phe Leu Glu Glu Arg Ser Val		
3025	3030	3035
Leu Leu Ala Ala Phe Arg Thr Glu Leu Thr Ala Leu Gly Thr Thr Asp		
3045	3050	3055
Ala Val Gly Leu Leu Asn Cys Leu Glu Gln Arg Ile Gln Glu Gln Gly		
3060	3065	3070
Val Glu Tyr Gln Ala Ala Met Glu Cys Leu Gln Lys Ala Asp Arg Arg		
3075	3080	3085
Ser Leu Leu Ser Glu Ile Gln Ala Leu His Ala Gln Met Asn Gly Arg		
3090	3095	3100
Lys Ile Thr Leu Lys Arg Glu Gln Glu Ser Glu Lys Pro Ser Gln Glu		
3105	3110	3115
Leu Leu Glu Tyr Asn Ile Gln Gln Lys Gln Ser Gln Met Leu Glu Met		
3125	3130	3135
Gln Val Glu Leu Ser Ser Met Lys Asp Arg Ala Thr Glu Leu Gln Glu		
3140	3145	3150

Gln Leu Ser Ser Glu Lys Met Val Val Ala Glu Leu Lys Ser Glu Leu
 3155 3160 3165
 Ala Gln Thr Lys Leu Glu Leu Glu Thr Thr Leu Lys Ala Gln His Lys
 3170 3175 3180
 His Leu Lys Glu Leu Glu Ala Phe Arg Leu Glu Val Lys Asp Lys Thr
 3185 3190 3195 3200
 Asp Glu Val His Leu Leu Asn Asp Thr Leu Ala Ser Glu Gln Lys Lys
 3205 3210 3215
 Ser Arg Glu Leu Gln Trp Ala Leu Glu Lys Glu Lys Ala Lys Leu Gly
 3220 3225 3230
 Arg Ser Glu Glu Arg Asp Lys Glu Glu Leu Glu Asp Leu Lys Phe Ser
 3235 3240 3245
 Leu Glu Ser Gln Lys Gln Arg Asn Leu Gln Leu Asn Leu Leu Leu Glu
 3250 3255 3260
 Gln Gln Lys Gln Leu Leu Asn Glu Ser Gln Gln Lys Ile Glu Ser Gln
 3265 3270 3275 3280
 Arg Met Leu Tyr Asp Ala Gln Leu Ser Glu Glu Gln Gly Arg Asn Leu
 3285 3290 3295
 Glu Leu Gln Val Leu Leu Glu Ser Glu Lys Val Arg Ile Arg Glu Met
 3300 3305 3310
 Ser Ser Thr Leu Asp Arg Glu Arg Glu Leu His Ala Gln Leu Gln Ser
 3315 3320 3325
 Ser Asp Gly Thr Gly Gln Ser Arg Pro Pro Leu Pro Ser Glu Asp Leu
 3330 3335 3340
 Leu Lys Glu Leu Gln Lys Gln Leu Glu Glu Lys His Ser Arg Ile Val
 3345 3350 3355 3360
 Glu Leu Leu Asn Glu Thr Glu Lys Tyr Lys Leu Asp Ser Leu Gln Thr
 3365 3370 3375
 Arg Gln Gln Met Glu Lys Asp Arg Gln Val His Arg Lys Thr Leu Gln
 3380 3385 3390
 Thr Glu Gln Glu Ala Asn Thr Glu Gly Gln Lys Lys Met His Glu Leu
 3395 3400 3405
 Gln Ser Lys Val Glu Asp Leu Gln Arg Gln Leu Glu Glu Lys Arg Gln
 3410 3415 3420
 Gln Val Tyr Lys Leu Asp Leu Glu Gly Gln Arg Leu Gln Gly Ile Met
 3425 3430 3435 3440
 Gln Glu Phe Gln Lys Gln Glu Leu Glu Arg Glu Glu Lys Arg Glu Ser
 3445 3450 3455
 Arg Arg Ile Leu Tyr Gln Asn Leu Asn Glu Pro Thr Thr Trp Ser Leu
 3460 3465 3470
 Thr Ser Asp Arg Thr Arg Asn Trp Val Leu Gln Gln Lys Ile Glu Gly
 3475 3480 3485
 Glu Thr Lys Glu Ser Asn Tyr Ala Lys Leu Ile Glu Met Asn Gly Gly
 3490 3495 3500
 Gly Thr Gly Cys Asn His Glu Leu Glu Met Ile Arg Gln Lys Leu Gln
 3505 3510 3515 3520
 Cys Val Ala Ser Lys Leu Gln Val Leu Pro Gln Lys Ala Ser Glu Arg
 3525 3530 3535
 Leu Gln Phe Glu Thr Ala Asp Asp Glu Asp Phe Ile Trp Val Gln Glu
 3540 3545 3550
 Asn Ile Asp Glu Ile Ile Leu Gln Leu Gln Lys Leu Thr Gly Gln Gln
 3555 3560 3565
 Gly Glu Glu Pro Ser Leu Val Ser Pro Ser Thr Ser Cys Gly Ser Leu
 3570 3575 3580
 Thr Glu Arg Leu Leu Arg Gln Asn Ala Glu Leu Thr Gly His Ile Ser
 3585 3590 3595 3600
 Gln Leu Thr Glu Glu Lys Asn Asp Leu Arg Asn Met Val Met Lys Leu
 3605 3610 3615
 Glu Glu Gln Ile Arg Trp Tyr Arg Gln Thr Gly Ala Gly Arg Asp Asn

3620 3625 3630
 Ser Ser Arg Phe Ser Leu Asn Gly Gly Ala Asn Ile Glu Ala Ile Ile
 3635 3640 3645
 Ala Ser Glu Lys Glu Val Trp Asn Arg Glu Lys Leu Thr Leu Gln Lys
 3650 3655 3660
 Ser Leu Lys Arg Ala Glu Ala Glu Val Tyr Lys Leu Lys Ala Glu Leu
 3665 3670 3675 3680
 Arg Asn Asp Ser Leu Gln Thr Leu Ser Pro Asp Ser Glu His Val
 3685 3690 3695
 Thr Leu Lys Arg Ile Tyr Gly Lys Tyr Leu Arg Ala Glu Ser Phe Arg
 3700 3705 3710
 Lys Ala Leu Ile Tyr Gln Lys Lys Tyr Leu Leu Leu Leu Leu Gly Gly
 3715 3720 3725
 Phe Gln Glu Cys Glu Asp Ala Thr Leu Ala Leu Leu Ala Arg Met Gly
 3730 3735 3740
 Gly Gln Pro Ala Phe Thr Asp Leu Glu Val Ile Thr Asn Arg Pro Lys
 3745 3750 3755 3760
 Gly Phe Thr Arg Phe Arg Ser Ala Val Arg Val Ser Ile Ala Ile Ser
 3765 3770 3775
 Arg Met Lys Phe Leu Val Arg Arg Trp His Arg Val Thr Gly Ser Val
 3780 3785 3790
 Ser Ile Asn Ile Asn Arg Asp Gly Phe Gly Leu Asn Gln Gly Ala Glu
 3795 3800 3805
 Lys Thr Asp Ser Phe Tyr His Ser Ser Gly Gly Leu Glu Leu Tyr Gly
 3810 3815 3820
 Glu Pro Arg His Thr Thr Tyr Arg Ser Arg Ser Asp Leu Asp Tyr Ile
 3825 3830 3835 3840
 Arg Ser Pro Leu Pro Phe Gln Asn Arg Tyr Pro Gly Thr Pro Ala Asp
 3845 3850 3855
 Phe Asn Pro Gly Ser Leu Ala Cys Ser Gln Leu Gln Asn Tyr Asp Pro
 3860 3865 3870
 Asp Arg Ala Leu Thr Asp Tyr Ile Thr Arg Leu Glu Ala Leu Gln Arg
 3875 3880 3885
 Arg Leu Gly Thr Ile Gln Ser Gly Ala Leu Ser Leu Thr Thr Ser Trp
 3890 3895 3900
 Gln His His Ser Ala Arg Pro Thr Ala Pro Leu Phe Phe Glu Ile Leu
 3905 3910 3915 3920
 Ser His Ser Leu Gly
 3925

<210> 7

<211> 12313

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 12031, 12102, 12264

<223> n = A,T,C or G

<400> 7

gaagatggcg gcggcggcgg cggtgacggc gcttcccgtg cggctgagga cgatccgcca 60
 gtgagcgcg agactgcttc cacttcgggc gggggagccc cggaccgaat cggctctcta 120
 ggccgtggag cttgccgtcc cacctccgtc caaatcgacc tttcctttct atccccaacc 180
 acccctcaac ccctgttttc ccctgccttc cttgcagagg ccatggagga cgaggagaga 240
 cagaagaagc tggaggccgg caaagccaag cttgccaggt ttcgacaaag aaaagctcag 300
 tcggatgggc agagtcttc caagaagcag aaaaaaaga gaaaaacgtc aagcagtaaa 360
 catgatgtgt cagcacacca tgatttgaat attgatcaat cacagtgtaa tgaaatgtac 420

ataaatagtt	ctcagagagt	agaatcaact	gtgattcctg	aatctacaat	aatgagaact	480
ctacatagtg	gagaaataac	cagtcacag	cagggcttct	ctgtggaact	ggaaagtga	540
atttcaacca	cagcagatga	ctgcagttca	gaggtaaagt	gttgcagttt	tgtgatgaga	600
acaggaaagc	ctacaaattt	attaagggaa	gaagaatttg	gtgttgatga	ttcttattct	660
gaacaaggag	cacaagacag	tccgactcat	ctagagatga	tggaaagtga	gttggctggg	720
aagcagcatg	agattgaaga	gctaaacaga	gagctggaag	aatgaggggt	tacctatggg	780
actgaaggac	tgcagcagtt	acaagaattt	gaagctgcca	ttaaacaaag	agatggcatt	840
ataaccagc	tcaactgctaa	tttacaacaa	gcaagaagag	aaaaggatga	gacaatgaga	900
gaatttttag	agttgacaga	acagagtcaa	aaattacaga	ttcaattttca	gcaattacag	960
gctagtga	ctctgagaaa	cagcactcat	agtagcacag	ctgcagactt	actacaagcc	1020
aaacaacaga	tcctcactca	tcaacagcag	cttgaagaac	aagaccactt	attagaagat	1080
tatcagaaaa	agaaagaaga	cttcacaatg	caaattagtt	tcttgcaaga	gaaaattaaa	1140
gtatatgaaa	tggacaaga	taaaaaagta	gaaaactcaa	ataaagaaga	aatacaggaa	1200
aaggagacaa	tcattgaaga	attaaacaca	aaaataatag	aagaagaaaa	gaaaactctt	1260
gagctaaagg	ataaattaac	aactgctgat	aaattactag	gagaattaca	agaacagatt	1320
gtgcaaaaga	accaagaaat	aaaaaacatg	aaattagagc	tgactaattc	taagcaaaaa	1380
gaaagacagt	cttctgaaga	aataaaacag	ttaatgggga	cagtogaaga	acttcagaag	1440
agaaatcata	aagacagcca	gttcgaaact	gatatagtac	aacgaatgga	acaagaaaaca	1500
caaagaaagt	tagaacaact	ccgggcagag	ctggatgaga	tgtatgggca	gcagatagtg	1560
caaattgaac	aagaattaat	aagacaacac	atggcacaga	tggaggaaat	gaaaacacgg	1620
cataagggag	aaatggagaa	tgctttaagg	tcattattcaa	atattacagt	taatgaagat	1680
cagataaagt	taatgaatgt	ggcaataaat	gaactgaata	taaaattgca	agataactaac	1740
tctcaaaagg	aaaaactcaa	ggaagaacta	ggactaattd	tagaagaaaa	gtgtgctcta	1800
cagagacagc	ttgaagacct	tgttgaagaa	ttgagctttt	caaggaaca	gattcagaga	1860
gctagacaga	caatagctga	acaagaaagt	aaacttaatg	aagcacataa	gtcccttagt	1920
acagtggaa	atttgaaagc	tgagattgtt	tctgcatctg	aatccagaaa	ggaactagaa	1980
ttaaaacatg	aagcagaagt	tacaaattac	aagataaaaac	ttgaaatggt	agaaaaagaa	2040
aagaatgctg	atgtgctgaa	aatggctgaa	tcacaagaag	ctgaattaga	gaggctgaga	2100
acacagcttc	tatttagtca	cgaagaagag	ctttccaaac	tgaagggaaga	tttagaaatt	2160
gaacatcgaa	taaatattga	aaaacttaaa	gataatttag	gcattcacta	taaacagcag	2220
atagatgggt	tacagaatga	aatgagtcaa	aagatagaaa	ccatgcagtt	tgaaaaggac	2280
aatttgataa	ctaagcagaa	tcaattaat	ttggaaattd	caaagctaaa	agattttacag	2340
cagtctcttg	taaattcaaa	gtcagaagaa	atgactcttc	aatcaatga	acttcaaaaa	2400
gaaattgaaa	tactcagaca	agaagaaaaa	gaaaagggtg	cacttgaaca	agaagttcaa	2460
gaattacaac	ttaaaacaga	attgttagaa	aaacagatga	aggaaaaaga	gaatgatctt	2520
caagaaaaat	ttgcacaact	tgaagcagag	aatagcattc	ttaaagatga	aaagaaaacc	2580
cttgaagaca	tgttgaaaat	acatactcct	gttagccaag	aagaaagatt	gattttctta	2640
gactccatta	agtccaaatc	caaagactct	gtgtgggaaa	aagaaataga	aatacttata	2700
gaggaaaatg	aggacctcaa	acaacaatgt	attcagctaa	atgaagagat	tgaaaagcaa	2760
aggaacactt	tttcatattg	tgaaaaaaac	tttgaagtta	actatcaaga	gttacaagag	2820
gagtatgctt	gccttctcaa	agtaaaagat	gatttagaag	acagtaaaaa	taaacaggaa	2880
ttagagtata	aaagtaaact	taaagcactt	aatgaagagc	ttcatttgca	aagaataaat	2940
ccaactacag	tgaaaatgaa	aagttctgtc	tttgatgaag	acaaaacttt	tgtagcagaa	3000
acattggaaa	tgggtgaggt	tgttgaaaag	gatacaacag	aactcatgga	aaaacttgag	3060
gtaaccaagc	gagagaaatt	agagctgtca	cagagactgt	ctgatctttc	tgaacaattg	3120
aaacagaaac	atgggtgagat	tagttttcta	aatgaagaag	ttaaatcttt	aaagcaagag	3180
aaagaacaag	tttcatgtgag	atgtagagag	ctagaaatca	ttattaacca	caacagggca	3240
gaaaatgtac	agtcattgtga	tactcaagta	agctctttat	tagatggagt	tgtgaccatg	3300
acaagcaggg	gtgctgaagg	atcagtttct	aaagtaaata	aaagtttttg	tgaagaatca	3360
aaaataatgg	tggagataaa	agtttctttt	gaaaatatga	ctgttggaga	agaaagtaag	3420
caagaacagt	tgatttttgga	tcacttacca	tctgtaacaa	aggaatcatc	acttagagca	3480
actcaaccaa	gtgaaaatga	taaacttcag	aaagaactca	atgtacttaa	atcagaacag	3540
aatgatttaa	ggctacagat	ggaagcccaa	cgcatttgcc	tctctctggt	ttattcaact	3600
catgtggatc	aggtttogtg	atatatggaa	aatgaaaaag	ataaagctct	ttgcagcttt	3660
aaagaagagc	ttatttttgc	tcaagaggaa	aagatcaagg	aacttcagaa	aataaccag	3720
ttagaactac	agactatgaa	aacacaagaa	acaggtgatg	aaggaaagcc	tttacatctg	3780
ctcattggaa	aacttcaaaa	ggcagtgctc	gaagaatggt	cttatttttt	acagacttta	3840
tgcagtgctc	ttgggtgaata	ttatactcct	gctttaaaat	gtgaagtaaa	tgcagaagac	3900
aaagagaatt	ctgggtgatta	catttctgaa	aatgaagatc	cagaattaca	agattataga	3960

tatgaagttc	aagactttca	agaaaatatg	cacactcttc	tcaacaaagt	aacagaagaa	4020
tacaacaaac	tcttgggtact	tcaaacacga	ctaagcaaga	tctggggaca	gcagacagat	4080
ggtatgaaac	ttgaattttg	agaagaaaac	cttccaaaag	aggaaacaga	gttttttatca	4140
atccattctc	agatgaccaa	tttggaagac	attgatgtca	atcataaaag	caagttatct	4200
tctctgcaag	atcttgaaaa	aactaaactt	gaagaacaag	ttcaagaatt	agaaagcctc	4260
atatacctct	tgcagcaaca	gttgaaagaa	actgaacaaa	actatgaggc	agagatccac	4320
tgtttacaga	agaggcttca	agctgttagt	gagtccacgg	ttccgccaa	cttacctgtt	4380
gattcggttg	taattacaga	atctgatgca	cagagaacaa	tgtaccctgg	aagttgtgtg	4440
aaaaagaata	ttgatggtac	aatagagttt	tctggtgaat	ttggagtga	agaggaaaca	4500
aatacgtta	agttgcttga	aaaacaatac	caagaacaat	tagaagaaga	agtagctaag	4560
gttattgtgt	caatgagtat	agcatttgc	caacaaactg	aactgtctag	aatatctggg	4620
ggaaaagaaa	atactgcata	atcaaagcaa	gcacatgctg	tgtgtcagca	agaacaacat	4680
tatttttaag	aaatgaaatt	atcacaggat	caaattgggt	ttcagacttt	tgagacagt	4740
gatgtgaaat	ttaaagaaga	atttaaacca	cttagtaaa	agttaggaga	acatggaaag	4800
gaaattttat	tatcaaatag	tgatcccat	gatataccag	aatcaaagga	ctgtgtgctg	4860
actattttcag	aagaaatggt	ctccaaagat	aaaacattta	tagttagaca	gtctattcat	4920
gatgagattt	cagtgtcaag	catggatgct	tctagacaac	taatgttgaa	tgaagaacag	4980
ttggaagata	tgagacagga	acttgtagca	caataccaag	aacatcaaca	ggcaacggaa	5040
ttgttaaggc	aagcacatat	gcggcaaatg	gagagacagc	gagaagacca	ggaacagcta	5100
caagaagaga	ttaaagagact	taatagacaa	ttagcccaga	gacccctccat	agataatgaa	5160
aacctgggtt	cagagagaga	gaggggtgct	ttagaggagc	tggaaagcact	aaagcagctg	5220
tcttttagctg	gaagagagaa	gctgtgttgt	gagctgcgca	acagcagtac	gcaaacacag	5280
aatggaaatg	aaaaccaagg	agaagttgaa	gaacaaacat	ttaaagaaaa	ggaattagac	5340
agaaaacctg	aagatgtgcc	tcctgagatt	ttgtctaatt	aaaggtatgc	actccagaaa	5400
gctaataata	gacttttgaa	gatcctctta	gaagtgtgaa	agacaacagc	agctgttgaa	5460
gaaacaattg	gtcgccatgt	ccttgggatt	ctagatagat	ctagtaaaag	ccagtcattc	5520
gccagcctaa	tttggaggtc	agaagcagag	gcactctgta	agtcattgtg	ccatgaggaa	5580
catacaagag	ttacagatga	atccattccc	tcttattctg	gaagtgatat	gccaagaaat	5640
gacattaaca	tgtggtcaaa	agtaactgag	gaaggaaacag	agctgtcaca	acgacttggtg	5700
aggagtgggt	ttgctggaac	tgaaatagac	cctgaaaatg	aagaacttat	gctgaacatt	5760
agctctcgac	tacaagcagc	agttgaaaaa	ctcctagaag	ccataagtga	aactagcagt	5820
cagcttgaac	atgcaagagt	gacacagaca	gagttgatgc	gtgagtcatt	tagacagaaa	5880
caagaagcaa	cagagtccct	taagtgccaa	gaggaaactc	gagagcgct	tcattgaggag	5940
tccagggccca	gagaacagct	agctgtggag	ctcagtaagg	ctgaggggct	cattgatggc	6000
tatgcagatg	aaaaaactct	ttttgaaaag	caaattcagg	aaaaaactga	tataatagat	6060
cgtcttgagc	aggagttggt	atgtgcaagt	aacaggttgc	aagaattgga	ggcagagcaa	6120
gagcagatcc	aagaagaaag	agaattactg	tccagacaaa	aggaagctat	gaaagcagag	6180
gcaggcccag	ttgaacaaca	attactacag	gagacagaaa	aattaatgaa	ggaaaaacta	6240
gaagtacaat	gtcaagctga	aaaagtacgt	gatgaccttc	aaaaacaagt	gaaagctcta	6300
gaaatagatg	tggaagaaca	agtcagtagg	tttatagagc	tggaacaaga	aaaaataact	6360
gaactaatgg	atttaagaca	gcaaaaccaa	gcattggaaa	agcagttaga	aaaaatgaga	6420
aaattttttag	atgagcaagc	cattgacaga	gaacatgaga	gagatgtatt	ccaacaggaa	6480
atacagaaac	tagaacagca	acttaagggt	gttcctcgat	tccagcctat	cagtgaacat	6540
caaactagag	aggttgaaaca	gttagcaaat	catctgaaa	aaaaaacaga	caaatgcagt	6600
gagcttttgc	tctctaaaga	gcagcttcaa	agggatatac	aagaaaggaa	tgaagaaata	6660
gagaaaactgg	agttcagagt	aagagaactg	gagcagcgcc	ttcttgtaga	ggaccgaaaa	6720
cacttttgag	ctgtagaagc	taaaaccagaa	ttgtccctag	aagtacaatt	gcaggctgaa	6780
cgagatgcc	tagacagaaa	ggaaaaagag	attacaaact	tagaagagca	attagaacag	6840
tttagagaag	aactggaaaa	taagaatgaa	gaagttcaac	aattacatat	gcaattagaa	6900
atacagaaaa	aggaatctac	taccgcctta	caagaacttg	aacaggaaaa	caaattattt	6960
aaggatgaca	tgagaaaact	gggacttgcc	ataaagggaat	ctgatgccat	gtctactcaa	7020
gaccaacatg	tgctattttg	gaaatttgct	caaataatac	aggaaaaaga	ggtagaaatt	7080
gaccaattaa	atgaacaagt	tacgaaactc	cagcagcaac	ttaaaattac	aacagataac	7140
aaggttattg	aagaaaaaaa	tgaactgata	agggatcttg	aaacccaaat	agaattgttg	7200
atgagtgatc	gaagagaaat	gaagagaag	agagaagaag	aaatagagca	gtcaagttaa	7260
gtgattgaaa	aacttcaaca	ggaattggca	aatattggac	agaagacatc	aatgaatgct	7320
cattccctct	cagaagaagc	agacagttta	aaacatcaat	tggtgtgtgt	tatagctgaa	7380
aagctggcct	tggaacagca	agtagaaacc	gctaatagag	aatgacctt	catgaaaaat	7440
gtacttaaa	aaaccaat	taaaatgaat	cagctaacac	aggaattatt	cagcttaaa	7500

agagaacgtg	aaagtgtgga	aaagattcaa	agcataccag	agaatagtgt	taacgtggct	7560
atagatcatc	tgagcaaaga	caaacctgaa	ctagaagtag	tccttacaga	ggatgctctt	7620
aaatccctag	aaaatcagac	atacttcaaa	tcttttgaag	aaaatggcaa	aggttccata	7680
attaatttgg	aaacaagggt	gctacaactt	gagagcactg	ttagtgc aaa	ggacttagaa	7740
cttaccctagt	gttataaaca	aataaaaagac	atgcaagaac	aaggccagtt	tgaaacagaa	7800
atgcttcaaa	agaagattgt	aaacctacag	aaaatagttg	aagaaaaagt	ggctgctgct	7860
cttgtcagtc	aaatccaact	tgaggcagtt	caggaatatg	caaaattctg	tcaagataat	7920
caaacaattt	catcagaacc	tgaaagaaca	aatattcaga	atttaaataca	actaagagaa	7980
gatgagttgg	ggtcagatat	atcagcatta	accttgagaa	tatcagaatt	agaaagccag	8040
gttggttgaag	tgcatactag	tttgatttta	gaaaaagaac	aagtagaaat	tcagaaaaaa	8100
aatgtttttag	aaaaagaaaa	gaagctgcta	gaactacaga	agctatttga	gggcaatgag	8160
aaaaaacaga	gagagaaaga	aaagaaaaga	agccctcaag	atggttgaagt	tctcaagaca	8220
actactgagc	tatttcatag	caatgaagaa	agtggatttt	ttaatgaact	cgaggctctt	8280
agagctgaat	cagtggctac	caaagcagaa	cttgccagtt	ataaagaaaa	ggctgaaaaa	8340
cttcaagaag	agcttttggg	aaaagaaaca	aatatgacat	ctcttcagaa	agacttaagc	8400
caagttaggg	atcacctcgc	agaggcaaaa	gagaaattgt	ccatttttaga	aaaagaagat	8460
gagactgagg	tacaagaaag	caaaaaggcc	tgcatgtttg	agccacttcc	tataaaaactg	8520
agtaagagca	ttgcatocca	gacagatggg	actctgaaga	tcagtagcag	caatcagact	8580
ccacaaattc	ttgttaaaaa	tgcaaggaata	caaattaatt	tacagagtga	atgttccctca	8640
gaagaagtta	ctgaaataat	cagtcagttt	actgaaaaaa	ttgagaagat	gcaagaaacta	8700
catgctgctg	aaattttgga	catggaatcc	agacatattt	cagaaactga	aaccttaaaag	8760
agggaacact	atgtttgcgt	tcagttactg	aaagaggaat	gtggtacctt	gaaggcagtg	8820
atacagtgtc	tgagaagtaa	agagggatcc	tcaattcctg	agctagcaca	ttctgatgct	8880
taccagacta	gagaaatatg	ctccagtgat	tctggatcag	actggggtca	gggaatttat	8940
cttacacaca	gtcagggatt	tgacatagca	tcagaaggcc	gaggagaaga	aagtgaaggt	9000
gcaacagatt	ccttttccaaa	gaaaataaaag	ggattactga	gagctgtcca	taatgaaggc	9060
atgcaggtgc	tttctctcac	tgagtctccc	tatagtgatg	gagaggacca	ttctatttcag	9120
caggttttcag	aaccttgggt	agaagagaga	aaagcttaca	tcaatacaat	ctcatctcta	9180
aagattttaa	ttacaaagat	gcaactgcaa	agagaagccg	aggtttatga	tagttctcaa	9240
tctcatgaga	gcttctcaga	ctggcgaggt	gaactactgc	ttgcccttca	acaagtttttc	9300
ttagaagagc	gtagtgtttt	actagcagca	tttcggacgg	agctgacagc	tctagggtact	9360
acagatgcag	ttggtttact	aaactgtttg	gaacagagaa	tacaagaaca	gggtgttgaa	9420
tatcaagcag	ctatggaatg	cctccagaaa	gcagatagaa	ggagtttggt	atctgaaatt	9480
caggcactgc	atgcacaaat	gaatggtagg	aaaattactc	tgaaaagaga	acaagagagt	9540
gagaaaccaa	gccaaagaact	cttggaatat	aatatacagc	agaagcagtc	tcaaagtctg	9600
gagatgcaag	tgagagctcag	cagtatgaaa	gacagagcaa	cggaaactgca	ggagcagctg	9660
agttctgaga	aaattggtgt	tgctgaactg	aagagttagc	ttgcacaaac	taaattggaa	9720
ctagaaacaa	cactcaaggc	acagcataaa	cacctaaaaag	aattggaggc	tttcagggtt	9780
gaagttaaaag	ataagacaga	tgaagtacat	ttgcttaatg	acacattagc	aagtgaacag	9840
aaaaaatcaa	gagagctcca	gtgggctttg	gagaaagaga	aagccaagtt	gggacgcagt	9900
gaagaacggg	ataaagaaga	acttgaggat	ctgaagtttt	cacttgagag	tcagaaacaa	9960
aggaatcttc	agctaaatct	acttttggaa	caacagaaac	aactactgaa	cgaatcccag	10020
caaaaaatag	aatcacagag	aatgctatat	gatgccaggt	tgtcagaaga	acaaggtcga	10080
aacttagagc	ttcagggtact	tcttgaatct	gagaaagttc	gaattcggga	aatgagtagt	10140
accctagata	gggagcggga	attgcacgca	cagctgcaga	gcagtgatgg	tactggacag	10200
tctcggccac	ccttgccctc	agaggaccta	ctgaaagagc	tgacagaaaca	gctagaggaa	10260
aaacacagtc	gcatagtaga	attgttaaata	gagactgaaa	aatataaaact	ggattctttg	10320
caaacacgac	agcaaatagga	aaaagatagg	caggttcaca	ggaaaacact	gcagacagaa	10380
caggaggcca	acactgaggg	acagaaaaaa	atgcatgagc	tccagtccaa	agtggagat	10440
cttcagcgcc	agctggaaga	gaaaagacaa	caagtttata	agtttagacct	tgaaggacag	10500
cgactacaag	gaatcatgca	ggaattccag	aagcaagaac	tagaacgaga	agaaaaacga	10560
gaaagtagaa	gaattctgta	tcagaacctt	aatgagccaa	ccacgtggag	cttaaccagt	10620
gatagaacta	gaaattgggt	tcttcaacag	aaaatagaag	gagaaacaaa	agaatcaaac	10680
tacgctaaat	tgattgaaat	gaatggagga	ggaaccggct	gtaatcatga	attagaaatg	10740
atcagacaaa	agcttcaatg	tgtagcttca	aaactcagag	ttctacccca	gaaagcctct	10800
gagagactac	agtttgaaac	agcagatgat	gaagatttca	tttgggttca	ggaaaatatt	10860
gatgaaatta	ttttacaact	acagaaatta	actggccagc	aaggtgaaga	gcccagcttg	10920
gtgtccccaa	gtacttcttg	tggctcattg	actgaaagac	tactgagaca	aaatgctgag	10980
ctgacagggc	atatcagtc	actgactgaa	gagaagaatg	acttaaggaa	catggttatg	11040


```

aagctggaag agcagatcag gtggtatcga cagacaggag ctggtagaga taattcttcc 11100
aggttttcat tgaatggtgg tgccaacatt gaagccatca ttgcctctga aaaagaagta 11160
tggaacagag aaaaattgac tctccagaaa tctttgaaaa gggcagaggc tgaagtatac 11220
aaactgaaag ctgaactaag aaatgactct ttacttcaaa ctctgagccc tgattctgaa 11280
catgtcactt taaagagaat ttatggtaaa tacttgaggg cagaaagttt tcgaaaggct 11340
ctcattttacc agaagaaata cctgctgctg ttactgggtg gggtccagga atgtgaagat 11400
gccaccttgg ccctgcttgc ccgatgggg gggcagccag ctttcacgga tctagagggtg 11460
atcaccaatc gcccaaaggg cttcaccagg tttcggctcg ccgtcagagt atccattgca 11520
atttccagaa tgaaattttt gggttcgacgg tggcatcgag tcacaggttc tgtttccatc 11580
aatattaaca gagatggcct tggactgaat caaggtgcag aaaagactga ctcattttat 11640
cattcttctg gtgggctgga gttatatgga gaaccaagac atactacgta tcgctcaaga 11700
tcagatctgg actatattag gtccccttta ccatttcaga ataggtacc aggactcca 11760
gctgatttca atcctgggtt tttagcatgt tctcagcttc agaattacga tcctgacaga 11820
gccctaacag attatatcac tcggctagag gcactgcaaa gacgacttgg aactatacag 11880
tcaggtgctc tgagtttaac cacatcttgg cagcaccaca gtgcgagacc cacagctccc 11940
cttttctttg aaattctttc acactcatta ggataatcaa agcttccagt ttagtgcattg 12000
agctaattat taagttagcc aaagcttaaa nttttgtaac cagcagagaa actgacttta 12060
aataatttaa gtgaaaatat gatttatcac cccagatccc antcctccca aaaatgattt 12120
cctactatgt tcattcagcg gactgatgac acaaaatgca caatgagcac cagtgtgcaa 12180
ggtaactctg gtttacagag cctaactgga gaacgtattc ctaagtagcg catggcagaa 12240
agtggtaagg ccgtgcgcga gcantccagc ctgggcagca gagcagagacc ctgtctcaaa 12300
gaaaaaaaaa aaa 12313

```

<210> 8

<211> 3917

<212> PRT

<213> Homo sapiens

<400> 8

```

Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
 1          5          10          15
Leu Ala Gln Phe Arg Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro
 20          25          30
Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
 35          40          45
Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
 50          55          60
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
 65          70          75          80
Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
 85          90          95
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100          105          110
Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115          120          125
Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
130          135          140
Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145          150          155          160
Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
165          170          175
Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
180          185          190
Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
195          200          205
Gln Leu Thr Ala Asn Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr
210          215          220
Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225          230          235          240

```

Gln	Phe	Gln	Gln	Leu	Gln	Ala	Ser	Glu	Thr	Leu	Arg	Asn	Ser	Thr	His	
				245					250					255		
Ser	Ser	Thr	Ala	Ala	Asp	Leu	Leu	Gln	Ala	Lys	Gln	Gln	Ile	Leu	Thr	
			260					265					270			
His	Gln	Gln	Gln	Leu	Glu	Glu	Gln	Asp	His	Leu	Leu	Glu	Asp	Tyr	Gln	
			275					280					285			
Lys	Lys	Lys	Glu	Asp	Phe	Thr	Met	Gln	Ile	Ser	Phe	Leu	Gln	Glu	Lys	
			290				295				300					
Ile	Lys	Val	Tyr	Glu	Met	Glu	Gln	Asp	Lys	Lys	Val	Glu	Asn	Ser	Asn	
305					310					315					320	
Lys	Glu	Glu	Ile	Gln	Glu	Lys	Glu	Thr	Ile	Ile	Glu	Glu	Leu	Asn	Thr	
				325					330					335		
Lys	Ile	Ile	Glu	Glu	Glu	Lys	Lys	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu	
			340					345					350			
Thr	Thr	Ala	Asp	Lys	Leu	Leu	Gly	Glu	Leu	Gln	Glu	Gln	Ile	Val	Gln	
		355					360					365				
Lys	Asn	Gln	Glu	Ile	Lys	Asn	Met	Lys	Leu	Glu	Leu	Thr	Asn	Ser	Lys	
	370					375					380					
Gln	Lys	Glu	Arg	Gln	Ser	Ser	Glu	Glu	Ile	Lys	Gln	Leu	Met	Gly	Thr	
385					390					395					400	
Val	Glu	Glu	Leu	Gln	Lys	Arg	Asn	His	Lys	Asp	Ser	Gln	Phe	Glu	Thr	
				405					410					415		
Asp	Ile	Val	Gln	Arg	Met	Glu	Gln	Glu	Thr	Gln	Arg	Lys	Leu	Glu	Gln	
			420					425					430			
Leu	Arg	Ala	Glu	Leu	Asp	Glu	Met	Tyr	Gly	Gln	Gln	Ile	Val	Gln	Met	
		435					440					445				
Lys	Gln	Glu	Leu	Ile	Arg	Gln	His	Met	Ala	Gln	Met	Glu	Glu	Met	Lys	
	450					455					460					
Thr	Arg	His	Lys	Gly	Glu	Met	Glu	Asn	Ala	Leu	Arg	Ser	Tyr	Ser	Asn	
465					470					475					480	
Ile	Thr	Val	Asn	Glu	Asp	Gln	Ile	Lys	Leu	Met	Asn	Val	Ala	Ile	Asn	
				485				490						495		
Glu	Leu	Asn	Ile	Lys	Leu	Gln	Asp	Thr	Asn	Ser	Gln	Lys	Glu	Lys	Leu	
			500					505					510			
Lys	Glu	Glu	Leu	Gly	Leu	Ile	Leu	Glu	Glu	Lys	Cys	Ala	Leu	Gln	Arg	
			515				520					525				
Gln	Leu	Glu	Asp	Leu	Val	Glu	Glu	Leu	Ser	Phe	Ser	Arg	Glu	Gln	Ile	
						535					540					
Gln	Arg	Ala	Arg	Gln	Thr	Ile	Ala	Glu	Gln	Glu	Ser	Lys	Leu	Asn	Glu	
545					550					555					560	
Ala	His	Lys	Ser	Leu	Ser	Thr	Val	Glu	Asp	Leu	Lys	Ala	Glu	Ile	Val	
				565				570						575		
Ser	Ala	Ser	Glu	Ser	Arg	Lys	Glu	Leu	Glu	Leu	Lys	His	Glu	Ala	Glu	
			580					585					590			
Val	Thr	Asn	Tyr	Lys	Ile	Lys	Leu	Glu	Met	Leu	Glu	Lys	Glu	Lys	Asn	
			595				600					605				
Ala	Val	Leu	Asp	Arg	Met	Ala	Glu	Ser	Gln	Glu	Ala	Glu	Leu	Glu	Arg	
						615					620					
Leu	Arg	Thr	Gln	Leu	Leu	Phe	Ser	His	Glu	Glu	Glu	Leu	Ser	Lys	Leu	
625					630					635					640	
Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys	
				645				650						655		
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn	
			660					665					670			
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu	
			675				680					685				
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp	
			690			695				700						
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln	

705		710		715		720
Ile Asn Glu Leu Gln Lys Glu Ile Glu Ile Leu Arg Gln Glu Glu Lys						
		725		730		735
Glu Lys Gly Thr Leu Glu Gln Glu Val Gln Glu Leu Gln Leu Lys Thr						
		740		745		750
Glu Leu Leu Glu Lys Gln Met Lys Glu Lys Glu Asn Asp Leu Gln Glu						
		755		760		765
Lys Phe Ala Gln Leu Glu Ala Glu Asn Ser Ile Leu Lys Asp Glu Lys						
		770		775		780
Lys Thr Leu Glu Asp Met Leu Lys Ile His Thr Pro Val Ser Gln Glu						
		785		790		795
Glu Arg Leu Ile Phe Leu Asp Ser Ile Lys Ser Lys Ser Lys Asp Ser						
		805		810		815
Val Trp Glu Lys Glu Ile Glu Ile Leu Ile Glu Glu Asn Glu Asp Leu						
		820		825		830
Lys Gln Gln Cys Ile Gln Leu Asn Glu Glu Ile Glu Lys Gln Arg Asn						
		835		840		845
Thr Phe Ser Phe Ala Glu Lys Asn Phe Glu Val Asn Tyr Gln Glu Leu						
		850		855		860
Gln Glu Glu Tyr Ala Cys Leu Leu Lys Val Lys Asp Asp Leu Glu Asp						
		865		870		875
Ser Lys Asn Lys Gln Glu Leu Glu Tyr Lys Ser Lys Leu Lys Ala Leu						
		885		890		895
Asn Glu Glu Leu His Leu Gln Arg Ile Asn Pro Thr Thr Val Lys Met						
		900		905		910
Lys Ser Ser Val Phe Asp Glu Asp Lys Thr Phe Val Ala Glu Thr Leu						
		915		920		925
Glu Met Gly Glu Val Val Glu Lys Asp Thr Thr Glu Leu Met Glu Lys						
		930		935		940
Leu Glu Val Thr Lys Arg Glu Lys Leu Glu Leu Ser Gln Arg Leu Ser						
		945		950		955
Asp Leu Ser Glu Gln Leu Lys Gln Lys His Gly Glu Ile Ser Phe Leu						
		965		970		975
Asn Glu Glu Val Lys Ser Leu Lys Gln Glu Lys Glu Gln Val Ser Leu						
		980		985		990
Arg Cys Arg Glu Leu Glu Ile Ile Asn His Asn Arg Ala Glu Asn						
		995		1000		1005
Val Gln Ser Cys Asp Thr Gln Val Ser Ser Leu Leu Asp Gly Val Val						
		1010		1015		1020
Thr Met Thr Ser Arg Gly Ala Glu Gly Ser Val Ser Lys Val Asn Lys						
		1025		1030		1035
Ser Phe Gly Glu Glu Ser Lys Ile Met Val Glu Asp Lys Val Ser Phe						
		1045		1050		1055
Glu Asn Met Thr Val Gly Glu Glu Ser Lys Gln Glu Gln Leu Ile Leu						
		1060		1065		1070
Asp His Leu Pro Ser Val Thr Lys Glu Ser Ser Leu Arg Ala Thr Gln						
		1075		1080		1085
Pro Ser Glu Asn Asp Lys Leu Gln Lys Glu Leu Asn Val Leu Lys Ser						
		1090		1095		1100
Glu Gln Asn Asp Leu Arg Leu Gln Met Glu Ala Gln Arg Ile Cys Leu						
		1105		1110		1115
Ser Leu Val Tyr Ser Thr His Val Asp Gln Val Arg Glu Tyr Met Glu						
		1125		1130		1135
Asn Glu Lys Asp Lys Ala Leu Cys Ser Leu Lys Glu Glu Leu Ile Phe						
		1140		1145		1150
Ala Gln Glu Glu Lys Ile Lys Glu Leu Gln Lys Ile His Gln Leu Glu						
		1155		1160		1165
Leu Gln Thr Met Lys Thr Gln Glu Thr Gly Asp Glu Gly Lys Pro Leu						
		1170		1175		1180

His Leu Leu Ile Gly Lys Leu Gln Lys Ala Val Ser Glu Glu Cys Ser
 1185 1190 1195 1200
 Tyr Phe Leu Gln Thr Leu Cys Ser Val Leu Gly Glu Tyr Tyr Thr Pro
 1205 1210 1215
 Ala Leu Lys Cys Glu Val Asn Ala Glu Asp Lys Glu Asn Ser Gly Asp
 1220 1225 1230
 Tyr Ile Ser Glu Asn Glu Asp Pro Glu Leu Gln Asp Tyr Arg Tyr Glu
 1235 1240 1245
 Val Gln Asp Phe Gln Glu Asn Met His Thr Leu Leu Asn Lys Val Thr
 1250 1255 1260
 Glu Glu Tyr Asn Lys Leu Leu Val Leu Gln Thr Arg Leu Ser Lys Ile
 1265 1270 1275 1280
 Trp Gly Gln Gln Thr Asp Gly Met Lys Leu Glu Phe Gly Glu Glu Asn
 1285 1290 1295
 Leu Pro Lys Glu Glu Thr Glu Phe Leu Ser Ile His Ser Gln Met Thr
 1300 1305 1310
 Asn Leu Glu Asp Ile Asp Val Asn His Lys Ser Lys Leu Ser Ser Leu
 1315 1320 1325
 Gln Asp Leu Glu Lys Thr Lys Leu Glu Glu Gln Val Gln Glu Leu Glu
 1330 1335 1340
 Ser Leu Ile Ser Ser Leu Gln Gln Gln Leu Lys Glu Thr Glu Gln Asn
 1345 1350 1355 1360
 Tyr Glu Ala Glu Ile His Cys Leu Gln Lys Arg Leu Gln Ala Val Ser
 1365 1370 1375
 Glu Ser Thr Val Pro Pro Ser Leu Pro Val Asp Ser Val Val Ile Thr
 1380 1385 1390
 Glu Ser Asp Ala Gln Arg Thr Met Tyr Pro Gly Ser Cys Val Lys Lys
 1395 1400 1405
 Asn Ile Asp Gly Thr Ile Glu Phe Ser Gly Glu Phe Gly Val Lys Glu
 1410 1415 1420
 Glu Thr Asn Ile Val Lys Leu Leu Glu Lys Gln Tyr Gln Glu Gln Leu
 1425 1430 1435 1440
 Glu Glu Glu Val Ala Lys Val Ile Val Ser Met Ser Ile Ala Phe Ala
 1445 1450 1455
 Gln Gln Thr Glu Leu Ser Arg Ile Ser Gly Gly Lys Glu Asn Thr Ala
 1460 1465 1470
 Ser Ser Lys Gln Ala His Ala Val Cys Gln Gln Glu Gln His Tyr Phe
 1475 1480 1485
 Asn Glu Met Lys Leu Ser Gln Asp Gln Ile Gly Phe Gln Thr Phe Glu
 1490 1495 1500
 Thr Val Asp Val Lys Phe Lys Glu Glu Phe Lys Pro Leu Ser Lys Glu
 1505 1510 1515 1520
 Leu Gly Glu His Gly Lys Glu Ile Leu Leu Ser Asn Ser Asp Pro His
 1525 1530 1535
 Asp Ile Pro Glu Ser Lys Asp Cys Val Leu Thr Ile Ser Glu Glu Met
 1540 1545 1550
 Phe Ser Lys Asp Lys Thr Phe Ile Val Arg Gln Ser Ile His Asp Glu
 1555 1560 1565
 Ile Ser Val Ser Ser Met Asp Ala Ser Arg Gln Leu Met Leu Asn Glu
 1570 1575 1580
 Glu Gln Leu Glu Asp Met Arg Gln Glu Leu Val Arg Gln Tyr Gln Glu
 1585 1590 1595 1600
 His Gln Gln Ala Thr Glu Leu Leu Arg Gln Ala His Met Arg Gln Met
 1605 1610 1615
 Glu Arg Gln Arg Glu Asp Gln Glu Gln Leu Gln Glu Glu Ile Lys Arg
 1620 1625 1630
 Leu Asn Arg Gln Leu Ala Gln Arg Ser Ser Ile Asp Asn Glu Asn Leu
 1635 1640 1645
 Val Ser Glu Arg Glu Arg Val Leu Leu Glu Glu Leu Glu Ala Leu Lys

1650	1655	1660
Gln Leu Ser Leu Ala Gly Arg Glu Lys Leu Cys Cys Glu Leu Arg Asn		
1665	1670	1675
Ser Ser Thr Gln Thr Gln Asn Gly Asn Glu Asn Gln Gly Glu Val Glu		1680
	1685	1690
Glu Gln Thr Phe Lys Glu Lys Glu Leu Asp Arg Lys Pro Glu Asp Val		1695
	1700	1705
Pro Pro Glu Ile Leu Ser Asn Glu Arg Tyr Ala Leu Gln Lys Ala Asn		1710
	1715	1720
Asn Arg Leu Leu Lys Ile Leu Leu Glu Val Val Lys Thr Thr Ala Ala		1725
	1730	1735
Val Glu Glu Thr Ile Gly Arg His Val Leu Gly Ile Leu Asp Arg Ser		1740
1745	1750	1755
Ser Lys Ser Gln Ser Ser Ala Ser Leu Ile Trp Arg Ser Glu Ala Glu		1760
	1765	1770
Ala Ser Val Lys Ser Cys Val His Glu Glu His Thr Arg Val Thr Asp		1775
	1780	1785
Glu Ser Ile Pro Ser Tyr Ser Gly Ser Asp Met Pro Arg Asn Asp Ile		1790
	1795	1800
Asn Met Trp Ser Lys Val Thr Glu Glu Gly Thr Glu Leu Ser Gln Arg		1805
	1810	1815
Leu Val Arg Ser Gly Phe Ala Gly Thr Glu Ile Asp Pro Glu Asn Glu		1820
1825	1830	1835
Glu Leu Met Leu Asn Ile Ser Ser Arg Leu Gln Ala Ala Val Glu Lys		1840
	1845	1850
Leu Leu Glu Ala Ile Ser Glu Thr Ser Ser Gln Leu Glu His Ala Lys		1855
	1860	1865
Val Thr Gln Thr Glu Leu Met Arg Glu Ser Phe Arg Gln Lys Gln Glu		1870
	1875	1880
Ala Thr Glu Ser Leu Lys Cys Gln Glu Glu Leu Arg Glu Arg Leu His		1885
	1890	1895
Glu Glu Ser Arg Ala Arg Glu Gln Leu Ala Val Glu Leu Ser Lys Ala		1900
1905	1910	1915
Glu Gly Val Ile Asp Gly Tyr Ala Asp Glu Lys Thr Leu Phe Glu Arg		1920
	1925	1930
Gln Ile Gln Glu Lys Thr Asp Ile Ile Asp Arg Leu Glu Gln Glu Leu		1935
	1940	1945
Leu Cys Ala Ser Asn Arg Leu Gln Glu Leu Glu Ala Glu Gln Gln Gln		1950
	1955	1960
Ile Gln Glu Glu Arg Glu Leu Leu Ser Arg Gln Lys Glu Ala Met Lys		1965
	1970	1975
Ala Glu Ala Gly Pro Val Glu Gln Gln Leu Leu Gln Glu Thr Glu Lys		1980
1985	1990	1995
Leu Met Lys Glu Lys Leu Glu Val Gln Cys Gln Ala Glu Lys Val Arg		2000
	2005	2010
Asp Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile Asp Val Glu Glu		2015
	2020	2025
Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu Lys Asn Thr Glu Leu		2030
	2035	2040
Met Asp Leu Arg Gln Gln Asn Gln Ala Leu Glu Lys Gln Leu Glu Lys		2045
	2050	2055
Met Arg Lys Phe Leu Asp Glu Gln Ala Ile Asp Arg Glu His Glu Arg		2060
2065	2070	2075
Asp Val Phe Gln Gln Glu Ile Gln Lys Leu Glu Gln Gln Leu Lys Val		2080
	2085	2090
Val Pro Arg Phe Gln Pro Ile Ser Glu His Gln Thr Arg Glu Val Glu		2095
	2100	2105
Gln Leu Ala Asn His Leu Lys Glu Lys Thr Asp Lys Cys Ser Glu Leu		2110
	2115	2120
		2125

Leu Leu Ser Lys Glu Gln Leu Gln Arg Asp Ile Gln Glu Arg Asn Glu
 2130 2135 2140
 Glu Ile Glu Lys Leu Glu Phe Arg Val Arg Glu Leu Glu Gln Ala Leu
 2145 2150 2155 2160
 Leu Val Glu Asp Arg Lys His Phe Gly Ala Val Glu Ala Lys Pro Glu
 2165 2170 2175
 Leu Ser Leu Glu Val Gln Leu Gln Ala Glu Arg Asp Ala Ile Asp Arg
 2180 2185 2190
 Lys Glu Lys Glu Ile Thr Asn Leu Glu Glu Gln Leu Glu Gln Phe Arg
 2195 2200 2205
 Glu Glu Leu Glu Asn Lys Asn Glu Glu Val Gln Gln Leu His Met Gln
 2210 2215 2220
 Leu Glu Ile Gln Lys Lys Glu Ser Thr Thr Arg Leu Gln Glu Leu Glu
 2225 2230 2235 2240
 Gln Glu Asn Lys Leu Phe Lys Asp Asp Met Glu Lys Leu Gly Leu Ala
 2245 2250 2255
 Ile Lys Glu Ser Asp Ala Met Ser Thr Gln Asp Gln His Val Leu Phe
 2260 2265 2270
 Gly Lys Phe Ala Gln Ile Ile Gln Glu Lys Glu Val Glu Ile Asp Gln
 2275 2280 2285
 Leu Asn Glu Gln Val Thr Lys Leu Gln Gln Gln Leu Lys Ile Thr Thr
 2290 2295 2300
 Asp Asn Lys Val Ile Glu Glu Lys Asn Glu Leu Ile Arg Asp Leu Glu
 2305 2310 2315 2320
 Thr Gln Ile Glu Cys Leu Met Ser Asp Gln Glu Cys Val Lys Arg Asn
 2325 2330 2335
 Arg Glu Glu Glu Ile Glu Gln Leu Asn Glu Val Ile Glu Lys Leu Gln
 2340 2345 2350
 Gln Glu Leu Ala Asn Ile Gly Gln Lys Thr Ser Met Asn Ala His Ser
 2355 2360 2365
 Leu Ser Glu Glu Ala Asp Ser Leu Lys His Gln Leu Asp Val Val Ile
 2370 2375 2380
 Ala Glu Lys Leu Ala Leu Glu Gln Gln Val Glu Thr Ala Asn Glu Glu
 2385 2390 2395 2400
 Met Thr Phe Met Lys Asn Val Leu Lys Glu Thr Asn Phe Lys Met Asn
 2405 2410 2415
 Gln Leu Thr Gln Glu Leu Phe Ser Leu Lys Arg Glu Arg Glu Ser Val
 2420 2425 2430
 Glu Lys Ile Gln Ser Ile Pro Glu Asn Ser Val Asn Val Ala Ile Asp
 2435 2440 2445
 His Leu Ser Lys Asp Lys Pro Glu Leu Glu Val Val Leu Thr Glu Asp
 2450 2455 2460
 Ala Leu Lys Ser Leu Glu Asn Gln Thr Tyr Phe Lys Ser Phe Glu Glu
 2465 2470 2475 2480
 Asn Gly Lys Gly Ser Ile Ile Asn Leu Glu Thr Arg Leu Leu Gln Leu
 2485 2490 2495
 Glu Ser Thr Val Ser Ala Lys Asp Leu Glu Leu Thr Gln Cys Tyr Lys
 2500 2505 2510
 Gln Ile Lys Asp Met Gln Glu Gln Gly Gln Phe Glu Thr Glu Met Leu
 2515 2520 2525
 Gln Lys Lys Ile Val Asn Leu Gln Lys Ile Val Glu Glu Lys Val Ala
 2530 2535 2540
 Ala Ala Leu Val Ser Gln Ile Gln Leu Glu Ala Val Gln Glu Tyr Ala
 2545 2550 2555 2560
 Lys Phe Cys Gln Asp Asn Gln Thr Ile Ser Ser Glu Pro Glu Arg Thr
 2565 2570 2575
 Asn Ile Gln Asn Leu Asn Gln Leu Arg Glu Asp Glu Leu Gly Ser Asp
 2580 2585 2590
 Ile Ser Ala Leu Thr Leu Arg Ile Ser Glu Leu Glu Ser Gln Val Val

2595	2600	2605
Glu Met His Thr Ser Leu Ile Leu Glu Lys Glu Gln Val Glu Ile Ala		
2610	2615	2620
Glu Lys Asn Val Leu Glu Lys Glu Lys Lys Leu Leu Glu Leu Gln Lys		
2625	2630	2635
Leu Leu Glu Gly Asn Glu Lys Lys Gln Arg Glu Lys Glu Lys Lys Arg		2640
2645	2650	2655
Ser Pro Gln Asp Val Glu Val Leu Lys Thr Thr Thr Glu Leu Phe His		
2660	2665	2670
Ser Asn Glu Glu Ser Gly Phe Phe Asn Glu Leu Glu Ala Leu Arg Ala		
2675	2680	2685
Glu Ser Val Ala Thr Lys Ala Glu Leu Ala Ser Tyr Lys Glu Lys Ala		
2690	2695	2700
Glu Lys Leu Gln Glu Glu Leu Leu Val Lys Glu Thr Asn Met Thr Ser		
2705	2710	2715
Leu Gln Lys Asp Leu Ser Gln Val Arg Asp His Leu Ala Glu Ala Lys		2720
2725	2730	2735
Glu Lys Leu Ser Ile Leu Glu Lys Glu Asp Glu Thr Glu Val Gln Glu		
2740	2745	2750
Ser Lys Lys Ala Cys Met Phe Glu Pro Leu Pro Ile Lys Leu Ser Lys		
2755	2760	2765
Ser Ile Ala Ser Gln Thr Asp Gly Thr Leu Lys Ile Ser Ser Ser Asn		
2770	2775	2780
Gln Thr Pro Gln Ile Leu Val Lys Asn Ala Gly Ile Gln Ile Asn Leu		
2785	2790	2795
Gln Ser Glu Cys Ser Ser Glu Glu Val Thr Glu Ile Ile Ser Gln Phe		
2805	2810	2815
Thr Glu Lys Ile Glu Lys Met Gln Glu Leu His Ala Ala Glu Ile Leu		
2820	2825	2830
Asp Met Glu Ser Arg His Ile Ser Glu Thr Glu Thr Leu Lys Arg Glu		
2835	2840	2845
His Tyr Val Ala Val Gln Leu Leu Lys Glu Glu Cys Gly Thr Leu Lys		
2850	2855	2860
Ala Val Ile Gln Cys Leu Arg Ser Lys Glu Gly Ser Ser Ile Pro Glu		
2865	2870	2875
Leu Ala His Ser Asp Ala Tyr Gln Thr Arg Glu Ile Cys Ser Ser Asp		
2885	2890	2895
Ser Gly Ser Asp Trp Gly Gln Gly Ile Tyr Leu Thr His Ser Gln Gly		
2900	2905	2910
Phe Asp Ile Ala Ser Glu Gly Arg Gly Glu Glu Ser Glu Ser Ala Thr		
2915	2920	2925
Asp Ser Phe Pro Lys Lys Ile Lys Gly Leu Leu Arg Ala Val His Asn		
2930	2935	2940
Glu Gly Met Gln Val Leu Ser Leu Thr Glu Ser Pro Tyr Ser Asp Gly		
2945	2950	2955
Glu Asp His Ser Ile Gln Gln Val Ser Glu Pro Trp Leu Glu Glu Arg		
2965	2970	2975
Lys Ala Tyr Ile Asn Thr Ile Ser Ser Leu Lys Asp Leu Ile Thr Lys		
2980	2985	2990
Met Gln Leu Gln Arg Glu Ala Glu Val Tyr Asp Ser Ser Gln Ser His		
2995	3000	3005
Glu Ser Phe Ser Asp Trp Arg Gly Glu Leu Leu Leu Ala Leu Gln Gln		
3010	3015	3020
Val Phe Leu Glu Glu Arg Ser Val Leu Leu Ala Ala Phe Arg Thr Glu		
3025	3030	3035
Leu Thr Ala Leu Gly Thr Thr Asp Ala Val Gly Leu Leu Asn Cys Leu		
3045	3050	3055
Glu Gln Arg Ile Gln Glu Gln Gly Val Glu Tyr Gln Ala Ala Met Glu		
3060	3065	3070

Cys Leu Gln Lys Ala Asp Arg Arg Ser Leu Leu Ser Glu Ile Gln Ala
 3075 3080 3085
 Leu His Ala Gln Met Asn Gly Arg Lys Ile Thr Leu Lys Arg Glu Gln
 3090 3095 3100
 Glu Ser Glu Lys Pro Ser Gln Glu Leu Leu Glu Tyr Asn Ile Gln Gln
 3105 3110 3115 3120
 Lys Gln Ser Gln Met Leu Glu Met Gln Val Glu Leu Ser Ser Met Lys
 3125 3130 3135
 Asp Arg Ala Thr Glu Leu Gln Glu Gln Leu Ser Ser Glu Lys Met Val
 3140 3145 3150
 Val Ala Glu Leu Lys Ser Glu Leu Ala Gln Thr Lys Leu Glu Leu Glu
 3155 3160 3165
 Thr Thr Leu Lys Ala Gln His Lys His Leu Lys Glu Leu Glu Ala Phe
 3170 3175 3180
 Arg Leu Glu Val Lys Asp Lys Thr Asp Glu Val His Leu Leu Asn Asp
 3185 3190 3195 3200
 Thr Leu Ala Ser Glu Gln Lys Lys Ser Arg Glu Leu Gln Trp Ala Leu
 3205 3210 3215
 Glu Lys Glu Lys Ala Lys Leu Gly Arg Ser Glu Glu Arg Asp Lys Glu
 3220 3225 3230
 Glu Leu Glu Asp Leu Lys Phe Ser Leu Glu Ser Gln Lys Gln Arg Asn
 3235 3240 3245
 Leu Gln Leu Asn Leu Leu Leu Glu Gln Gln Lys Gln Leu Leu Asn Glu
 3250 3255 3260
 Ser Gln Gln Lys Ile Glu Ser Gln Arg Met Leu Tyr Asp Ala Gln Leu
 3265 3270 3275 3280
 Ser Glu Glu Gln Gly Arg Asn Leu Glu Leu Gln Val Leu Leu Glu Ser
 3285 3290 3295
 Glu Lys Val Arg Ile Arg Glu Met Ser Ser Thr Leu Asp Arg Glu Arg
 3300 3305 3310
 Glu Leu His Ala Gln Leu Gln Ser Ser Asp Gly Thr Gly Gln Ser Arg
 3315 3320 3325
 Pro Pro Leu Pro Ser Glu Asp Leu Leu Lys Glu Leu Gln Lys Gln Leu
 3330 3335 3340
 Glu Glu Lys His Ser Arg Ile Val Glu Leu Leu Asn Glu Thr Glu Lys
 3345 3350 3355 3360
 Tyr Lys Leu Asp Ser Leu Gln Thr Arg Gln Gln Met Glu Lys Asp Arg
 3365 3370 3375
 Gln Val His Arg Lys Thr Leu Gln Thr Glu Gln Glu Ala Asn Thr Glu
 3380 3385 3390
 Gly Gln Lys Lys Met His Glu Leu Gln Ser Lys Val Glu Asp Leu Gln
 3395 3400 3405
 Arg Gln Leu Glu Glu Lys Arg Gln Gln Val Tyr Lys Leu Asp Leu Glu
 3410 3415 3420
 Gly Gln Arg Leu Gln Gly Ile Met Gln Glu Phe Gln Lys Gln Glu Leu
 3425 3430 3435 3440
 Glu Arg Glu Glu Lys Arg Glu Ser Arg Arg Ile Leu Tyr Gln Asn Leu
 3445 3450 3455
 Asn Glu Pro Thr Thr Trp Ser Leu Thr Ser Asp Arg Thr Arg Asn Trp
 3460 3465 3470
 Val Leu Gln Gln Lys Ile Glu Gly Glu Thr Lys Glu Ser Asn Tyr Ala
 3475 3480 3485
 Lys Leu Ile Glu Met Asn Gly Gly Gly Thr Gly Cys Asn His Glu Leu
 3490 3495 3500
 Glu Met Ile Arg Gln Lys Leu Gln Cys Val Ala Ser Lys Leu Gln Val
 3505 3510 3515 3520
 Leu Pro Gln Lys Ala Ser Glu Arg Leu Gln Phe Glu Thr Ala Asp Asp
 3525 3530 3535
 Glu Asp Phe Ile Trp Val Gln Glu Asn Ile Asp Glu Ile Ile Leu Gln


```

          3540                      3545                      3550
Leu Gln Lys Leu Thr Gly Gln Gln Gly Glu Glu Pro Ser Leu Val Ser
          3555                      3560                      3565
Pro Ser Thr Ser Cys Gly Ser Leu Thr Glu Arg Leu Leu Arg Gln Asn
          3570                      3575                      3580
Ala Glu Leu Thr Gly His Ile Ser Gln Leu Thr Glu Glu Lys Asn Asp
3585                      3590                      3595                      3600
Leu Arg Asn Met Val Met Lys Leu Glu Glu Gln Ile Arg Trp Tyr Arg
          3605                      3610                      3615
Gln Thr Gly Ala Gly Arg Asp Asn Ser Ser Arg Phe Ser Leu Asn Gly
          3620                      3625                      3630
Gly Ala Asn Ile Glu Ala Ile Ile Ala Ser Glu Lys Glu Val Trp Asn
          3635                      3640                      3645
Arg Glu Lys Leu Thr Leu Gln Lys Ser Leu Lys Arg Ala Glu Ala Glu
          3650                      3655                      3660
Val Tyr Lys Leu Lys Ala Glu Leu Arg Asn Asp Ser Leu Leu Gln Thr
3665                      3670                      3675                      3680
Leu Ser Pro Asp Ser Glu His Val Thr Leu Lys Arg Ile Tyr Gly Lys
          3685                      3690                      3695
Tyr Leu Arg Ala Glu Ser Phe Arg Lys Ala Leu Ile Tyr Gln Lys Lys
          3700                      3705                      3710
Tyr Leu Leu Leu Leu Leu Gly Gly Phe Gln Glu Cys Glu Asp Ala Thr
          3715                      3720                      3725
Leu Ala Leu Leu Ala Arg Met Gly Gly Gln Pro Ala Phe Thr Asp Leu
          3730                      3735                      3740
Glu Val Ile Thr Asn Arg Pro Lys Gly Phe Thr Arg Phe Arg Ser Ala
3745                      3750                      3755                      3760
Val Arg Val Ser Ile Ala Ile Ser Arg Met Lys Phe Leu Val Arg Arg
          3765                      3770                      3775
Trp His Arg Val Thr Gly Ser Val Ser Ile Asn Ile Asn Arg Asp Gly
          3780                      3785                      3790
Phe Gly Leu Asn Gln Gly Ala Glu Lys Thr Asp Ser Phe Tyr His Ser
          3795                      3800                      3805
Ser Gly Gly Leu Glu Leu Tyr Gly Glu Pro Arg His Thr Thr Tyr Arg
          3810                      3815                      3820
Ser Arg Ser Asp Leu Asp Tyr Ile Arg Ser Pro Leu Pro Phe Gln Asn
3825                      3830                      3835                      3840
Arg Tyr Pro Gly Thr Pro Ala Asp Phe Asn Pro Gly Ser Leu Ala Cys
          3845                      3850                      3855
Ser Gln Leu Gln Asn Tyr Asp Pro Asp Arg Ala Leu Thr Asp Tyr Ile
          3860                      3865                      3870
Thr Arg Leu Glu Ala Leu Gln Arg Arg Leu Gly Thr Ile Gln Ser Gly
          3875                      3880                      3885
Ala Leu Ser Leu Thr Thr Ser Trp Gln His His Ser Ala Arg Pro Thr
          3890                      3895                      3900
Ala Pro Leu Phe Phe Glu Ile Leu Ser His Ser Leu Gly
3905                      3910                      3915

```

<210> 9

<211> 2850

<212> DNA

<213> Homo sapiens

<400> 9

```

gttgtgactt tccctttcga attcctcggt atatcttggg gactggagga cctgtctggt 60
tattatacag acgcataact ggaggtggga tccacacagc tcagaacagc tggatcttgc 120
tcagtctctg ccaggggaag attccttggg ggaggccctg cagcgacatg gagggagctg 180
ctttgctgag agtctctgtc ctctgcatct ggatgagtgc acttttcctt ggtgtgagag 240

```

```

tgagggcgaga ggaagctgga gcgaggggtgc aacaaaacgt tccaagtggg acagatactg 300
gagatcctca aagtaagccc ctcggtgact gggctgctgg caccatggac ccagagagca 360
gtatctttat tgaggatgcc attaatgtatt tcaaggaaaa agtgagcaca cagaatctgc 420
tactcctgct gactgataat gaggcctgga acggattcgt ggctgctgct gaactgcccc 480
ggaatgagggc agatgagctc cgtaaagctc tggacaacct tgcaagacaa atgatcatga 540
aagacaaaaa ctggcacgat aaaggccagc agtacagaaa ctgggtttctg aaagagtttc 600
ctcggttgaa aagtaagctt gaggataaca taagaaggct ccgtgccctt gcagatgggg 660
ttcagaaggt ccacaaaggc accaccatcg ccaatgtggg gtctggctct ctgagcattt 720
cctctggcat cctgaccctc gtcggcatgg gtctggcacc cttcacagag ggaggcagcc 780
ttgtactctt ggaacctggg atggagttgg gaatcacagc cgctttgacc gggattacca 840
gcagtagcat agactacgga aagaagtggg ggacacaagc ccaagccac gacctggtca 900
tcaaaagcct tgacaaattg aaggaggtga aggagttttt gggtgagaac atatccaact 960
ttctttcctt agctggcaat acttaccac tccacagagg cattgggaag gacatccgtg 1020
ccctcagacg agccagagcc aatcttcagt cagtaccgca tgccctcagcc tcacgcccc 1080
gggtcactga gccaatctca gctgaaagcg gtgaacaggt ggagaggggt aatgaaccca 1140
gcctcctgga aatgagcaga ggagtcaagc tcacggatgt ggcccttgta agcttctttc 1200
ttgtgctgga tgtagtctac ctggtgtacg aatcaaagca cttacatgag ggggcaaagt 1260
cagagacagc tgaggagctg aagaagggtg ctcaggagct ggaggagaag ctaaaccattc 1320
tcaacaataa ttataagatt ctgcaggcgg accaagaact gtgaccacag ggcagggcag 1380
ccaccaggag agatatgcct ggcaggggcc aggacaaaaat gcaaacctttt ttttttttct 1440
gagacagagt cttgctctgt cgccaagttg gagtgcattg gtgcatctc agctcactgc 1500
aagctctgcc tcccggttgc aagcgattct cctgccttgg cctcccaagt agctgggact 1560
acaggcgcc accaccatgc ccagctaatt tttgtatttt taatagagat ggggtttcac 1620
catgttgccc aggatgggtc cgatctcctg acctcttgat ctgccacot tggcctccca 1680
aagtgtggg attacaggcg tgagccatcg cttttgaccc aaatgcaaac attttattag 1740
ggggataaag aggggtgaggt aaagtttatg gaactgagtg ttagggactt tggcatttcc 1800
atagctgagc acagcagggg aggggttaat gcagatggca gtgcagcaag gagaaggcag 1860
gaacatttga gctgcaata agggaaaaat gggaaactgga gagtgtgggg aatgggaaga 1920
agcagtttac tttagactaa agaatatatt ggggggcccg gtgtagtggc tcatgcctgt 1980
aatccgagca ctttgggagg ccaaggccgg cggatcacga ggtcaggaga tcaagaccat 2040
cctggctaac acagtgaac cccgtctcta ctaaaaatac aaaaaattag ccgggcatgg 2100
tgccggcgcc tgtagtcca gctaactggg cggctgaggg aggagaatgg cgtgaacctg 2160
ggaggtggag cttgcagtga gccgagatat cgccactgca ctccagcctg ggtgacagag 2220
cgagactcca tctcaaaaaa aaaaaaaaaa agaatatatt gacggaagaa tagagaggag 2280
gcttgaagga accagcaatg agaaggccag gaaaagaaag agctgaaaat ggagaaagcc 2340
caagagttag aacagttgga tacaggagaa gaaacagcgg ctccactaca gaccagccc 2400
caggttcaat gtccctcgaa gaatgaagtc tttccctggt gatgggtccc tgccctgtct 2460
ttccagcatc cactctccct tgtcctcctg ggggcatatc tcagtcaggc agcggcttcc 2520
tgatgatggg cgttgggggtg gttgtcatgt gatgggtccc tccaggttac taaagggtgc 2580
atgtcccctg cttgaacact gaagggcagg tgggtggcca tggccatggt cccagctga 2640
ggagcaggtg tccctgagaa cccaaacttc ccagagagta tgtgagaacc aaccaatgaa 2700
aacagtccca tcgctcttac ccgtaagta aacagtcaga aaattagcat gaaagcagtt 2760
tagcattggg aggaagctca gatctctaga gctgtcttgt cgccgcccag gattgacctg 2820
tgtgtaagtc ccaataaact cacctactca 2850

```

<210> 10
 <211> 383
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly
 1 5 10 15
 Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro
 20 25 30
 Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu
 35 40 45
 Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val
 50 55 60

Ser	Thr	Gln	Asn	Leu	Leu	Leu	Leu	Leu	Thr	Asp	Asn	Glu	Ala	Trp	Asn	
65				70					75						80	
Gly	Phe	Val	Ala	Ala	Ala	Glu	Leu	Pro	Arg	Asn	Glu	Ala	Asp	Glu	Leu	
			85					90						95		
Arg	Lys	Ala	Leu	Asp	Asn	Leu	Ala	Arg	Gln	Met	Ile	Met	Lys	Asp	Lys	
			100					105					110			
Asn	Trp	His	Asp	Lys	Gly	Gln	Gln	Tyr	Arg	Asn	Trp	Phe	Leu	Lys	Glu	
		115					120					125				
Phe	Pro	Arg	Leu	Lys	Ser	Lys	Leu	Glu	Asp	Asn	Ile	Arg	Arg	Leu	Arg	
	130					135					140					
Ala	Leu	Ala	Asp	Gly	Val	Gln	Lys	Val	His	Lys	Gly	Thr	Thr	Ile	Ala	
145					150					155					160	
Asn	Val	Val	Ser	Gly	Ser	Leu	Ser	Ile	Ser	Ser	Gly	Ile	Leu	Thr	Leu	
				165					170					175		
Val	Gly	Met	Gly	Leu	Ala	Pro	Phe	Thr	Glu	Gly	Gly	Ser	Leu	Val	Leu	
		180						185					190			
Leu	Glu	Pro	Gly	Met	Glu	Leu	Gly	Ile	Thr	Ala	Ala	Leu	Thr	Gly	Ile	
		195					200					205				
Thr	Ser	Ser	Thr	Ile	Asp	Tyr	Gly	Lys	Lys	Trp	Trp	Thr	Gln	Ala	Gln	
	210					215						220				
Ala	His	Asp	Leu	Val	Ile	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Glu	Val	Lys	
225					230					235					240	
Glu	Phe	Leu	Gly	Glu	Asn	Ile	Ser	Asn	Phe	Leu	Ser	Leu	Ala	Gly	Asn	
				245					250					255		
Thr	Tyr	Gln	Leu	Thr	Arg	Gly	Ile	Gly	Lys	Asp	Ile	Arg	Ala	Leu	Arg	
			260					265					270			
Arg	Ala	Arg	Ala	Asn	Leu	Gln	Ser	Val	Pro	His	Ala	Ser	Ala	Ser	Arg	
	275						280					285				
Pro	Arg	Val	Thr	Glu	Pro	Ile	Ser	Ala	Glu	Ser	Gly	Glu	Gln	Val	Glu	
	290					295					300					
Arg	Val	Asn	Glu	Pro	Ser	Ile	Leu	Glu	Met	Ser	Arg	Gly	Val	Lys	Leu	
305					310					315					320	
Thr	Asp	Val	Ala	Pro	Val	Ser	Phe	Phe	Leu	Val	Leu	Asp	Val	Val	Tyr	
				325					330					335		
Leu	Val	Tyr	Glu	Ser	Lys	His	Leu	His	Glu	Gly	Ala	Lys	Ser	Glu	Thr	
		340						345					350			
Ala	Glu	Glu	Leu	Lys	Lys	Val	Ala	Gln	Glu	Leu	Glu	Glu	Lys	Leu	Asn	
		355					360					365				
Ile	Leu	Asn	Asn	Asn	Tyr	Lys	Ile	Leu	Gln	Ala	Asp	Gln	Glu	Leu		
	370					375						380				

<210> 11

<211> 3004

<212> DNA

<213> Homo sapiens

<400> 11

```

gttgtgactt tcccttttoga attcctcggt atatcttggg gactggagga cctgtctggt 60
tattatacag acgcataact ggaggtggga tccacacagc tcagaacagc tggatcttgc 120
tcagtctctg ccaggggaag attccttgac ttctgggggtg atggagaaga aacaggctgt 180
gctgtgtccc taatgggaaa cgtggctgag acaggggagt gagaagggtg cgttgaagaa 240
tggtgcctgt ggcatgatgc cagctttgca atcatgagat tcaaaagcca cactgtggaa 300
ttgaggaggc cctgcagcga catggaggga gctgctttgc tgagagtctc tgtcctctgc 360
atctggatga gtgcactttt ccttggtgtg agagtgaggg cagaggaagc tggagcgagg 420
gtgcaacaaa acgttocaag tgggacagat actggagatc ctcaaagtaa gccctcggt 480
gactgggctg ctggcaccat ggacccagag agcagtatct ttattgagga tgccattaag 540
tatttcaagg aaaaagttag cacacagaat ctgctactcc tgctgactga taatgaggcc 600
tggaacggat tcgtggctgc tgctgaactg cccaggaatg aggcagatga gctccgtaaa 660

```

```

gctctggaca accttgcaag acaaattgatc atgaaagaca aaaactggca cgataaaggc 720
cagcagtaca gaaactgggt tctgaaagag tttcctcggt tgaaaagtaa gcttgaggat 780
aacataagaa ggctccgtgc ccttgagat ggggttcaga aggtccacaa aggcaccacc 840
atcgccaatg tgggtgtctgg ctctctcagc atttcctctg gcatcctgac cctcgtcggc 900
atgggtctgg cacccttcac agagggaggc agccttgtag tcttggaacc tgggatggag 960
ttgggaatca cagccgcttt gaccgggatt accagcagta ccatagacta cggaaagaag 1020
tgggtggacac aagcccaagc ccacgacctg gtcatacaaaa gccttgacaa attgaaggag 1080
gtgaaggagt ttttgggtga gaacatatcc aactttcttt ccttagctgg caatacttac 1140
caactcacac gaggcattgg gaaggacatc cgtgccctca gacgagccag agccaatctt 1200
cagtcagtac cgcattgcctc agcctcacgc cccgggttca ctgagccaat ctgagctgaa 1260
agcgggtgaa aggtggagag ggttaatgaa ccagcatcc tggaaatgag cagaggagtc 1320
aagctcacgg atgtggcccc tgtaagcttc tttcttctgc tggatgtagt ctacctcgtg 1380
tacgaatcaa agcacttaca tgagggggca aagtcagaga cagctgagga gctgaagaag 1440
gtggctcagg agctggagga gaagctaaac attctcaaca ataattataa gattctgcag 1500
gcggaaccaag aactgtgacc acagggcagg gcagccacca ggagagatat gcctggcagg 1560
ggccaggaca aaatgcaaac tttttttttt ttctgagaca gactcttgct ctgtcgccaa 1620
gttgagagtgc aatgggtgcga tctcagctca ctgcaagctc tgccctccgt gttcaagcga 1680
ttctcctgcc ttggcctccc aagtagctgg gactacagge gcctaccacc atgccagct 1740
aatttttgtta tttttaatag agatgggggtt tcaccatgtt ggccaggatg gtctcgatct 1800
cctgacctct tgatctgccc accttggcct cccaaagtgc tgggattaca ggcgtgagcc 1860
atcgcttttg acccaaatgc aaacatttta tttaggggat aaagaggggt aggtaaagt 1920
tatggaactg agtggttaggg actttggcat ttccatagct gagcacagca ggggaggggt 1980
taatgcagat ggcagtgcag caaggagaag gcaggaacat tggagcctgc aataagggaa 2040
aaatgggaac tggagagtgt ggggaatggg aagaagcagt ttactttaga ctaaagaata 2100
tattgggggg ccgggtgtag tggctcatgc ctgtaatccg agcactttgg gaggccaagg 2160
cgggcggatc acgaggtcag gagatcaaga ccattcctggc taacacagtg aaaccccgtc 2220
tctactaaaa atacaaaaaa ttagccgggc atggtgcggg cgccctgtagt tccagctaac 2280
tgggcggctg aggcaggaga atggcgtgaa cctgggaggt ggagcttgca gtgagccgag 2340
atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa aaaaaaaaaa 2400
aaaaagaata tattgacgga agaattagaga ggagccttga aggaaccagc aatgagaagg 2460
ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt tggatacagg 2520
agaagaaaca gcggctccac tacagacca gccccagggt caatgtcctc cgaagaatga 2580
agtctttccc tgggtgatggg cccctgccct gtctttccag catccactct ccttgtcct 2640
cctgggggca tatctcagtc aggcagcggc ttcctgatga tggctggttg ggtggttgtc 2700
atgtgatggg tccctccagg ttactaaagg gtgcatgtcc cctgcttgaa cactgaaggg 2760
caggtggttg gccatggcca tgggtccccag ctgaggagca ggtgtccctg agaaccctaaa 2820
cttcccagag agtatgtgag aaccaacca tgaaaacagt cccatcgctc ttaccgggta 2880
agtaaacagt cagaaaatta gcatgaaagc agtttagcat tgggaggaag ctgagatctc 2940
tagagctgtc ttgtcgccgc ccaggattga cctgtgtgta agtcccaata aactcaccta 3000
ctca 3004

```

<210> 12

<211> 414

<212> PRT

<213> Homo sapiens

<400> 12

```

Met Arg Phe Lys Ser His Thr Val Glu Leu Arg Arg Pro Cys Ser Asp
 1           5           10          15
Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
          20          25          30
Ser Ala Leu Phe Leu Gly Val Arg Ala Glu Glu Ala Gly Ala
      35          40          45
Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
      50          55          60
Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
      65          70          75          80
Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
          85          90          95

```

Thr	Gln	Asn	Leu	Leu	Leu	Leu	Leu	Thr	Asp	Asn	Glu	Ala	Trp	Asn	Gly	
		100						105					110			
Phe	Val	Ala	Ala	Ala	Glu	Leu	Pro	Arg	Asn	Glu	Ala	Asp	Glu	Leu	Arg	
		115					120					125				
Lys	Ala	Leu	Asp	Asn	Leu	Ala	Arg	Gln	Met	Ile	Met	Lys	Asp	Lys	Asn	
		130				135					140					
Trp	His	Asp	Lys	Gly	Gln	Gln	Tyr	Arg	Asn	Trp	Phe	Leu	Lys	Glu	Phe	
145				150					155						160	
Pro	Arg	Leu	Lys	Ser	Lys	Leu	Glu	Asp	Asn	Ile	Arg	Arg	Leu	Arg	Ala	
			165					170						175		
Leu	Ala	Asp	Gly	Val	Gln	Lys	Val	His	Lys	Gly	Thr	Thr	Ile	Ala	Asn	
		180						185					190			
Val	Val	Ser	Gly	Ser	Leu	Ser	Ile	Ser	Ser	Gly	Ile	Leu	Thr	Leu	Val	
		195					200				205					
Gly	Met	Gly	Leu	Ala	Pro	Phe	Thr	Glu	Gly	Gly	Ser	Leu	Val	Leu	Leu	
	210					215					220					
Glu	Pro	Gly	Met	Glu	Leu	Gly	Ile	Thr	Ala	Ala	Leu	Thr	Gly	Ile	Thr	
225					230					235					240	
Ser	Ser	Thr	Ile	Asp	Tyr	Gly	Lys	Lys	Trp	Trp	Thr	Gln	Ala	Gln	Ala	
			245						250					255		
His	Asp	Leu	Val	Ile	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Glu	Val	Lys	Glu	
		260						265					270			
Phe	Leu	Gly	Glu	Asn	Ile	Ser	Asn	Phe	Leu	Ser	Leu	Ala	Gly	Asn	Thr	
		275					280					285				
Tyr	Gln	Leu	Thr	Arg	Gly	Ile	Gly	Lys	Asp	Ile	Arg	Ala	Leu	Arg	Arg	
	290				295						300					
Ala	Arg	Ala	Asn	Leu	Gln	Ser	Val	Pro	His	Ala	Ser	Ala	Ser	Arg	Pro	
305					310					315					320	
Arg	Val	Thr	Glu	Pro	Ile	Ser	Ala	Glu	Ser	Gly	Glu	Gln	Val	Glu	Arg	
			325					330						335		
Val	Asn	Glu	Pro	Ser	Ile	Leu	Glu	Met	Ser	Arg	Gly	Val	Lys	Leu	Thr	
		340						345					350			
Asp	Val	Ala	Pro	Val	Ser	Phe	Phe	Leu	Val	Leu	Asp	Val	Val	Tyr	Leu	
		355				360						365				
Val	Tyr	Glu	Ser	Lys	His	Leu	His	Glu	Gly	Ala	Lys	Ser	Glu	Thr	Ala	
	370					375					380					
Glu	Glu	Leu	Lys	Lys	Val	Ala	Gln	Glu	Leu	Glu	Glu	Lys	Leu	Asn	Ile	
385					390					395					400	
Leu	Asn	Asn	Asn	Tyr	Lys	Ile	Leu	Gln	Ala	Asp	Gln	Glu	Leu			
			405					410								

<210> 13

<211> 2298

<212> DNA

<213> Homo sapiens

<400> 13

```

ctaaaggtct ggttattatg cagatgcacg gctggaggtg ggatccacac agctcagaac 60
agctggatct tgctcacact ctttcaagag aagcttcctt ggacaaaagg accctgcctt 120
ggtgtgagag tgagggcaga gggagctgga gcaagtagaa tttctctaaa taccagctgg 180
ctggggccca ggagattaaa aaacaccggg ctaggttggt cttggcattt gctgacacgc 240
aaagggattg cagagatcca gcccttccaa cctccctctg tccacaggtg gctcacattc 300
agtcccacaa tttgctttct cctcctcaag ggttaagaaa aaaaacgaac ccttccagtc 360
aggtcagtga ctggagagct ccaaggaaa tctctcagtg acctggctgc tggcaccatg 420
gactcagaaa agaaacgctt tactgaagag gccaccaaact acttccggga gagagtcagc 480
ccagtgcatt tgcaaactct gctgactaac aatgaagcct ggaagagatt cgtgactgcg 540
gctgaattgc ccagggatga ggcagatgct ctctacgaag ctctgaagaa gcttagaaca 600
tatgcagcta ttgaggacga atatgtgcag cagaaagatg agcagtttag ggaatggttt 660

```

```

ttgaaagagt ttccccaagt caagaggaag atccaggagt ccatagaaaa gcttcgtgcc 720
cttgcaaatg gtattgaaga ggtccacaga ggctgcacca tctccaatgt ggtgtccagc 780
tccactggcg ctgcctctgg catcatgtcc cttgctggtc ttgttttggc accatttaca 840
gcagggacga gtctggccct tactgcagct ggggtagggc tgggagcagc gtctgctgtg 900
actgggatca ccaccagcat cgtggagcac tcatacacat catcagcaga agctgaagcc 960
agcaggctga ctgcaaccag cattgaccga ttgaaggat ttaaggaagt tatgctgac 1020
atcacacca acttactttc ccttcttaat aattattacg aagccacaca aaccattggg 1080
agtgaatcc gtgccatcag gcaagccaga gccagggccc gactccctgt gaccacctgg 1140
cgaatctcag ctggaagtgg tggtaagca gagagaacga ttgcaggcac cacccgggca 1200
gtgagcagag gagcccgat cctgagtgcg accacttcag gcatcttcct tgcactggat 1260
gtggtcaacc ttgtatacga gtcaaagcac ttgcatgagg gggcaaagtc tgcactctgt 1320
gaggagctga ggcggcaggc tcaggagctg gaggagaatc taatggagct cactcagatc 1380
tatcagcgtc tgaatccatg ccatacccac tgaccccaga ccagtgcagc cagcagggga 1440
ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga taaagagggc 1500
aaggtaaagt ttatggagct gagtgttagt gacttttgga tttctgtagc tgagcacagc 1560
aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat gctggagcct 1620
ggaataaggg agragagggg actggagagt gtggggaata ggaagaagaa atttccttta 1680
gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc agcaatgaga 1740
aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac ttttgatac 1800
agcagaagaa acagcggctc cactaccgac ctgccccggg ttcgatgtcc ttccaagaat 1860
gaagtctttc cctgggtgat gtcctctgcc ctgtctttcm agcatccact ctgtcttgte 1920
ctcctggaag tgtatctcag tcagccagtg gcttcttgat gatggccggt gaaggtggtg 1980
gtttagtgt gatggatccc ctttaggtta tttaggggta tatgtcccct gcttgaacct 2040
tgaaggccag gtaatgagcc atggccattg tccccagctg aggaccaggt gtctctaaaa 2100
acccaaacat cctggagagt atgcgagaac ctaccaagaa aaacagtctc attactcata 2160
tacagcaggc aaagagacag aaaattaact gaaaagcagt ttagagactg ggggaggccg 2220
gatctctaga gccatcctgc tgagtgcctt gtgtgtaagt cctaataaac tcacctactc 2280
accaaaaaaa aaaaaaaa 2298

```

<210> 14
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe
 1 5 10 15
 Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn
 20 25 30
 Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu
 35 40 45
 Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala
 50 55 60
 Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp
 65 70 75 80
 Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile
 85 90 95
 Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly
 100 105 110
 Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly
 115 120 125
 Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr
 130 135 140
 Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala
 145 150 155 160
 Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser
 165 170 175
 Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu
 180 185 190

Lys	Val	Phe	Lys	Glu	Val	Met	Arg	Asp	Ile	Thr	Pro	Asn	Leu	Leu	Ser
	195						200					205			
Leu	Leu	Asn	Asn	Tyr	Tyr	Glu	Ala	Thr	Gln	Thr	Ile	Gly	Ser	Glu	Ile
	210					215					220				
Arg	Ala	Ile	Arg	Gln	Ala	Arg	Ala	Arg	Ala	Arg	Leu	Pro	Val	Thr	Thr
225					230					235					240
Trp	Arg	Ile	Ser	Ala	Gly	Ser	Gly	Gly	Gln	Ala	Glu	Arg	Thr	Ile	Ala
				245					250					255	
Gly	Thr	Thr	Arg	Ala	Val	Ser	Arg	Gly	Ala	Arg	Ile	Leu	Ser	Ala	Thr
			260					265					270		
Thr	Ser	Gly	Ile	Phe	Leu	Ala	Leu	Asp	Val	Val	Asn	Leu	Val	Tyr	Glu
		275					280					285			
Ser	Lys	His	Leu	His	Glu	Gly	Ala	Lys	Ser	Ala	Ser	Ala	Glu	Glu	Leu
	290					295					300				
Arg	Arg	Gln	Ala	Gln	Glu	Leu	Glu	Glu	Asn	Leu	Met	Glu	Leu	Thr	Gln
305					310					315					320
Ile	Tyr	Gln	Arg	Leu	Asn	Pro	Cys	His	Thr	His					
				325						330					

<210> 15
 <211> 1316
 <212> DNA
 <213> Homo sapiens

<400> 15
 agctagacgc cccgaggtcg gagtgaagcg cggggaccga gcccgtctc ccagggagtc 60
 cggggcgcac ggcaccgagg agagcgcggg agccaacctg ggcgcatcat gcgcagggcc 120
 cgggacgctg ggccggtcta caccgcgcgc tgggtcacgt ggcccggacg gcccggcggc 180
 tgccccggcc gggggggcgg ggctcgcgcc gggttgcgt ggacgacgga gacggcggg 240
 cccgcagcgg cctggagcct cccaacccgc gccgcgctgg ccctcgagcg taggagccgc 300
 cccctgcccc cccgcgcggg ccccgcgccc ggccgcccgc cccctatata gcgcgcccc 360
 gcagggcccg cgccaggccg ccagcctcgg agtgggcgcg ggacagtgcg cggcgccccg 420
 cagccaggcc cccgcccccg ccgcatccac ctccctcgcc gcctgcgacc caacgggcgc 480
 cccccgcggc cagctcgcgc cgggcccccg cggccaccat gaagaaggag gtgtgtctcg 540
 tggccttcct caaggcctg ttcgcagagt tcttgccac cctcatcttc gtcttctttg 600
 gcctgggctc ggccctcaag tggccgtcgg cgctgcctac catcctgcag atcgcgctgg 660
 gttttggcct ggccataggc acgctggccc aggcctggg acccgtgagc ggcgccaca 720
 tcaacccgcg catcacctg gccctcttgg tgggcaacca gatctcgctg ctccgggctt 780
 tcttctacgt ggcgccccag ctggtgggcg ccattgccgg ggctggcatc ctctacggtg 840
 tggcaccgct caatgcccgg ggcaatctgg ccgtcaacgc gctcaacaac aacacaacgc 900
 agggccaggc catggtggtg gagctgattc tgaccttcca gctggcactc tgcattctcg 960
 cctccactga ctccgcgcg accagccctg tgggctcccc agccctgtcc attggcctgt 1020
 ctgtcacctt gggccacctt gtcggaatct acttcaactg ctgtccatg aaccagccc 1080
 gctcttttgg ccctgcgggtg gtcattgaatc ggctcagccc cgctcactgg gttttctggg 1140
 tagggcccat cgtgggggcg gtcctggctg ccattcttta cttctacctg ctcttcccca 1200
 actccctgag cctgagtgag cgtgtggcca tcatcaaagg cacgtatgag cctgacgagg 1260
 actgggagga gcagcgggaa gagcgggaaga agaccatgga gctgaccacc cgctga 1316

<210> 16
 <211> 265
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Lys Lys Glu Val Cys Ser Val Ala Phe Leu Lys Ala Val Phe Ala
 1 5 10 15
 Glu Phe Leu Ala Thr Leu Ile Phe Val Phe Phe Gly Leu Gly Ser Ala
 20 25 30

Leu	Lys	Trp	Pro	Ser	Ala	Leu	Pro	Thr	Ile	Leu	Gln	Ile	Ala	Leu	Ala
	35						40				45				
Phe	Gly	Leu	Ala	Ile	Gly	Thr	Leu	Ala	Gln	Ala	Leu	Gly	Pro	Val	Ser
	50					55					60				
Gly	Gly	His	Ile	Asn	Pro	Ala	Ile	Thr	Leu	Ala	Leu	Leu	Val	Gly	Asn
	65				70					75					80
Gln	Ile	Ser	Leu	Leu	Arg	Ala	Phe	Phe	Tyr	Val	Ala	Ala	Gln	Leu	Val
			85						90					95	
Gly	Ala	Ile	Ala	Gly	Ala	Gly	Ile	Leu	Tyr	Gly	Val	Ala	Pro	Leu	Asn
			100					105					110		
Ala	Arg	Gly	Asn	Leu	Ala	Val	Asn	Ala	Leu	Asn	Asn	Asn	Thr	Thr	Gln
		115					120					125			
Gly	Gln	Ala	Met	Val	Val	Glu	Leu	Ile	Leu	Thr	Phe	Gln	Leu	Ala	Leu
	130					135					140				
Cys	Ile	Phe	Ala	Ser	Thr	Asp	Ser	Arg	Arg	Thr	Ser	Pro	Val	Gly	Ser
	145					150				155					160
Pro	Ala	Leu	Ser	Ile	Gly	Leu	Ser	Val	Thr	Leu	Gly	His	Leu	Val	Gly
			165						170					175	
Ile	Tyr	Phe	Thr	Gly	Cys	Ser	Met	Asn	Pro	Ala	Arg	Ser	Phe	Gly	Pro
			180					185					190		
Ala	Val	Val	Met	Asn	Arg	Phe	Ser	Pro	Ala	His	Trp	Val	Phe	Trp	Val
		195					200					205			
Gly	Pro	Ile	Val	Gly	Ala	Val	Leu	Ala	Ala	Ile	Leu	Tyr	Phe	Tyr	Leu
	210					215					220				
Leu	Phe	Pro	Asn	Ser	Leu	Ser	Leu	Ser	Glu	Arg	Val	Ala	Ile	Ile	Lys
	225				230					235					240
Gly	Thr	Tyr	Glu	Pro	Asp	Glu	Asp	Trp	Glu	Glu	Gln	Arg	Glu	Glu	Arg
			245						250					255	
Lys	Lys	Thr	Met	Glu	Leu	Thr	Thr	Arg							
			260					265							

<210> 17
 <211> 1258
 <212> DNA
 <213> Homo sapiens

<400> 17
 cacatatata atgaaaagta atcagtctcc aaagttttta tgtgtcatgt aagattactg 60
 cttgcctctc taaggaaggt cgtgactggt taaatagacg ggcaagggtg aaccttttga 120
 aagatgagct tttgaatata agttgtctgc tagatcatgg tttgtattga actaacaagg 180
 tttgcagatc tgctgactta tataaagcct tttgattcct actaagcttt aagattttaa 240
 aaatgttcaa tgttgaaatt tctgtggggc tctatttttg ctttggcttt ctggtgagag 300
 agtgaggaag cattctttcc ttcaactaagt ttgtctttct tgtcttctgg atagattgat 360
 ttttaagagac taagggaatt tacaaactaa agatttttagt catctggtgg aaaaggagac 420
 ttttaagattg ttttagggctg ggcgggggtga ctcacatctg taatcccagc actttgggag 480
 gccgaggcag gcagaacact tgaaggagtt caagaccagc gtggccaacg tggtgaaacc 540
 ctgtctctac taaaaataca aaaattgttt agctctgttt ttcataatag aaatagaaaa 600
 ggtaaaattg cttttcttct gaaaagaaca agtattgttc atccaagaag ggtttttgtg 660
 actgaatcag cagtgcctgc cctagtcata gctgtgcttc aaaaacctca gcatgattag 720
 tgttggagca aaacaaggaa gcaaagcaaa tactgttttt gaaattctat ctgttgcttg 780
 aactattttg taataattaa actttgatgt tgagaaatca caactttatt gtacacttca 840
 ttgcaacttg aaattcatgg tcttaaagtg agatttgaat ttctattgag cgctttttaa 900
 aaagtaatac caaaccataa agttaaaatc tatgtatatt gagtcatatc taaaaccacg 960
 tataaacata aattgtattt cctgttttaa ttccagggga agtactgttt gggaaagcta 1020
 ttattaggta aatgttttac aaattactgt ttctcacttt cagtcatacc ctaatgatcc 1080
 cagcaagata atgtcctgtc ttctaagatg tgcatacagc ctggtacata ctgaaaaccc 1140
 tataaggtcc tggataattt ttgtttgatt attcattgaa gaaacattta ttttccaatt 1200
 gtgtgaagtt tttgactggt aataaaagaa tctgtcaacc atcaaaaaaa aaaaaaaa 1258

<210> 18
 <211> 22
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Val Cys Ile Glu Leu Thr Arg Phe Ala Asp Leu Leu Thr Tyr Ile
 1 5 10 15
 Lys Leu Phe Asp Ser Tyr
 20

<210> 19
 <211> 983
 <212> DNA
 <213> Homo sapiens

<400> 19
 gtggaattca tggcatctac ttcgatgac tattgcagag tgcccatgga agacggggat 60
 aagcgtgtga agcttctgct ggggatagga attctggtgc tcctgatcat cgtgattctg 120
 ggggtgccct tgattatctt caccatcaag gccaacagcg aggcctgccg ggacggcctt 180
 cgggcagtga tggagtgtcg caatgtcacc catctcctgc aacaagagct gaccgaggcc 240
 cagaagggct ttcaggatgt ggaggcccag gccgccacct gcaaccacac tgtgatggcc 300
 ctaatggctt ccctggatgc agagaaggcc caaggacaaa agaaagtgga ggagcttgag 360
 ggagagatca ctacattaaa ccataagctt caggacgcgt ctgcagaggt ggagcgactg 420
 agaagagaaa accaggtctt aagcgtgaga atcgcgagaca agaagtacta cccagctcc 480
 caggactcca gctccgctgc ggcgccccag ctgctgattg tgctgctggg cctcagcgct 540
 ctgctgcagt gagatcccag gaagctggca catcttgaa ggtccgtcct gctcggcttt 600
 tcgcttgaac attcccttga tctcatcagt tctgagcggg tcatggggca acacgggttag 660
 cggggagagc acggggtagc cggagaaggc cctctggagc aggtctggag gggccatggg 720
 gcagtcctgg gtgtggggac acagtcgggt tgaccaggg ctgtctccct ccagagcctc 780
 cctccggaca atgagtcctt cctcttgtct cccaccctga gattgggcat ggggtgcggg 840
 gtggggggca tgtgtgtcct gttgttatgg gttttttttg cggggggggg tgcttttttc 900
 tggggctctt gagctccaaa aaataaacac ttccttttag ggagagcaaa aaaaaaaaaa 960
 aaaaaaaaaa aaaaaaaaaa aaa 983

<210> 20
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
 1 5 10 15
 Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
 20 25 30
 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
 35 40 45
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 50 55 60
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 65 70 75 80
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 85 90 95
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 100 105 110
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 115 120 125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 130 135 140
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 145 150 155 160
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 165 170 175
 Ala Leu Leu Gln
 180

<210> 21
 <211> 4859
 <212> DNA
 <213> Homo sapiens

<400> 21
 cacgttgggt gacataatgg ggttttttta attatagatt cacactgcat ttattcatca 60
 cccctgtcct ctcatccata actcaaattt actaccagca acacaaaata caaagatgtg 120
 tccagtttca ctacagctct tcgcgtttac aagtgtcgag cgcttgcttt cggaacgcc 180
 ttgtgattgg ccgagccaat gccagtgaca tcaaccaact tacttttgat tggaaggctg 240
 gttgctggga ctgtagcgtt tgcaggaagt cacttaactg tttgggagct ggaaaaccga 300
 agctgaagtt ctcttttggc ataggaacga gcgcaactga ctaggaaaga tgtgtcccaa 360
 agctccgcaa gctggaacgt gagccaggag gcccggaccg gccacgggac cgcgaggcac 420
 tccgaaagtg tgcggctgcc ccttccctgc ctcccagctg ttaccctttt aaatgtcagt 480
 gttcgaggct gtaggggtag cacgaggcag cgaaacggaa cagtcggatt ggccgcacgc 540
 ctcagttcta gacgcacctc tccaccgaag ccgttctgac tggcaggggg agaaagtaaa 600
 cagagttgaa tcaccctccc cactggccaa ttggaggggg tttggtttgt gacgtgatgg 660
 gattctgcga aattgttact gagcaagaga atgccggaac gtgcggaccg gccggagcag 720
 gggttcagaa gccgtcagtg gactcgggaa aaagtgtctc ttagacctgg cgctcggcgg 780
 ggccctcgcc acccgctcg ggggtgatcg gtgaatgtcc tggggctttg gctcgacggc 840
 gaggcggccg agggcgtgca cctctcttgc agtttctctc cccagcgcct cgggggctgt 900
 ttcagtcgaa taaacttgcg accgccacgt gtggcatctt tccaaggag cgggctcaga 960
 ggggccggcg cgcccgctcg gggatcgcg ccggcgcggg gcagggggcg cggctagagg 1020
 cggcgcgcg gcggagccc gggccgtgga tgctgcgtgc ggagggcgtg ccggttacgt 1080
 aaagatgagg ggctgaggtc gcctcgcgcc tcctgcgagt cggaagcgcc ccgcgcccc 1140
 gcccccttgg ccgcgcgcgc gtgcggggcg ggcggtcgt cgtccgaggc cagggagggc 1200
 gagccgaacc tccgcagcca ccgocaaagt tgtccgcgcc gcctgggctg ccgtcgccc 1260
 caccatgtcc gcggccgcct acatggactt cgtggctgcc cagtgtctgg tttccatttc 1320
 gaaccgcgct gcggtgccgg agcatggggt cgtccggac gccgagcggc tgcgactacc 1380
 tgagcgcgag gtgaccaagg agcacggtga cccgggggac acctggaagg attactgcac 1440
 actggtcacc atcgccaaga gcttggttga cctgaacaag taccgacca tccagacccc 1500
 ctccgtgtgc agcgacagtc tggaaagtcc agatgaggat atgggatccg acagcgacgt 1560
 gaccaccgaa tctgggtcga gtccttccca cagcccggag gagagacagg atcctggcag 1620
 cgcgcccagc ccgctctccc tctctcatcc tggagtggct gcgaagggga aacacgcctc 1680
 cgaaaagagg cacaagtgcc cctacagtgg ctgtgggaaa gtctatggaa aatcctccca 1740
 tctcaaagcc cattacagag tgcatacagg tgaacggccc ttcccctgca cgtggccaga 1800
 ctgccttaaa aagtctctcc gctcagacga gctgacccgc cactaccgga cccacactgg 1860
 ggaaaagcag ttccgctgtc cgctgtgtga gaagcgcttc atgaggagt accacctcac 1920
 aaagcacgcc cggcggcaca ccgagttcca cccagcatg atcaagcgat cgaaaaaggc 1980
 gctggccaac gctttgtgag gtgctgccc tggagccag ggagggatg accccgaaag 2040
 gacaaaagta ctcccaggaa acagacgcgt gaaaactgag cccagaaga ggcacacttg 2100
 acggcacagg aagtcactgc tcttttgtca atattctgat tttcctctcc ctgcattgtt 2160
 tttaaaaagc acattgtagc ctaagatcaa agtcaacaac actcggctcc cttgaagagg 2220
 caactctctg aaccgctctc tgactgttgg agggaaggca aatgcttttg ggttttttgg 2280
 tttttgtttt tgtttttttt tctcctttta tttttttgcg ggggagggtg gggagtgggt 2340
 gggggggagg gggtaaggcc aagactgggt agattttaaa gattcaacac tgggtgtacat 2400
 atgtccgctg ggtgagttga cctgtggcct cgcacagtga ttctaggccc tttatgcttg 2460
 ctgtctctca gaattgtttt cttacctttt aatgtaatga cgagtgtgct tcagtttgtt 2520
 tagcaaaacc actctcttga atcacgttaa cttttgagat taaaaaaaaa aacgccatag 2580

```

cacagctgtc tttatgcaag caagagcaca tctactccag catgatctgt catctaaaga 2640
cttgaataca aaaaacagtt acttatagtc aatgggtaag cagagtctga atttatacta 2700
atcaagacaa acotttgaaa gggttacctt agtacagAAC ttttaaacct tgccttctgt 2760
gagttgtact ttttgaacat aagctgcact tttatcttct aatgcagagg atgaataagt 2820
taaatacatg ctttgaggat agaagcagat gttctgtttg gcaccacgtt ataactctgt 2880
tatttttaca tatacacgtt tccctaagaa atcatgCGCA gagatgtgag ggcagaatat 2940
acacaacaga tgctgaagga gaaggagggt agtgttttgc aaaagaaaaa gaaaagaacc 3000
aacagaattt taactctatt aacttttcca aatttttcta tgcttttagt taacatcatt 3060
attgtatcct aatgccacta ggggagagag cttttgactc tgttgggttt tatttgaatg 3120
tgtgcataac agtaatgaga tctggaaaca cctatctttt ggggaaaaag gtttgttggg 3180
ctccttcctg tgttcctaca aaactccac tctcaggtgc aagagttatg tagaaggaaa 3240
gggagctgaa ataggaacag aaaaatcaac ccctataact agtgaacacc aagggaat 3300
accacaatga tttcagagga gactctgcaa aatcgtccct tgtggagaat gcaggcaaca 3360
tggaatacta cgaatgaaat cacatcactg tatcttttac atcaatagcc tcaccactaa 3420
tatatcttgt atctaggtgt ctataatggc tgaaaccact acatccatct atgccattta 3480
cctgaaaact taactgtggc ctttatgagg ccagaaaagt gaactgagtt ttgtagttaa 3540
gacctcaaat gaggggagtc agcagtgatc atgggggaaa tgtttacatt ttttttttct 3600
tcagaagtaa cgctttctga tgatttttat tgatatttaa aacagggagc tatggtgcac 3660
tctagtttat acttgcgtc tgaaatgtgt aaacataggg tgcctacctt tttcacctga 3720
cccatactcg tttctgattc agaatcagtg tgggctcctg cagtgggCGC gggtcacggc 3780
tgactccaac ttccaataca acagccatca ctagcacagt gtttttttgt ttaaccaacg 3840
tagtgttatt agtagttcta taaagagaac tgcttttaac attagggact gggagcagtc 3900
catgggataa aaaggaaagt gttttctcac gagaaaacat gtcaggaaaa ataaagaaca 3960
ctttctacct ctgtttcaga tttttgaaac acttatttta aaccaaattt taatttctgt 4020
gtccaaaata agttttaagg acatctgttc ttccatacga aatagggttag gctgcctatt 4080
tctcactgag ctcatggaat ggttctgctt atgatactct gcacgctgcc ttttagtgag 4140
tgaggagttt ggggttgctt agcacttgct aacttgtaaa aagtcactct tccctcacag 4200
aaagaaacga aagaaagcaa agcaaagtcA gtgaaagaca atctttatag tttcaggagt 4260
aaatctaaat gtggcttttg tcaagcactt agatggatat aaatgcagca acttgtttta 4320
aaaaaatgca catttacttc ccaaaaaagt tgttacttgc cttttcaagt gtgacaaaact 4380
cacatttgat attctcttat atgttatagt aatgtaacgt ataaactcaa gcctttttat 4440
tctttgtgat taaatcctgt tttaaaatgt cacaaaacag gaaccagcat tctaattaga 4500
tttactatat caagatatgg ttcaaatagg actactagag ttcattgaac actaaaacta 4560
tgaaacaatt actttttata ttaaaaagac catggattta acttatgaaa atccaaatgc 4620
aggatagtaa tttttgttta cttttttaac caaactgaat ttttgaaaga ctattgcagg 4680
tgtttaaaaa gaaagaaaag ttgttttatc taatactgta agtagttgtc atattctgga 4740
aaatttaata gtttttaggt taagatatct cctctctttg gttagggaag aagaaagccc 4800
ttcaccattg tggaatgatg ccctggcttt aagggttagc tccacatcat gottctctt 4859

```

<210> 22
 <211> 244
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Ser Ala Ala Ala Tyr Met Asp Phe Val Ala Ala Gln Cys Leu Val
 1 5 10 15
 Ser Ile Ser Asn Arg Ala Ala Val Pro Glu His Gly Val Ala Pro Asp
 20 25 30
 Ala Glu Arg Leu Arg Leu Pro Glu Arg Glu Val Thr Lys Glu His Gly
 35 40 45
 Asp Pro Gly Asp Thr Trp Lys Asp Tyr Cys Thr Leu Val Thr Ile Ala
 50 55 60
 Lys Ser Leu Leu Asp Leu Asn Lys Tyr Arg Pro Ile Gln Thr Pro Ser
 65 70 75 80
 Val Cys Ser Asp Ser Leu Glu Ser Pro Asp Glu Asp Met Gly Ser Asp
 85 90 95
 Ser Asp Val Thr Thr Glu Ser Gly Ser Ser Pro Ser His Ser Pro Glu
 100 105 110

Glu Arg Gln Asp Pro Gly Ser Ala Pro Ser Pro Leu Ser Leu Leu His
 115 120 125
 Pro Gly Val Ala Ala Lys Gly Lys His Ala Ser Glu Lys Arg His Lys
 130 135 140
 Cys Pro Tyr Ser Gly Cys Gly Lys Val Tyr Gly Lys Ser Ser His Leu
 145 150 155 160
 Lys Ala His Tyr Arg Val His Thr Gly Glu Arg Pro Phe Pro Cys Thr
 165 170 175
 Trp Pro Asp Cys Leu Lys Lys Phe Ser Arg Ser Asp Glu Leu Thr Arg
 180 185 190
 His Tyr Arg Thr His Thr Gly Glu Lys Gln Phe Arg Cys Pro Leu Cys
 195 200 205
 Glu Lys Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala Arg Arg
 210 215 220
 His Thr Glu Phe His Pro Ser Met Ile Lys Arg Ser Lys Lys Ala Leu
 225 230 235 240
 Ala Asn Ala Leu

<210> 23
 <211> 1304
 <212> DNA
 <213> Homo sapiens

<400> 23
 ttcccagatg cacaggagga gaagcaggag ctgtcgggaa gatcagaagc cagtcatgga 60
 tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctggggc ggcgccctgg 120
 ggccccggag agcaagtga gccggggagc cctgtacaca ggcttttcca tctggtgac 180
 tctgtcctc gctggccagg ccaccaccgc ctacttcctg taccagcagc agggccggct 240
 ggacaaactg acagtcacct ccagaaacct gcagctggag aacctgcgca tgaagcttcc 300
 caagcctccc aagcctgtga gcaagatgag catggccacc ccgctgctga tgcaggcgct 360
 gcccatggga gccctgcccc aggggcccac gcagaatgcc accaagtatg gcaacatgac 420
 agaggaccat gtgatgcacc tgctccagaa tgctgacccc ctgaagggtg acccgccact 480
 gaagggggagc ttcccggaga acctgagaca ccttaagaac accatggaga ccatagactg 540
 gaaggtcttt gagagctgga tgcaccattg gctcctgttt gaaatgagca ggcactcctt 600
 ggagcaaaag cccactgacg ctccaccgaa agagtcaact gaactggagg acccgtcttc 660
 tgggctgggt gtgaccaagc aggatctggg ccagatcccc atgtgagagc agcagaggcg 720
 gtcttcaaca tcctgccagc ccacacacgc tacagctttc ttgctccctt cagcccccag 780
 cccctcccc atgtcccacc ctgtacctca tcccatgaga cctggtgcct ggctctttcg 840
 tcacccttgt acaagacaaa ccaagtggga acagcagata acaatgcagc aaggccctgc 900
 tgcccaatct ccatctgtca acaggggagt gaggtcccag gaagtggcca aaagctagac 960
 agatccccgt tcctgacatc acagcagcct ccaacacaag gctccaagac ctagggtcat 1020
 ggacgagatg ggaaggcaca gggagaaggg ataaccctac acccagacct caggctggac 1080
 atgctgactg tcctctcccc tcagcccttt ggccttggct tttctagcct atttacctgc 1140
 aggctgagcc actctcttcc ctttccccag catcactccc caaggaagag ccaatgtttt 1200
 ggacccataa tcctttctgc cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260
 ctttcagggc catggttcac attagaataa aaggtagtaa ttag 1304

<210> 24
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val
 1 5 10 15
 Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met
 20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala
 35 40 45
 Leu Tyr Thr Gly Phe Ser Ile Leu Val Thr Leu Leu Leu Ala Gly Gln
 50 55 60
 Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys
 65 70 75 80
 Leu Thr Val Thr Ser Gln Asn Leu Gln Leu Glu Asn Leu Arg Met Lys
 85 90 95
 Leu Pro Lys Pro Pro Lys Pro Val Ser Lys Met Arg Met Ala Thr Pro
 100 105 110
 Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met
 115 120 125
 Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His
 130 135 140
 Leu Leu Gln Asn Ala Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly
 145 150 155 160
 Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile
 165 170 175
 Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu
 180 185 190
 Met Ser Arg His Ser Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys
 195 200 205
 Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys
 210 215 220
 Gln Asp Leu Gly Pro Val Pro Met
 225 230

<210> 25
 <211> 1615
 <212> DNA
 <213> Homo sapiens

<400> 25
 gaattcggca cgaggcaagg acccctcccc ctgcgggcgc tcccatggca cagttcgcgt 60
 tcgagagtga cctgcactcg ctgcttcagc tggatgcacc catccccaat gcacccctg 120
 cgcgctggca gcgcaaagcc aaggaagccg caggcccggc cccctcacc atgcgggccg 180
 ccaaccgata ccacagcgcc ggcaggactc cgggccgaac tcctggcaaa tccagttcca 240
 aggttcagac cactcctagc aaacctggcg gtgaccgcta tatcccccac cgcagtgtcg 300
 ccagatgga ggtggccagc ttctcctga gcaaggagaa ccagcctgaa aacagccaga 360
 cgccaccaa gaaggaacat cagaaagcct gggctttgaa cctgaacggg tttgatgtag 420
 aggaagcaa gatccttcgg ctgagtggaa aaccacaaaa tgcgccagag ggttatcaga 480
 acagactgaa agtactctac agccaaaagg ccactcctgg ctccagccgg aagacctgcc 540
 gttacattcc ttccctgcca gaccgtatcc tggatgcgcc tgaaatccga aatgactatt 600
 acctgaacct tgtggattgg agttctggga atgtactggc cgtggcactg gacaacagt 660
 tgtacctgtg gagtgcagg tctggtgaca tcctgcagct tttgcaaatg gagcagcctg 720
 gggaatatat atcctctgtg gcctggatca aagagggcaa ctacttggct gtgggcacca 780
 gcagtgtgta ggtgcagcta tgggatgtgc agcagcagaa acgggttcga aatatgacca 840
 gtcactctgc ccgagtgggc tccetaagct ggaacagcta tatcctgtcc agtggttcac 900
 gttctggcca catccaccac catgatgttc gggtagcaga acaccatgtg gccacactga 960
 gtggccacag ccaggaagtg tgtgggctgc gctgggcccc agatggacga catttggcca 1020
 gtggtggtaa tgataacttg gtcaatgtgt ggcctagtgc tcctggagag ggtggctggg 1080
 ttctcttgca gacattcacc cagcatcaag gggctgtcaa ggccgtagca tgggtgtccct 1140
 ggcagtccaa tgtcctggca acaggagggg gcaccagtga tcgacacatt cgcactctgga 1200
 atgtgtgctc tggggcctgt ctgagtgccg tggagtccca ttcccaggtg tgctccatcc 1260
 tctggtctcc ccattacaag gagctcatct caggccatgg ctttgcacag aaccagctag 1320
 ttatttggaa gtacccaacc atggccaagg tggctgaact caaagggtcac acatccgggg 1380
 tcctgagtct gaccatgagc ccagatgggg ccacagtggc atccgcagca gcagatgaga 1440
 ccctgaggct atggcgctgt tttgagttgg accctgcgcg gcggcggggag cgggagaagg 1500

ccagtgcagc caaaagcagc ctcattccacc aaggcatccg ctgaagacca acccatcacc 1560
 tcagttgttt tttatttttc taataaagtc atgtctccct tcatgttttt ttttt 1615

<210> 26
 <211> 499
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Ala Gln Phe Ala Phe Glu Ser Asp Leu His Ser Leu Leu Gln Leu
 1 5 10 15
 Asp Ala Pro Ile Pro Asn Ala Pro Pro Ala Arg Trp Gln Arg Lys Ala
 20 25 30
 Lys Glu Ala Ala Gly Pro Ala Pro Ser Pro Met Arg Ala Ala Asn Arg
 35 40 45
 Ser His Ser Ala Gly Arg Thr Pro Gly Arg Thr Pro Gly Lys Ser Ser
 50 55 60
 Ser Lys Val Gln Thr Thr Pro Ser Lys Pro Gly Gly Asp Arg Tyr Ile
 65 70 75 80
 Pro His Arg Ser Ala Ala Gln Met Glu Val Ala Ser Phe Leu Leu Ser
 85 90 95
 Lys Glu Asn Gln Pro Glu Asn Ser Gln Thr Pro Thr Lys Lys Glu His
 100 105 110
 Gln Lys Ala Trp Ala Leu Asn Leu Asn Gly Phe Asp Val Glu Glu Ala
 115 120 125
 Lys Ile Leu Arg Leu Ser Gly Lys Pro Gln Asn Ala Pro Glu Gly Tyr
 130 135 140
 Gln Asn Arg Leu Lys Val Leu Tyr Ser Gln Lys Ala Thr Pro Gly Ser
 145 150 155 160
 Ser Arg Lys Thr Cys Arg Tyr Ile Pro Ser Leu Pro Asp Arg Ile Leu
 165 170 175
 Asp Ala Pro Glu Ile Arg Asn Asp Tyr Tyr Leu Asn Leu Val Asp Trp
 180 185 190
 Ser Ser Gly Asn Val Leu Ala Val Ala Leu Asp Asn Ser Val Tyr Leu
 195 200 205
 Trp Ser Ala Ser Ser Gly Asp Ile Leu Gln Leu Leu Gln Met Glu Gln
 210 215 220
 Pro Gly Glu Tyr Ile Ser Ser Val Ala Trp Ile Lys Glu Gly Asn Tyr
 225 230 235 240
 Leu Ala Val Gly Thr Ser Ser Ala Glu Val Gln Leu Trp Asp Val Gln
 245 250 255
 Gln Gln Lys Arg Leu Arg Asn Met Thr Ser His Ser Ala Arg Val Gly
 260 265 270
 Ser Leu Ser Trp Asn Ser Tyr Ile Leu Ser Ser Gly Ser Arg Ser Gly
 275 280 285
 His Ile His His His Asp Val Arg Val Ala Glu His His Val Ala Thr
 290 295 300
 Leu Ser Gly His Ser Gln Glu Val Cys Gly Leu Arg Trp Ala Pro Asp
 305 310 315 320
 Gly Arg His Leu Ala Ser Gly Gly Asn Asp Asn Leu Val Asn Val Trp
 325 330 335
 Pro Ser Ala Pro Gly Glu Gly Gly Trp Val Pro Leu Gln Thr Phe Thr
 340 345 350
 Gln His Gln Gly Ala Val Lys Ala Val Ala Trp Cys Pro Trp Gln Ser
 355 360 365
 Asn Val Leu Ala Thr Gly Gly Gly Thr Ser Asp Arg His Ile Arg Ile
 370 375 380
 Trp Asn Val Cys Ser Gly Ala Cys Leu Ser Ala Val Asp Ala His Ser
 385 390 395 400

Gln	Val	Cys	Ser	Ile	Leu	Trp	Ser	Pro	His	Tyr	Lys	Glu	Leu	Ile	Ser
				405					410					415	
Gly	His	Gly	Phe	Ala	Gln	Asn	Gln	Leu	Val	Ile	Trp	Lys	Tyr	Pro	Thr
			420					425					430		
Met	Ala	Lys	Val	Ala	Glu	Leu	Lys	Gly	His	Thr	Ser	Arg	Val	Leu	Ser
		435					440					445			
Leu	Thr	Met	Ser	Pro	Asp	Gly	Ala	Thr	Val	Ala	Ser	Ala	Ala	Ala	Asp
	450					455					460				
Glu	Thr	Leu	Arg	Leu	Trp	Arg	Cys	Phe	Glu	Leu	Asp	Pro	Ala	Arg	Arg
465					470					475					480
Arg	Glu	Arg	Glu	Lys	Ala	Ser	Ala	Ala	Lys	Ser	Ser	Leu	Ile	His	Gln
				485					490					495	
Gly	Ile	Arg													

<210> 27
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 27
 ctctgacgag cctccttaaa actctgccgt taaaatgggg gcgggttttt caactcaaaa 60
 agcgtcaat ttttttcttt tcaaaaaaag ctgatgaggt cggaaaaaag ggagaagaaa 120
 ccggcaccct ctctgagagg caacagaagc agcaattgtt tcagcgaaaa aagcagcaag 180
 ggagggagtg aaggaaaaaa gcaaaaaaag gggcgacacg caagtgcctg taggggtgaa 240
 aggagcaggg accggcgatc taggggggga tcagctacaa aagaaactgt cactgggagc 300
 ggtgcggcca aggaggaagc agtgctgcca ggctctgctc cagggcacag ctggctggcg 360
 gctgccctgt ccgcagcaaa ggggcacagg ccggggacag cgagaggtgg caaagtggca 420
 ccgggcgcgg aggctgctga gcgctcgccg agacgcggac cggactggct gccccggaac 480
 tgcggcgact ctccctaact agaacttggc ctacgtttcc caggactctc cccatctcca 540
 gagggcccca caaaaccggg aaaggaagga aaggacagcg gcggcagcag ctcaatgagt 600
 gcctacagca gaaagcctga acgagctcgg tcgtaggcgg gaagttcccg ggggctgccc 660
 agtgcagccg caatgctgcc gcgagctgcc ccagcagtcg gggctccgta gacgctttcc 720
 gcatcactct ccttctctcg gctgccggga gtcccgggac ctggcggggc cggcatgacg 780
 ggcttctcgg gggcccgccg cacgcccggc agcctccgga gacgcgcgcc gagcccggt 840
 cccacggcct ctgaggctcg gcggggctgc ggctgcctgg cgggcgggct ccggagcttt 900
 cctgagccgg cattagccca cggcttgccc cggacgcgac caaaggctct tctggagaag 960
 cccagagcac tgggcaatcg ttacgacctg taacttgagg gccaccgaac tgctactccc 1020
 gttcgctttt ggcatcatc ttttaaccct ccggagcagc tcagcatcca gccaccgcgg 1080
 cgctctccca gcagcggagg acccaggact atcccttcgg cgagacggat ggaaaccgag 1140
 ccccctggag gacctgccc tgcagttctg cctcacacgg ctcaagtcac caccgtgaac 1200
 aagggaccct aaagaatggc cgagccttgg gggaacgagt tggcgtccgc agctgccagg 1260
 ggggacctag agcaacttac tagtttgttg caaaataatg taaacgtcaa tgcacaaaat 1320
 ggatttgaa ggactgcgct gcaggttatg aaacttgaa atcccagat tgccaggaga 1380
 ctgctactta gaggtgctaa tcccgatttg aaagaccgaa ctggtttcgc tgtcattcat 1440
 gatgcggcca gagcaggttt cctggacact ttacagactt tgctggagtt tcaagctgat 1500
 gttaacatcg aggataatga agggaaacct cccttgcact tggctgcaa agaaggtcac 1560
 ctccgggttg tggagtctct ggtgaagcac acggccagca atgtggggca tcggaaccat 1620
 aagggggaca ccgcctgtga tttggccagg ctctatggga ggaatgaggt tgttagcctg 1680
 atgcaggcaa acggggctgg gggagccaca aatcttcaat aaacgtgggg agggctcccc 1740
 cacgttgccct ctactttatc aattaactga gtagctctcc tgacttttaa tgtcatttgt 1800
 taaaatacag ttctgtcata tgtaagcag ctaaattttc tgaaactgca taagtgaaaa 1860
 tcttacaaca ggtttatgaa tatatttaag caacatcttt ttaacctgca aaatctgttc 1920
 taacatgtaa ttgcagataa ctttgacttt cttctgaata ttttatcttt ccttggcctt 1980
 tcccttgctt ccccttttgc caatctcaac acccaagttg aagactttgt ttttaaatg 2040
 gtttgccttg atgcttttgt ctaattaaaa cactttcaaa acaggaaaaa aaaaaaaaaa 2100
 aaa 2103

<210> 28
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Ala Glu Pro Trp Gly Asn Glu Leu Ala Ser Ala Ala Ala Arg Gly
 1 5 10 15
 Asp Leu Glu Gln Leu Thr Ser Leu Leu Gln Asn Asn Val Asn Val Asn
 20 25 30
 Ala Gln Asn Gly Phe Gly Arg Thr Ala Leu Gln Val Met Lys Leu Gly
 35 40 45
 Asn Pro Glu Ile Ala Arg Arg Leu Leu Leu Arg Gly Ala Asn Pro Asp
 50 55 60
 Leu Lys Asp Arg Thr Gly Phe Ala Val Ile His Asp Ala Ala Arg Ala
 65 70 75 80
 Gly Phe Leu Asp Thr Leu Gln Thr Leu Leu Glu Phe Gln Ala Asp Val
 85 90 95
 Asn Ile Glu Asp Asn Glu Gly Asn Leu Pro Leu His Leu Ala Ala Lys
 100 105 110
 Glu Gly His Leu Arg Val Val Glu Phe Leu Val Lys His Thr Ala Ser
 115 120 125
 Asn Val Gly His Arg Asn His Lys Gly Asp Thr Ala Cys Asp Leu Ala
 130 135 140
 Arg Leu Tyr Gly Arg Asn Glu Val Val Ser Leu Met Gln Ala Asn Gly
 145 150 155 160
 Ala Gly Gly Ala Thr Asn Leu Gln
 165

<210> 29
 <211> 4049
 <212> DNA
 <213> Homo sapiens

<400> 29
 gcggccgcac tcagcgccac gcgtcgaaag cgcaggcccc gaggaccgc cgcactgaca 60
 gtatgagccg cacagcctac acggtgggag cctgtcttct cctcttgggg accctgctgc 120
 cggtgtctga agggaaaaag aaaggggtccc aaggtgccat ccccccgcga gacaaggccc 180
 agcacaatga ctacagagcag actcagtcgc ccagcagcc tggctccagg aaccgggggc 240
 ggggccaaag gcggggcact gccatgcccg gggaggaggt gctggagtcc agccaagagg 300
 ccctgcatgt gacggagcgc aaatacctga agcgagactg gtgcaaaacc cagccgctta 360
 agcagaccat ccacgaggaa ggctgcaaca gtcgcaccat catcaaccgc ttctgttacg 420
 gccagtgcaa ctctttctac atccccaggc acatccggaa ggaggaaggt tccttttcagt 480
 cctgtctcct ctgcaagccc aagaattca ctaccatgat ggtcacactc aactgccctg 540
 aactacagcc acctaccaag aagaagagag tcacacgtgt gaagcagtgt cgttgcatat 600
 ccatcgattt ggattaagcc aaatccaggt gcaccagca tgtcctagga atgcagcccc 660
 aggaagtccc agacctaaaa caaccagatt cttacttggc ttaaacctag aggccagaag 720
 aacccccagc tgcctcctgg caggagcctg cttgtgcgta gttcgtgtgc atgagtgtgg 780
 atgggtgcct gtgggtgttt ttagacacca gagaaaacac agtctctgct agagagcact 840
 ccctattttg taaacatata tgctttaatg gggatgtacc agaaaccac ctcaccccg 900
 ctcacatcta aaggggcggg gccgtggtct ggttctgact ttgtgttttt gtgccctcct 960
 ggggaccaga atctcctttc ggaatgaatg ttcatggaag aggtcctctt gagggcaaga 1020
 gacctgtttt agtgctgcat tcgacatgga aaagtccctt taacctgtgc ttgcatcctc 1080
 ctttctctct cctcctcaca atccatctct tcttaagttg atagtacta tgtcagtcta 1140
 atctcttggt tgccaagggt cctaaattaa ttcaactaac catgatgcaa atgtttttca 1200
 ttttgtgaag accctccaga ctctgggaga ggctgggtgt ggcaaggaca agcaggatag 1260
 tggagtgaga aagggagggt ggagggtgag gccaaatcag gtccagcaaa agtcagtagg 1320
 gacattgcag aagcttgaaa ggccaataacc agaacacagg ctgatgcttc tgagaaagtc 1380


```

ttttcctagt atttaacaga acccaagtga acagaggaga aatgagattg ccagaaagtg 1440
attaacttttg gccgttgcaa tctgctcaaa cctaaccacca aactgaaaac ataaatactg 1500
accactccta tgttcggacc caagcaagtt agctaaacca aaccaactcc tctgctttgt 1560
ccctcaggtg gaaaagagag gtagtttaga actctctgca taggggtggg aattaatcaa 1620
aaacckcaga ggctgaaatt cctaatacct ttcctttatc gtggttatag tcagctcatt 1680
tccattccac tatttcccat aatgcttctg agagccacta acttgattga taaagatcct 1740
gcctctgctg agtgtaacctg acagtaagtc taaagatgar agagtttagg gactactctg 1800
ttttagcaag aratatktg ggggtctttt tgttttaact attgtcagga gattgggcta 1860
ragagaagac gacgagagta aggaaataaa gggrattgcc tctggctaga gagtaagtta 1920
gggtttaata cctggtagaa atgtaaggga tatgacctcc ctttctttat gtgctcactg 1980
aggatctgag gggacctgt taggagagca tagcatcatg atgtattagc tgttcatctg 2040
ctactggttg gatggacata actattgtaa ctattcagta tttactggta ggcaactgcc 2100
tctgattaaa cttggcctac tggcaatggc tacttaggat tgatctaagg gccaaagtgc 2160
agggtgggtg aactttattg tactttggat ttggttaacc tgttttcttc aagcctgagg 2220
ttttatatac aaactccctg aatactcttt ttgccttgta tcttctcagc ctctagcca 2280
agtcctatgt aatatggaaa acaaactctg cagacttgag attcagttgc cgatcaaggc 2340
tctggcatto agagaacctt tgcaactcga gaagctgttt ttatttcgtt tttgttttga 2400
tccagtgtc tcccatctaa caactaaaca ggagccattt caaggcgga gatattttta 2460
acacccaaaa tgttggtct gattttcaaa cttttaaact cactactgat gattctcagc 2520
ctaggcgaat ttgtccaaac acatagtgtg tgtgttttgt atacactgta tgaccccacc 2580
ccaaatcttt gtattgtcca cattctccaa caataaagca cagagtggat ttaattaagc 2640
acacaaatgc taaggcagaa ttttgagggt gggagagaag aaaagggaag gaagctgaaa 2700
atgtaaaacc acaccagga ggaaaaatga cattcagaac cagcaaacac tgaatttctc 2760
ttgttgtttt aactctgcca caagaatgca atttcgttaa tggagatgac ttaagttggc 2820
agcagtaatc ttcttttagg agcttgtaac acagtcttgc acataagtgc agatttggt 2880
caagtaaaga gaatttcctc aacactaact tcaactggat aatcagcagc gtaactacco 2940
taaaagcata tcaactagcca aagagggaag tatctgttct tcttactgtg cctatattaa 3000
gactagtaca aatgtggtgt gtcttccaac tttcattgaa aatgccatat ctataccata 3060
ttttattcga gtcactgatg atgtaatgat atatttttctc attattatag tagaatattt 3120
ttatggcaag atatttgtgg tcttgatcat acctattaaa ataatgcaa acaccaaata 3180
tgaattttat gatgtacact ttgtgcttgg cattaaaaga aaaaaacaca catcctggaa 3240
gtctgtaagt tgttttttgt tactgtaggt cttcaaagtt aagagtgtaa gtgaaaaatc 3300
tggaggagag gataatttcc actgtgtgga atgtgaatag ttaaatagaaa agttatgggt 3360
atttaatgta attattactt caaatccctt ggtcactgtg atttcaagca tgttttcttt 3420
ttctccttta tatgactttc tctgagttgg gcaaagaaga agctgacaca ccgtatgttg 3480
ttagagtctt ttatctggtc aggggaacaa aaactctgac ccagctgaac atgtcttctc 3540
gagtcagtgc ctgaatcttt attttttaaa ttgaatgttc cttaaagggt aacatttcta 3600
aagcaatatt aagaaagact ttaaattgta ttttggaga cttacgatgc atgtatacaa 3660
acgaatagca gataatgatg actagttcac acataaagtc cttttaagga gaaaatctaa 3720
aatgaaaagt ggataaacag aacatttata agtgatcagt taatgcctaa gagtgaagt 3780
agttctattg acattcctca agatatttaa tatcaactgc attatgtatt atgtctgctt 3840
aaatcattta aaaacggcaa agaattatat agactatgag gtaccttgct gtgtaggagg 3900
atgaaagggg agttgatagt ctcataaaaac taatttggct tcaagtttca tgaatctgta 3960
actagaattt aattttcacc ccaataatgt tctatatagc ctttgctaaa gagcaactaa 4020
taaattaaac ctattcttcc aaaaaaaaaa 4049

```

```

<210> 30
<211> 184
<212> PRT
<213> Homo sapiens

```

```

<400> 30
Met Ser Arg Thr Ala Tyr Thr Val Gly Ala Leu Leu Leu Leu Gly
 1             5             10             15
Thr Leu Leu Pro Ala Ala Glu Gly Lys Lys Lys Gly Ser Gln Gly Ala
 20             25             30
Ile Pro Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln Thr Gln
 35             40             45
Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln Gly Arg

```

50		55		60
Gly Thr Ala Met Pro Gly Glu Glu Val Leu Glu Ser Ser Gln Glu Ala				
65		70		75
Leu His Val Thr Glu Arg Lys Tyr Leu Lys Arg Asp Trp Cys Lys Thr				80
	85		90	95
Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser Arg Thr				
	100		105	110
Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro				
	115		120	125
Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser Phe Cys				
	130		135	140
Lys Pro Lys Lys Phe Thr Met Met Val Thr Leu Asn Cys Pro Glu				
145		150		155
Leu Gln Pro Pro Thr Lys Lys Lys Arg Val Thr Arg Val Lys Gln Cys				160
	165		170	175
Arg Cys Ile Ser Ile Asp Leu Asp				
	180			

<210> 31
 <211> 3443
 <212> DNA
 <213> Homo sapiens

<400> 31

gagcaacctc	agcttctagt	atccagactc	cagcgccgcc	ccggggcgccg	accccaaccc	60
cgacccagag	cttctccagc	ggcggcgag	cgagcagggc	tccccgcctt	aacttcctcc	120
gcggggccca	gccaccttcg	ggagtccggg	ttgcccacct	gcaaactctc	cgcttctgc	180
acctgccacc	cctgagccag	cgcgggcgcc	cgagcgagtc	atggccaacg	cggggctgca	240
gctgttgggc	ttcattctcg	ccttcctggg	atggatcggc	gccatcgtea	gcactgccct	300
gccccagtgg	aggatttact	cctatgcccg	cgacaacatc	gtgacggccc	aggccatgta	360
cgaggggctg	tggatgtcct	gcgtgtcgca	gagcaccggg	cagatccagt	gcaaagtctt	420
tgactccttg	ctgaatctga	gcagcacatt	gcaagcaacc	cgtgccttga	tgggtggttg	480
catcctcctg	ggagtgatag	caatctttgt	ggccaccgtt	ggcatgaagt	gtatgaagtg	540
cttggaagac	gatgaggtgc	agaagatgag	gatggctgtc	attgggggtg	cgatatttct	600
tcttgacagg	ctggctatct	tagttgccac	agcatggtat	ggcaatagaa	tcgttcaaga	660
attctatgac	cctatgaccc	cagtcaatgc	caggtacgaa	tttggtcagg	ctctcttcac	720
tggctgggct	gctgcttctc	tctgccttct	gggaggtgcc	ctactttgct	gttcctgtcc	780
ccgaaaaaca	acctcttacc	caacaccaag	gccctatcca	aaacctgcac	cttcacggcg	840
gaaagactac	gtgtgacaca	gaggcaaaag	gagaaaatca	tgttgaaaaca	aaccgaaaat	900
ggacattgag	atactatcat	taacattagg	accttagaat	tttgggtatt	gtaatctgaa	960
gtatggtatt	acaaaacaaa	caaaacaaaca	aaaaacccat	gtgttaaaat	actcagtgtc	1020
aaacatggct	taatcttatt	ttatcttctt	tcctcaatat	aggagggaag	attttaccat	1080
ttgtattact	gcttcccatt	gagtaatcat	actcaaattg	gggaaggggt	gctccttaaa	1140
tatatataga	tatgtatata	tacatgtttt	tctattaaaa	atagacagta	aaatactatt	1200
ctcattatgt	tgatactagc	atacttaaaa	tatctctaaa	ataggtaaat	gtatttaatt	1260
ccatattgat	gaagatgttt	attggtatat	tttctttttc	gtccttatat	acatatgtaa	1320
cagtcaaata	tcattttactc	ttcttcatta	gctttgggtg	cctttgccac	aagacctagc	1380
ctaattttacc	aaggatgaat	tctttcaatt	cttcatgctg	gcccttttca	tatacttatt	1440
ttatttttta	ccataatctt	atagcacttg	catcgttatt	aagcccttat	ttgttttctg	1500
tttcattggg	ctctatctcc	tgaatctaac	acatttcata	gcctacattt	tagtttctaa	1560
agccaagaag	aattttattac	aaatcagaac	tttgagggca	aatctttctg	catgaccaa	1620
gtgataaatt	cctgttgacc	ttcccacaca	atccctgtac	tctgacccat	agcactcttg	1680
tttgctttga	aaatatattgt	ccaattgagt	agctgcatgc	tgttccccca	ggtgttgtaa	1740
cacaacttta	ctgattgaat	ttttaagcta	cttattcata	gttttatatc	cccctaaact	1800
acctttttgt	tccccattcc	ttaattgtat	tgttttccca	agtgtaatga	tcatgcgttt	1860
tatatcttcc	taataagggtg	tgggtctgtt	gtctgaacaa	agtgttagac	tttctggagt	1920
gataatctgg	tgacaaatat	tctctctgta	gctgtgaagca	agtcacttaa	tctttctacc	1980
tcttttttct	atctgocaaa	ttgagataat	gatacttaac	cagttagaag	aggtagtgtg	2040

```

aatattaatt agtttatatt actctcattc tttgaacatg aactatgcct atgtagtgtc 2100
tttatttgct cagctggctg agacactgaa gaagtcactg aacaaaacct acacacgtac 2160
cttcatgtga ttcactgcct tcctctctct accagtctat ttccactgaa caaaacctac 2220
acacatacct tcatgtgggt cagtgccttc ctctctctac cagtctatit ccactgaaca 2280
aaacctacgc acataccttc atgtggctca gtgccttcct ctctctacca gtctatttcc 2340
attctttcag ctgtgtctga catgtttgtg ctctgttcca ttttaacaac tgctcttact 2400
tttccagtct gtacagaatg ctatttccact tgagcaagat gatgtatgga aagggtgttg 2460
gcactgggtg ctggagacct ggatttgagt cttggtgcta tcaatcaccg tctgtgtttg 2520
agcaaggcat ttggctgctg taagcttatt gcttcatctg taagcgggtg tttgtaattc 2580
ctgatcttcc cacctcacag tgatgttggt gggatccagt gagatagaat acatgtaagt 2640
gtgggtttgt aatttgaaaa gtgctatact aagggaaga attgaggaat taactgcata 2700
cgttttggtg ttgcttttca aatgtttgaa aataaaaaaa tgtaagaaa tgggttttct 2760
gccttaacca gtctctcaag tgatgagaca gtgaagtaaa attgagtgc ctaaacgaat 2820
aagattctga ggaagtctta tcttctgcag tgagtatggc ccaatgcttt ctgtggctaa 2880
acagatgtaa tgggaagaaa taaaagccta cgtgttggtg aatccaacag caaggagat 2940
ttttgaatca taataactca taagggtgcta tctgttcagt gatgccctca gagctcttgc 3000
tgtagctgg cagctgacgc tgctaggata gttagtttgg aaatggtact tcataataaa 3060
ctacacaagg aaagtacgac accgtgtctt atgaggaatt ggacctaata aattttagt 3120
tgccttccaa acctgagaat atatgctttt ggaagttaaa atttaaatgg cttttgccac 3180
atacatagat cttcatgatg tgtgagtgtg attccatgtg gatatcagtt accaaacatt 3240
acaaaaaaat tttatggccc aaaatgacca acgaaattgt tacaatagaa tttatccaat 3300
tttgatcttt ttatattctt ctaccacacc tggaaacaga ccaatagaca ttttggggtt 3360
ttataatggg aatttgtata aagcattact ctttttcaat aaattgtttt ttaatttaaa 3420
aaaaggaaaa aaaaaaaaaa aaa 3443

```

<210> 32

<211> 211

<212> PRT

<213> Homo sapiens

<400> 32

```

Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe Leu
 1          5          10          15
Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp Arg Ile
          20          25          30
Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala Met Tyr Glu
          35          40          45
Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly Gln Ile Gln Cys
          50          55          60
Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser Thr Leu Gln Ala Thr
65          70          75          80
Arg Ala Leu Met Val Gly Ile Leu Leu Gly Val Ile Ala Ile Phe
          85          90          95
Val Ala Thr Val Gly Met Lys Cys Met Lys Cys Leu Glu Asp Asp Glu
          100          105          110
Val Gln Lys Met Arg Met Ala Val Ile Gly Gly Ala Ile Phe Leu Leu
          115          120          125
Ala Gly Leu Ala Ile Leu Val Ala Thr Ala Trp Tyr Gly Asn Arg Ile
          130          135          140
Val Gln Glu Phe Tyr Asp Pro Met Thr Pro Val Asn Ala Arg Tyr Glu
145          150          155          160
Phe Gly Gln Ala Leu Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu
          165          170          175
Leu Gly Gly Ala Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser
          180          185          190
Tyr Pro Thr Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys
          195          200          205
Asp Tyr Val
210

```

<210> 33
 <211> 4318
 <212> DNA
 <213> Homo sapiens

<400> 33
 aagcggctcg ggctgcggct ggctcagagt gccgcggggg gcgtggggcg gtgctgagga 60
 gctgaagccg tggccagctc gactccggac agtcacagca gcagcagcag cagccctcgc cgttcgcgga 120
 agccggagca gtcccgagc agaagcagca gcagcagcag cagccctcgc cgttcgcgga 180
 gcgcagccga gccggccatg gcgttgctga tgcgcgtgaa tgggctgaag gaggaggaca 240
 aagagcccct catcgagctc ttctgcaagg ctggcagtgaa tggtgaaagc ataggaaaact 300
 gccctttttc ccagaggctc ttcatgattc tttggctcaa aggagttgta tttagtgtga 360
 cgactgttga cctgaaaagg aagccagcag acctgcagaa cttgggtccc gggacccacc 420
 caccatttat aactttcaac agtgaagtca aaacggatgt aaataagatt gaggaatttc 480
 ttgaagaggt cttatgccct cccaagtact taaagctttc accaaaacac ccagaatcaa 540
 atactgctgg aatggacatc tttgccaaat tctctgcata tatcaagaat tcaaggccag 600
 aggctaatag agcactggag aggggtctcc tgaaaaccct gcagaaactg gatgaatatc 660
 tgaattctcc tctccctgat gaaattgatg aaaatagtat ggaggacata aagttttcta 720
 cacgtaaatt tctggatggc aatgaaatga cattagctga ttgcaacctg ctgccccaaac 780
 tgcataattgt caaggtgggt gccaaaaaat atcgcaactt tgatattcca aaagaaatga 840
 ctggcatctg gagataccta actaatgcat acagtaggga cgagttcacc aatacctgtc 900
 ccagtataaa ggaggttgaa atagcatata gtgatgtagc caaaagactc accaagtaaa 960
 atcgcgtttg taaaagagat gtcttcatgt cttcccctaa gaatacgctt ttcctaacag 1020
 gctactcctt cctgtagagc agaaattgta ttttgcacga acatgcagtt attgaagatt 1080
 aggatcaagg atagacaagg tatagtagtt atcttaaaat atacactcct aagcagtatt 1140
 attttaaaat cctttaccct ggctaccctc cctaccggg ttcctctctc ttttaatttg 1200
 agacactcca ccacaaactt ttcactttag aggtagcttg ccatctctca ggagccctca 1260
 ccattgtgtc cattcaactgt gtatagatgg cagaactttt gaggtgcaat gtttaattgt 1320
 taaaaatagt agccacgact ttatcaggca gcccacaaact ggtgcataat gcatggtaca 1380
 agaaatattt atgtattttt tggaattttg taatattttg taggagtata tgaaaggatt 1440
 gctactgtat cagaaatatt gtttcaattt agtctatcct ggatatgtac taacgaatat 1500
 taccaccaga gaagagagct ttctacaaaa gtcactacag attttgctat attgctttgt 1560
 agatagattt ttacttttgc ctaaaagcat ttatccttca taccaattgt aacatctgac 1620
 accatgtaga agctaaaagt ttagagggag tgagcgtttt ctcaagacct tctcaagca 1680
 ttttatcttt agaagagaaa ctgatggcca cctgatactc tgtctaaata cgtttgttat 1740
 atgtgttttg ccctgtgcca ttcatttgga actttattgc attctttatt ttaaaaagct 1800
 tgtttttacg taatcataga gcttgctatt tgtacatctg ttgagcaaca ctacataact 1860
 gatttttagt tgacttagct atagcagtac aatgattagt aatgtaaaaa ttaacacaga 1920
 aattaaccta aggaatgaag ggtgggtttg tcaaaatatc aagtaaatat ttgtttctaa 1980
 agtacattta atgtagatga cctaaagaat gcgttatcca tcctatataa aagaaagata 2040
 aaacacaggt caccaatttt ctcatttcac ccattttacc ttgtatagag gattgttcat 2100
 tcttttgga ctaagttata gttatgggtg gtgtgtattt actgtagttt tgccatgatc 2160
 cactcattgc acttccctga gttaaatttt ccaacagcca tgttgaggaa tagcactctg 2220
 catgtttttg ttttggtttt cgggggtttt ttttaattgaa gccctaaacc aggaattatt 2280
 tgtgttctaa caggaggatg aacttgctga aaataaaact ttgctatgta tttactcttt 2340
 tttaaaagac aaaagcaaaa ccagactttc tacgtactac tccaaagact gtgattgtga 2400
 ctataatata tttttggtaa tttttttata cctaatttgt ataggaagtg ctatttctca 2460
 taggctgttt cttgaaattt taagtttatt gctttaaaat ggcagtgttt ctccactttt 2520
 gatatgctaa catttagtaa gcaactggctt tatgaaagcg gctttttata agtatactgc 2580
 attttttgag cctatcatta attagcttag tatgaaagat aagaaaatct ccatgttgta 2640
 tccatttggc tcaggaagat tctttgcctt acctttctta gaactcttta ttgcttatca 2700
 aaagtttgag taaccgttg agtttttttt gtaattttaa tattgtatga tttatctggt 2760
 tcaaggaaga tgcactatcc agttatctat tgagaaatta ttttgagtg gtttttagtg 2820
 gtgaaaatgt cccatctgca ccagtacaca ggcaggcatt atcattcttc acctactttt 2880
 taaatagtgg caacttggga ttctttctgg tgattctgaa ccttgccctca tagcttaaag 2940
 tataaaaaaa gattcaagag cagtgaaggt tgttctttcc agtgaatggt ggactgagtg 3000
 gtgcgaggtg gagggctaac aagaggaaaag aactacattc ttcagaatac agtgaatgaa 3060

```

attcatttttg aaactcaaat attttcattt tggatattct cctgttttta ttaaaccagt 3120
gattacacct ggccatccct ctaaatgttc taggaaggca tgtctattgt gattttgatg 3180
aagacagaat tattttttctc tgtagaaaca cagataccac tttatcaggg aagttagtca 3240
aatgaaatgg aaattggtaa atggacaaaa gctagctagt aaaaaggacg acccagcaac 3300
atgctttaac ccattgtat gtttgtggaa agagcatagt ttaacatctt gagaaatttg 3360
ggacataaag ttttcatggt agacagttca tgcagtatat gaattgacat aatggaaata 3420
atctgatttt atttttacaa ctaacatcca ttccccttca tttaaacacc ttttgtgttt 3480
tacttcagtg aggagattgg agtctgaatg gatctgtttt ccaagagatt ctgagaaatt 3540
tttgtattca gcagttggaa agctctctat tctagttgat aaaacttccc ttttttgatg 3600
tagatgcaga tattctatac agttctgttg tcttttacta ggactgtaaa cttttgtgat 3660
aaaattcaaa taagattttta tttctttgta attttggctt tcacaattta tctttaaatc 3720
cttgagcaat ctgtatacaa ttaagagatt tctgacattt attctttacac taaatggatc 3780
aactctagga tttaggcatg ttaacttctg ttgtgttttg aatctctcca gagttgcatg 3840
tagatagcat ttatttctgt gcccttaaac ccatttagaa aataactaca aagtaaaaaat 3900
gtagaggaaa tagaaatgta ttttttcatg aacattttga taaaaatttc atcatttaat 3960
gattcaccaa tttcttgcac taatttgaat ttaagcattt aattcaaaga gaggggagca 4020
tccattattg gtacatgtgg gcttttaaaa actccatcct ttataaatag tcaagggttg 4080
ggccacacaa agtatatttt tatcatggaa aaatttcaac tcctcaagcc gtaatgttga 4140
acagaattgg agtattttct ttataatttc ttgaacaggc aaatgaaagc ttattataga 4200
atgcatgtat tttcttttat ctttggaaac tcagcaccag tatattgctg gcagctattg 4260
tattaaaaaa taaagtatat tttcactatc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4318

```

<210> 34

<211> 253

<212> PRT

<213> Homo sapiens

<400> 34

```

Met Ala Leu Ser Met Pro Leu Asn Gly Leu Lys Glu Glu Asp Lys Glu
 1          5          10          15
Pro Leu Ile Glu Leu Phe Val Lys Ala Gly Ser Asp Gly Glu Ser Ile
          20          25          30
Gly Asn Cys Pro Phe Ser Gln Arg Leu Phe Met Ile Leu Trp Leu Lys
          35          40          45
Gly Val Val Phe Ser Val Thr Thr Val Asp Leu Lys Arg Lys Pro Ala
          50          55          60
Asp Leu Gln Asn Leu Ala Pro Gly Thr His Pro Pro Phe Ile Thr Phe
65          70          75          80
Asn Ser Glu Val Lys Thr Asp Val Asn Lys Ile Glu Glu Phe Leu Glu
          85          90          95
Glu Val Leu Cys Pro Pro Lys Tyr Leu Lys Leu Ser Pro Lys His Pro
          100          105          110
Glu Ser Asn Thr Ala Gly Met Asp Ile Phe Ala Lys Phe Ser Ala Tyr
          115          120          125
Ile Lys Asn Ser Arg Pro Glu Ala Asn Glu Ala Leu Glu Arg Gly Leu
          130          135          140
Leu Lys Thr Leu Gln Lys Leu Asp Glu Tyr Leu Asn Ser Pro Leu Pro
145          150          155          160
Asp Glu Ile Asp Glu Asn Ser Met Glu Asp Ile Lys Phe Ser Thr Arg
          165          170          175
Lys Phe Leu Asp Gly Asn Glu Met Thr Leu Ala Asp Cys Asn Leu Leu
          180          185          190
Pro Lys Leu His Ile Val Lys Val Val Ala Lys Lys Tyr Arg Asn Phe
          195          200          205
Asp Ile Pro Lys Glu Met Thr Gly Ile Trp Arg Tyr Leu Thr Asn Ala
210          215          220
Tyr Ser Arg Asp Glu Phe Thr Asn Thr Cys Pro Ser Asp Lys Glu Val
225          230          235          240
Glu Ile Ala Tyr Ser Asp Val Ala Lys Arg Leu Thr Lys

```

245

250

<210> 35
 <211> 6728
 <212> DNA
 <213> Homo sapiens

<400> 35
 agcagacggg agtttctcct cgggggtcgga gcaggaggca cgcggagtgt gaggccacgc 60
 atgagcggac gctaaccctc tccccagcca caaagagtct acatgtctag ggtctagaca 120
 tgttcagctt tgtggacctc cggctcctgc tcctcttagc ggccaccgcc ctccctgacgc 180
 acggccaaga ggaaggccaa gtcgagggcc aagacgaaga catcccacca atcacctgcg 240
 tacagaacgg cctcaggtac catgaccgag acgtgtggaa acccgagccc tgccggatct 300
 gcgtctgcga caacggcaag gtgttgtgcg atgacgtgat ctgtgacgag accaagaact 360
 gccccggcgc cgaagtcccc gagggcgagt gctgtcccgt ctgccccgac ggctcagagt 420
 caccacccga ccaagaaacc accggcgtcg agggacccaa gggagacact ggcccccgag 480
 gcccaagggg acccgagggc cccctggccc gagatggcat ccctggacag cctggacttc 540
 ccggaccccc cggaccccc ggacctcccg gacccctgg cctcggagga aactttgctc 600
 ccagctgtgc ttatggctat gatgagaaat caaccggagg aatttccgtg cctggcccca 660
 tgggtccctc tggctcctcg ggtctccctg gccccctgg tgcaacctgg cccaaggct 720
 tccaagggtc ccctgggtgag cctggcgagc ctggagcttc aggtcccatg ggtccccgag 780
 gtccccaggg tccccctgga aagaatggag atgatgggga agctggaaaa cctggctgctc 840
 ctgggtgagcg tgggcctcct gggcctcagg gtgctcgagg attgcccgga acagctggcc 900
 tccctggaat gaaggacac agaggtttca gtggtttgga tggtgccaag ggagatgctg 960
 gtccctgctgg tcctaagggt gagcctggca gccctggtga aaatggagct cctggtcaga 1020
 tgggcccccg tggcctgcct ggtgagagag gtgcacctgg agccctggc cctgctggtg 1080
 ctcgtggaaa tgatgggtg actggtgctg cggggcccc tgggtcccac ggccccgctg 1140
 gtccctcctg cttccctggt gctgttggtg ctaagggtag agctggtccc caagggcccc 1200
 gaggtctctg aggtccccag ggtgtgcgtg gtgagcctgg cccctctggc cctgctggtg 1260
 ctgctggccc tgctggaaac cctggtgctg atggacagcc tgggtgctaaa ggtgccaatg 1320
 gtgctcctgg tattgctggt gctcctggct tccttgggtc ccgaggcccc tctggacccc 1380
 agggcccccg cggccctcct ggtcccaagg gtaacagcgg tgaacctggt gctcctggca 1440
 gcaaaggaga cactggtgct aaggagagc ctggccctgt tgggtgtcaa ggacccctg 1500
 gccctgctgg agaggaagga aagcgaggag ctcgaggtga acccggaccc actggcctgc 1560
 ccggaccccc tggcgagcgt ggtggacctg gttagccgtg tttccctggc gcagatggtg 1620
 ttgctggtgc caagggtccc gctggtgaac gtggttctcc tggccccgct ggccccaaag 1680
 gatctcctgg tgaagctggt cgtcccgtg aagctggtct gcctggtgcc aagggtctga 1740
 ctggaagccc tggcagccct ggtcctgatg gcaaaactgg cccctctggt ccgcccgtc 1800
 aagatggtcg ccccgaccc ccaggccac ctggtgccc tggtcaggct ggtgtgatgg 1860
 gattccctgg acctaaaggt gctgctggag agcccgga ggctggagag cgaggtgttc 1920
 ccggaccccc tggcgctgtc ggtcctgctg gcaaagatgg agaggctgga gctcaggac 1980
 cccctggccc tgctggtccc gctggcgaga gaggtgaaca aggcctgct ggctcccccg 2040
 gattccagggt tctccctggt cctgctggtc ctccaggtga agcaggcaaa cctggtgaac 2100
 aggggtgttc tggagacctt ggcgccccct gcccctctgg agcaagaggc gagagaggtt 2160
 tccctggcga gcgtggtgtg caaggtcccc ctggtcctgc tggaccccgga ggggccaacg 2220
 gtgctcccg caacgatggt gctaagggtg atgctggtgc ccctggagct ccggtagcc 2280
 agggcgcccc tggccttcag ggaatgctg gtgaacgtgg tgcagctggt cttccagggc 2340
 ctaagggtga cagaggtgat gctggtccca aaggtgctga tggctctcct ggcaaagatg 2400
 gcgtccgtgg tctgaccggc ccattgggtc ctccctggcc tgctggtgcc cctggtgaca 2460
 aggggtgaaag tgggtcccagc ggccctgctg gtcccactgg agctcgtggt gcccccgag 2520
 accgtggtga gcctggtccc ccggccctg ctggctttgc tggccccct ggtgctgacg 2580
 gccaacctgg tgctaaaggc gaacctggtg atgctggtgc caaaggcgat gctggtcccc 2640
 ctgggcctgc cggacccgct ggacccccct gcccattgg taatgttgg gctcctggag 2700
 ccaagggtgc tcgcggcagc gctggtcccc ctggtgctac tggtttccct ggtgctgctg 2760
 gcgagctcg tctcctggc cctctggaa atgctggacc ccctggccct cctggtcctg 2820
 ctggcaaaaga aggcggcaaa ggtccccgtg gtgagactgg ccctgctgga cgtcctggtg 2880
 aagttggtcc ccctggtccc cctggccctg ctggcgagaa aggatccct ggtgctgatg 2940
 gtccctgctgg tgctcctggt actccgggc ctcaaggtat tgctggacag cgtggtggtg 3000

tgggcctgcc	tgggtcagaga	ggagagagag	gcttcctctgg	tcttcctggc	ccctctggtg	3060
aacctggcaa	acaaggtccc	tctggagcaa	gtggtgaacg	tggtecccc	ggtcccatgg	3120
gccccctgg	attggctgga	ccccctggtg	aatctggacg	tgagggggct	cctgctgccg	3180
aaggttcccc	tggacgagac	ggttctcctg	gcgccaaggg	tgaccgtggt	gagaccggcc	3240
ccgctggacc	ccctggtgct	cctggtgctc	ctggtgcccc	tggccccgtt	ggccctgctg	3300
gcaagagtgg	tgatcgtggt	gagactggtc	ctgctgggtc	cgccggtccc	gtcggccccg	3360
tggcgccccg	tggccccgcc	ggaccccaag	gccccctggt	tgacaagggt	gagacaggcg	3420
aacaggggcg	cagaggcata	aagggtcacc	gtggcttctc	tggcctccag	ggtccccctg	3480
gccctcctgg	ctctcctggt	gaacaaggtc	cctctggagc	ctctggtcct	gctggtcccc	3540
gaggtcccc	tggctctgct	ggtgctcctg	gcaaagatgg	actcaacggt	ctccctggcc	3600
ccattgggccc	ccctgggtcct	cgcggtcgca	ctggtgatgc	tggteoctgtt	ggtccccccg	3660
gccctcctgg	acctcctggt	ccccctggtc	ctcccagcgc	tggtttcgac	ttcagcttcc	3720
tgccccagcc	acctcaagag	aaggctcacg	atggtggccg	ctaactaccg	gctgatgatg	3780
ccaatgtggt	tctgtaccgt	gacctcgagg	tggacaccac	cctcaagagc	ctgagccagc	3840
agatcgagaa	catccggagc	ccagagggaa	gccgcaagaa	ccccgcccgc	acctgccgtg	3900
acctcaagat	gtgocactct	gactggaaga	gtggagagta	ctggattgac	cccaaccaag	3960
gctgcaacct	ggatgccatc	aaagtcttct	gcaacatgga	gactggtgag	acctgcgtgt	4020
accccaactca	gcccagtggt	gcccagaaga	actggtacat	cagcaagaac	cccaaggaca	4080
agaggcatgt	ctggttcggc	gagagcatga	ccgatggatt	ccagttcgag	tatggcgggc	4140
agggtccgga	ccctgccgat	gtggccatcc	agctgacctt	cctgcgcctg	atgtccaccg	4200
aggcctccca	gaacatcacc	taccactgca	agaacagcgt	ggcctacatg	gaccacgaga	4260
ctggcaacct	caagaaggcc	ctgctcctca	agggctccaa	cgagatcgag	atccgcgccg	4320
agggcaacag	ccgttccacc	tacagcgtca	ctgtcgatgg	ctgcacgagt	cacaccggag	4380
cctggggcaa	gacagtgatt	gaatacaaaa	ccaccaagtc	ctccgcctg	cccatcatcg	4440
atgtggcccc	cttggacggt	ggtgccccag	accaggaatt	cggcttcgac	gttggccccg	4500
tctgcttctc	gtaaaactcc	tccatcccaa	cctggctccc	tcccacccaa	ccaaactttc	4560
ccccaaaccg	gaaacagaca	agcaacccaa	actgaacccc	cccaaaagcc	aaaaaatggg	4620
agacaatttc	acatggactt	tggaaaatat	tttttctctt	tgcatttcac	tctcaaactt	4680
agttttttatc	tttgaccaac	cgaacatgac	caaaaaccaa	aagtgcattc	aaccttacca	4740
aaaaaaaaaaaa	aaaaaaaaaaaa	agaataaata	aataagtttt	taaaaaagga	agcttggtcc	4800
acttgcttga	agacccatgc	gggggtaagt	ccctttctgc	ccgttgggtt	atgaaacccc	4860
aatgctgccc	tttctgctcc	tttctccaca	cccccttgg	cctccctcc	actccttccc	4920
aatctgtct	ccccagaaga	cacaggaaac	aatgtattgt	ctgcccagca	atcaaaggca	4980
atgctcaaac	acccaagtgg	ccccaccct	cagcccgctc	ctgcccgcgc	agcaccacca	5040
ggccctgggg	acctgggggt	ctcagactgc	caaagaagcc	ttgccatctg	gcgtcccat	5100
ggctatttga	acatctcccc	ttcgtttttg	agggggtcat	gccgggggag	ccaccagccc	5160
ctcactgggt	tcggaggaga	gtcaggaagg	gccacgacaa	agcagaaaca	tcggatttgg	5220
ggaacgcgtg	tcatcccttg	tgccgcaggc	tgggcgggag	agactgttct	gttctgttcc	5280
ttgtgtaact	gtgttgctga	aagactacct	cgttcttgtc	ttgatgtgtc	accggggcaa	5340
ctgcctgggg	gcggggatgg	gggcagggtg	gaagcggctc	cccattttta	taccaaaggt	5400
gctacatcta	tgtgatgggt	ggggtgggga	gggaatcact	ggtgctatag	aaattgagat	5460
gcccccccag	gccagcaaat	gttccttttt	gttcaaagtc	tattttttatt	ccttgatatt	5520
ttttctttct	tttttttttt	ttttgtggat	ggggacttgt	gaatttttct	aaagggtgcta	5580
tttaacatgg	gaggagagcg	tgtgcgtctc	agcccagccc	gctgctcact	ttccaccctc	5640
tctccacctg	cctctggcct	ctcaggcctc	tgctctccga	cctctctcct	ctgaaacccc	5700
cctccacagc	tgcagcccat	cctcccgct	ccctcctagt	ctgtcctgcg	tcctctgtcc	5760
ccgggtttca	gagacaactt	cccaaagcac	aaagcagttt	ttccctaggg	gtggggaggaa	5820
gcaaaagact	ctgtacctat	tttgtatgtg	tataataatt	tgagatgttt	tttaattattt	5880
tgattgctgg	aataaagcat	gtggaaatga	cccaaacata	atccgcagtg	gcctcctaatt	5940
ttccttcttt	ggagttgggg	gaggggtaga	catggggaag	gggccttggg	gtgatgggct	6000
tgccttccat	tcctgcocct	tcctcccca	ctattctctt	ctagatccct	ccataacccc	6060
actccctttt	ctctcaccct	tcttataccg	caaacctttc	tacttctctc	ttcattttct	6120
attcttgcaa	tttctttgca	cctttttcaa	atcctcttct	cccctgcaat	accatacagg	6180
caatccacgt	gcacaacaca	cacacacact	cttcacatct	ggggttgtcc	aaacctcata	6240
ccactccccc	ttcaagccca	tcactctccc	acccctgga	tgccctgcac	ttggtggcgg	6300
tgggatgctc	atggatactg	ggaggggtgag	gggagtggaa	cccgtgagga	ggacctgggg	6360
gcctctcctt	gaactgacat	gaaggggtcat	ctggcctctg	ctcccttctc	accacgcgtg	6420
acctcctgcc	gaaggagcaa	cgcaacagga	gaggggtctg	ctgagcctgg	cgaggggtctg	6480
ggagggacca	ggaggaaggc	gtgctccctg	ctcgtgtctc	tggccctggg	ggagtgaggg	6540

```

agacagacac ctgggagagc tgtggggaag gcactcgcac cgtgctcttg ggaaggaagg 6600
agacctggcc ctgctcacca cggactgggt gcctcgacct cctgaatccc cagaacacaa 6660
ccccctggg ctggggtggt ctggggaacc atcgtgcccc cgcctccgcg ctactccttt 6720
ttaagctt                                     6728

```

<210> 36
 <211> 1464
 <212> PRT
 <213> Homo sapiens

<400> 36

Met	Phe	Ser	Phe	Val	Asp	Leu	Arg	Leu	Leu	Leu	Leu	Leu	Ala	Ala	Thr	1	5	10	15
Ala	Leu	Leu	Thr	His	Gly	Gln	Glu	Glu	Gly	Gln	Val	Glu	Gly	Gln	Asp	20	25	30	
Glu	Asp	Ile	Pro	Pro	Ile	Thr	Cys	Val	Gln	Asn	Gly	Leu	Arg	Tyr	His	35	40	45	
Asp	Arg	Asp	Val	Trp	Lys	Pro	Glu	Pro	Cys	Arg	Ile	Cys	Val	Cys	Asp	50	55	60	
Asn	Gly	Lys	Val	Leu	Cys	Asp	Asp	Val	Ile	Cys	Asp	Glu	Thr	Lys	Asn	65	70	75	80
Cys	Pro	Gly	Ala	Glu	Val	Pro	Glu	Gly	Glu	Cys	Cys	Pro	Val	Cys	Pro	85	90	95	
Asp	Gly	Ser	Glu	Ser	Pro	Thr	Asp	Gln	Glu	Thr	Thr	Gly	Val	Glu	Gly	100	105	110	
Pro	Lys	Gly	Asp	Thr	Gly	Pro	Arg	Gly	Pro	Arg	Gly	Pro	Ala	Gly	Pro	115	120	125	
Pro	Gly	Arg	Asp	Gly	Ile	Pro	Gly	Gln	Pro	Gly	Leu	Pro	Gly	Pro	Pro	130	135	140	
Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Gly	Gly	Asn	Phe	Ala	145	150	155	160
Pro	Gln	Leu	Ser	Tyr	Gly	Tyr	Asp	Glu	Lys	Ser	Thr	Gly	Gly	Ile	Ser	165	170	175	
Val	Pro	Gly	Pro	Met	Gly	Pro	Ser	Gly	Pro	Arg	Gly	Leu	Pro	Gly	Pro	180	185	190	
Pro	Gly	Ala	Pro	Gly	Pro	Gln	Gly	Phe	Gln	Gly	Pro	Pro	Gly	Glu	Pro	195	200	205	
Gly	Glu	Pro	Gly	Ala	Ser	Gly	Pro	Met	Gly	Pro	Arg	Gly	Pro	Pro	Gly	210	215	220	
Pro	Pro	Gly	Lys	Asn	Gly	Asp	Asp	Gly	Glu	Ala	Gly	Lys	Pro	Gly	Arg	225	230	235	240
Pro	Gly	Glu	Arg	Gly	Pro	Pro	Gly	Pro	Gln	Gly	Ala	Arg	Gly	Leu	Pro	245	250	255	
Gly	Thr	Ala	Gly	Leu	Pro	Gly	Met	Lys	Gly	His	Arg	Gly	Phe	Ser	Gly	260	265	270	
Leu	Asp	Gly	Ala	Lys	Gly	Asp	Ala	Gly	Pro	Ala	Gly	Pro	Lys	Gly	Glu	275	280	285	
Pro	Gly	Ser	Pro	Gly	Glu	Asn	Gly	Ala	Pro	Gly	Gln	Met	Gly	Pro	Arg	290	295	300	
Gly	Leu	Pro	Gly	Glu	Arg	Gly	Arg	Pro	Gly	Ala	Pro	Gly	Pro	Ala	Gly	305	310	315	320
Ala	Arg	Gly	Asn	Asp	Gly	Ala	Thr	Gly	Ala	Ala	Gly	Pro	Pro	Gly	Pro	325	330	335	
Thr	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Phe	Pro	Gly	Ala	Val	Gly	Ala	Lys	340	345	350	
Gly	Glu	Ala	Gly	Pro	Gln	Gly	Pro	Arg	Gly	Ser	Glu	Gly	Pro	Gln	Gly	355	360	365	
Val	Arg	Gly	Glu	Pro	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Ala	Ala	Gly	Pro	370	375	380	

Ala	Gly	Asn	Pro	Gly	Ala	Asp	Gly	Gln	Pro	Gly	Ala	Lys	Gly	Ala	Asn
385					390					395					400
Gly	Ala	Pro	Gly	Ile	Ala	Gly	Ala	Pro	Gly	Phe	Pro	Gly	Ala	Arg	Gly
				405					410					415	
Pro	Ser	Gly	Pro	Gln	Gly	Pro	Gly	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Asn
			420					425					430		
Ser	Gly	Glu	Pro	Gly	Ala	Pro	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Ala	Lys
		435					440				445				
Gly	Glu	Pro	Gly	Pro	Val	Gly	Val	Gln	Gly	Pro	Pro	Gly	Pro	Ala	Gly
	450					455					460				
Glu	Glu	Gly	Lys	Arg	Gly	Ala	Arg	Gly	Glu	Pro	Gly	Pro	Thr	Gly	Leu
465					470					475					480
Pro	Gly	Pro	Pro	Gly	Glu	Arg	Gly	Gly	Pro	Gly	Ser	Arg	Gly	Phe	Pro
				485					490					495	
Gly	Ala	Asp	Gly	Val	Ala	Gly	Pro	Lys	Gly	Pro	Ala	Gly	Glu	Arg	Gly
			500					505					510		
Ser	Pro	Gly	Pro	Ala	Gly	Pro	Lys	Gly	Ser	Pro	Gly	Glu	Ala	Gly	Arg
		515					520					525			
Pro	Gly	Glu	Ala	Gly	Leu	Pro	Gly	Ala	Lys	Gly	Leu	Thr	Gly	Ser	Pro
	530					535					540				
Gly	Ser	Pro	Gly	Pro	Asp	Gly	Lys	Thr	Gly	Pro	Pro	Gly	Pro	Ala	Gly
545					550					555					560
Gln	Asp	Gly	Arg	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Arg	Gly	Gln
				565					570					575	
Ala	Gly	Val	Met	Gly	Phe	Pro	Gly	Pro	Lys	Gly	Ala	Ala	Gly	Glu	Pro
			580					585					590		
Gly	Lys	Ala	Gly	Glu	Arg	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	Gly
		595					600					605			
Pro	Ala	Gly	Lys	Asp	Gly	Glu	Ala	Gly	Ala	Gln	Gly	Pro	Pro	Gly	Pro
	610					615					620				
Ala	Gly	Pro	Ala	Gly	Glu	Arg	Gly	Glu	Gln	Gly	Pro	Ala	Gly	Ser	Pro
625					630					635					640
Gly	Phe	Gln	Gly	Leu	Pro	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Glu	Ala	Gly
				645					650					655	
Lys	Pro	Gly	Glu	Gln	Gly	Val	Pro	Gly	Asp	Leu	Gly	Ala	Pro	Gly	Pro
			660					665					670		
Ser	Gly	Ala	Arg	Gly	Glu	Arg	Gly	Phe	Pro	Gly	Glu	Arg	Gly	Val	Gln
		675					680					685			
Gly	Pro	Pro	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Ala	Asn	Gly	Ala	Pro	Gly
	690					695					700				
Asn	Asp	Gly	Ala	Lys	Gly	Asp	Ala	Gly	Ala	Pro	Gly	Ala	Pro	Gly	Ser
705					710					715					720
Gln	Gly	Ala	Pro	Gly	Leu	Gln	Gly	Met	Pro	Gly	Glu	Arg	Gly	Ala	Ala
				725					730					735	
Gly	Leu	Pro	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Asp	Ala	Gly	Pro	Lys	Gly
			740					745					750		
Ala	Asp	Gly	Ser	Pro	Gly	Lys	Asp	Gly	Val	Arg	Gly	Leu	Thr	Gly	Pro
		755					760					765			
Ile	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Ala	Pro	Gly	Asp	Lys	Gly	Glu	Ser
	770					775					780				
Gly	Pro	Ser	Gly	Pro	Ala	Gly	Pro	Thr	Gly	Ala	Arg	Gly	Ala	Pro	Gly
785					790					795					800
Asp	Arg	Gly	Glu	Pro	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Phe	Ala	Gly	Pro
				805					810					815	
Pro	Gly	Ala	Asp	Gly	Gln	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Asp	Ala
			820					825					830		
Gly	Ala	Lys	Gly	Asp	Ala	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Pro	Ala	Gly
		835					840				845				
Pro	Pro	Gly	Pro	Ile	Gly	Asn	Val	Gly	Ala	Pro	Gly	Ala	Lys	Gly	Ala

850	855	860
Arg Gly Ser Ala Gly Pro	Pro Gly Ala Thr Gly	Phe Pro Gly Ala Ala
865	870	875
Gly Arg Val Gly Pro	Pro Gly Pro Ser Gly	Asn Ala Gly Pro Pro Gly
885	890	895
Pro Pro Gly Pro Ala Gly	Lys Glu Gly Gly Lys Gly	Pro Arg Gly Glu
900	905	910
Thr Gly Pro Ala Gly Arg	Pro Gly Glu Val Gly	Pro Pro Gly Pro Pro
915	920	925
Gly Pro Ala Gly Glu Lys	Gly Ser Pro Gly Ala	Asp Gly Pro Ala Gly
930	935	940
Ala Pro Gly Thr Pro Gly	Gln Gly Ile Ala Gly	Gln Arg Gly Val
945	950	955
Val Gly Leu Pro Gly Gln	Arg Gly Glu Arg Gly	Phe Pro Gly Leu Pro
965	970	975
Gly Pro Ser Gly Glu Pro	Gly Lys Gln Gly Pro	Ser Gly Ala Ser Gly
980	985	990
Glu Arg Gly Pro Pro Gly	Pro Met Gly Pro Pro	Gly Leu Ala Gly Pro
995	1000	1005
Pro Gly Glu Ser Gly Arg	Glu Gly Ala Pro Ala	Ala Glu Gly Ser Pro
1010	1015	1020
Gly Arg Asp Gly Ser Pro	Gly Ala Lys Gly Asp	Arg Gly Glu Thr Gly
1025	1030	1035
Pro Ala Gly Pro Pro Gly	Ala Pro Gly Ala Pro	Gly Ala Pro Gly Pro
1045	1050	1055
Val Gly Pro Ala Gly Lys	Ser Gly Asp Arg Gly	Glu Thr Gly Pro Ala
1060	1065	1070
Gly Pro Ala Gly Pro Val	Gly Pro Val Gly Ala	Arg Gly Pro Ala Gly
1075	1080	1085
Pro Gln Gly Pro Arg Gly	Asp Lys Gly Glu Thr	Gly Glu Gln Gly Asp
1090	1095	1100
Arg Gly Ile Lys Gly His	Arg Gly Phe Ser Gly	Leu Gln Gly Pro Pro
1105	1110	1115
Gly Pro Pro Gly Ser Pro	Gly Glu Gln Gly Pro	Ser Gly Ala Ser Gly
1125	1130	1135
Pro Ala Gly Pro Arg Gly	Pro Pro Gly Ser Ala	Gly Ala Pro Gly Lys
1140	1145	1150
Asp Gly Leu Asn Gly Leu	Pro Gly Pro Ile Gly	Pro Pro Gly Pro Arg
1155	1160	1165
Gly Arg Thr Gly Asp Ala	Gly Pro Val Gly Pro	Pro Gly Pro Pro Gly
1170	1175	1180
Pro Pro Gly Pro Pro Gly	Pro Pro Ser Ala Gly	Phe Asp Phe Ser Phe
1185	1190	1195
Leu Pro Gln Pro Pro Gln	Glu Lys Ala His Asp	Gly Gly Arg Tyr Tyr
1205	1210	1215
Arg Ala Asp Asp Ala Asn	Val Val Arg Asp Arg	Leu Glu Val Asp
1220	1225	1230
Thr Thr Leu Lys Ser Leu	Ser Gln Gln Ile Glu	Asn Ile Arg Ser Pro
1235	1240	1245
Glu Gly Ser Arg Lys Asn	Pro Ala Arg Thr Cys	Arg Asp Leu Lys Met
1250	1255	1260
Cys His Ser Asp Trp Lys	Ser Gly Glu Tyr Trp	Ile Asp Pro Asn Gln
1265	1270	1275
Gly Cys Asn Leu Asp Ala	Ile Lys Val Phe Cys	Asn Met Glu Thr Gly
1285	1290	1295
Glu Thr Cys Val Tyr Pro	Thr Gln Pro Ser Val	Ala Gln Lys Asn Trp
1300	1305	1310
Tyr Ile Ser Lys Asn Pro	Lys Asp Lys Arg His	Val Trp Phe Gly Glu
1315	1320	1325

Ser Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly Gly Gln Gly Ser Asp
 1330 1335 1340
 Pro Ala Asp Val Ala Ile Gln Leu Thr Phe Leu Arg Leu Met Ser Thr
 1345 1350 1355 1360
 Glu Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Val Ala Tyr
 1365 1370 1375
 Met Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala Leu Leu Leu Lys Gly
 1380 1385 1390
 Ser Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn Ser Arg Phe Thr Tyr
 1395 1400 1405
 Ser Val Thr Val Asp Gly Cys Thr Ser His Thr Gly Ala Trp Gly Lys
 1410 1415 1420
 Thr Val Ile Glu Tyr Lys Thr Thr Lys Ser Ser Arg Leu Pro Ile Ile
 1425 1430 1435 1440
 Asp Val Ala Pro Leu Asp Val Gly Ala Pro Asp Gln Glu Phe Gly Phe
 1445 1450 1455
 Asp Val Gly Pro Val Cys Phe Leu
 1460

<210> 37
 <211> 5086
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 27, 46
 <223> n = A,T,C or G

<400> 37
 agcaccacgg cagcaggagg tttcgggcta agttggaggt actgggccac gactgcatgc 60
 ccgcgcccgc caggtgatac ctccgcoggt gaccagggg ctctgcgaca caaggagtct 120
 gcatgtctaa gtgctagaca tgctcagctt tgtggatacg cggactttgt tgctgcttgc 180
 agtaacctta tgcctagcaa catgccaatc tttaacaagag gaaactgtaa gaaagggccc 240
 agccggagat agaggaccac gtggagaaaag ggtccacca ggccccccag gcagagatgg 300
 tgaagatggt cccacaggcc ctctcgtgctt acctggctct cctggcccc ctggtctcgg 360
 tgggaacttt gctgctcagt atgatggaaa aggagttgga ctgggccctg gaccaatggg 420
 cttaatggga cctagaggcc cacctgggtgc agctggagcc ccaggccctc aagggtttcca 480
 aggacctgct ggtgagcctg gtgaacctgg tcaaaactggt cctgcagggtg ctgctgggtc 540
 agctggccct cctggcaagg ctggtgaaga tggtcaccct ggaaaaccgc gacgacctgg 600
 tgagagagga gttgttgac cacagggtgc tctggtttc cctggaactc ctggacttcc 660
 tggcttcaaa ggcattaggg gacacaatgg tctggatgga ttgaaggagc agcccggtgc 720
 tctggtgtg aagggtgaac ctggtgcccc tggtgaaaat ggaactccag gtcaaacagg 780
 agcccggtgg ctctcgtggt agagaggacg tgttggtgcc cctggcccag ctggtgcccg 840
 tggcagtgat ggaagtgtgg gtcccgtggg tcctgctggt ccattgggt ctgctggccc 900
 tccaggcttc ccaggtgccc ctggcccaaa gggtgaaatt ggagctgttg gtaacgctgg 960
 tctgctggt cccgcgggtc ccctggtgga agtgggtctt ccaggcctct ccggccccgt 1020
 tggacctcct ggtaatcctg gagcaaacgg ccttactggt gccagggtg ctgctggcct 1080
 tcccggcgtt gctggggctc ccggcctccc tggacccgc ggtattcctg gccctgttgg 1140
 tgctgccggt gctactggtg ccagaggact tgttggtgag cctggtccag ctggctccaa 1200
 aggagagagc ggtaacaagg gtgagcccgg ctctgctggg cccaagggtc ctctggtcc 1260
 cagtggtgaa gaaggaaaga gaggccctaa tggggaagct ggatctgccg gccctccagg 1320
 acctcctggg ctgagaggta gtccctggtt tcgtggtctt cctggagctg atggcagagc 1380
 tggcgtcatg ggcctcctg gttagtcgtg tgcaagtggc cctgctggag tccgaggacc 1440
 taatggagat ctggttcgcc ctggggagcc tgggtctcat ggaccagag gtcttctctg 1500
 tccccctgga aatatcggcc ccgtggaaa agaaggtcct gtcggcctcc ctggcatcga 1560
 cggcaggcct ggcccaattg gccagctgg agcaagagga gagcctggca acattggatt 1620
 ccctggaccc aaaggcccca ctggtgatcc tggcaaaaac ggtgataaag gtcattgctg 1680

tcttgcgtggt	gctcgggggtg	ctccagggtcc	tgatggaaac	aatggtgctc	agggacctcc	1740
tggaccacag	ggtgttcaag	gtggaaaagg	tgaacagggt	cccgctgggtc	ctccaggcctt	1800
ccagggtctg	cctggccctc	cagggtccgc	tggtgaagtt	ggcaaaccag	gagaaagggg	1860
tctccatggt	gagtttggtc	tccctggtcc	tgctggtcca	agaggggaaac	gcgggtcccc	1920
agggtgagagt	ggtgctgccg	gtcctactgg	tcctatttga	agccgagggtc	cttctggacc	1980
cccagggcct	gatggaaaca	agggtgaacc	tggtgtggtt	ggtgctgtgg	gcactgctgg	2040
tccatctggt	cctagtggac	tcccaggaga	gaggggtgct	gctggcatac	ctggaggcaa	2100
gggagaaaaag	ggtgaacctg	gtctcagagg	tgaaattggt	aaccttggtca	gagatggtgc	2160
tcgtggtgct	catggtgctg	taggtgcccc	tggtcctgct	ggagccacag	gtgaccgggg	2220
cgaagctggg	gctgctgggtc	ctgctgggtcc	tgctggtcct	cggggaagcc	ctggtgaacg	2280
tggcgagggtc	ggtcctgctg	gccccaacgg	atttgctggt	cgggctgggtg	ctgctggtca	2340
acccgggtgct	aaaggagaaa	gaggagccaa	agggcctaag	ggtgaaaacg	gtgttgttgg	2400
tcccacaggc	cccggttgag	ctgctggccc	agctggtcca	aatggtcccc	ccggtcctgc	2460
tggaaagtctg	ggtgatggag	gccccctgg	tatgactggt	ttccctgggtg	ctgctggacg	2520
gactggtccc	ccaggacctc	ctggtatttc	tggccctcct	ggtccccctg	gtcctgctgg	2580
gaaagaaggg	cttcgtgggtc	ctcgtggtga	ccaagggtcca	gttggccgaa	ctggagaagt	2640
agggtgcagtt	ggtccccctg	gcttcgctgg	tgagaaggggt	ccctctggag	aggctggtac	2700
tgctggacct	cctggcactc	caggtcctca	gggtccttct	ggtgctcctg	gtattctggg	2760
tctccctggc	tcgagagggtg	aacgtggtct	acctggtggt	gctggtgctg	tgggtgaacc	2820
tggctcctct	ggcattggcg	gccctcctgg	ggcccggtgg	cctcctgggtg	ctgtgggtag	2880
tcctggagtc	aacggtgctc	ctggtgaagc	tggtcgtgat	ggcaaccctg	ggaacgatgg	2940
tcccccagggt	cgcgatgggtc	aaccgggaca	caaggagag	cgcgggttacc	ctggcaatat	3000
tgggtcccggt	ggtgctgcag	gtgcacctgg	tcctcatggc	cccgtgggtc	ctgctggcaa	3060
acatggaaac	cgtggtgaaa	ctggtccttc	tggtcctggt	ggtcctgctg	gtgctgttgg	3120
cccaagaggt	cctagtggcc	cacaaggcat	tcgtggcgat	aaggagagagc	ccggtgaaaa	3180
ggggcccgaga	ggtcttcctg	gcttaaagg	acacaatgga	ttgcaagggtc	tgcctggtat	3240
cgctggtcac	catggtgatc	aagggtctcc	tggtcctggt	ggtcctgctg	gtcctagggg	3300
ccctgctggt	ccttctggcc	ctgctggaaa	agatggctgc	actggacatc	ctggtacggt	3360
tggacgtgct	ggcattcgag	gccctcagg	tcaccaaggc	cctgctggcc	cccctggtcc	3420
ccctggccct	cctggacctc	cagggtgtaag	cgggtggtgt	tatgactttg	gttacgatgg	3480
agactttctac	agggtgacc	agcctcgctc	agcaccttct	ctcagaccca	aggactatga	3540
agttgatgct	actctgaagt	ctctcaacaa	ccagattgag	acccttctta	ctcctgaagg	3600
ctctagaaaag	aaccagctc	gcacatgccg	tgacttgaga	ctcagccacc	cagagtggag	3660
cagtggttac	tactggattg	accctaacca	aggatgcact	atggatgcta	tcaaagtata	3720
ctgtgatttc	tctactggcg	aaacctgtat	ccgggcccaa	cctgaaaaca	tcccagccaa	3780
gaactgggat	aggagctcca	aggacaagaa	acacgtctgg	ctaggagaaa	ctatcaatgc	3840
tggcagccag	tttgaatata	atgtagaagg	agtgaattcc	aaggaaatgg	ctacccaact	3900
tgccttcattg	cgctcgtggtg	ccaactatgc	ctctcagaac	atcacctacc	actgcaagaa	3960
cagcatttga	tacatggatg	aggagactgg	caacctgaaa	aaggctgtca	ttctacaggg	4020
ctctaattgat	gttgaaacttg	ttgctgaggg	caacagcagg	ttcacttaca	ctgttcttgt	4080
agatggctgc	tctaaaaaga	caaatgaatg	gggaaagaca	atcattgaat	acaaaacaaa	4140
taagccatca	cgctgcccct	tccttgatat	tgcacctttg	gacatcggtg	gtgctgacca	4200
tgaattcttt	gtggacattg	gccagtcctg	tttcaaataa	atgaactcaa	tctaaattaa	4260
aaaagaaaaga	aatttgaaaa	aactttctct	ttgccatttc	ttcttcttct	tttttaactg	4320
aaagctgaat	ccttccattt	cttctgcaca	tctacttgct	taaattgtgg	gcaaaagaga	4380
aaaagaagga	ttgatcagag	cattgtgcaa	tacagtttca	ttactcctt	ccccgctcc	4440
cccaaaaatt	tgaatttttt	tttcaacact	cttacacctg	ttatggaaaa	tgtcaacctt	4500
tgtaagaaaa	ccaaaataaa	aattgaaaaa	taaaaaccat	aaacattttg	accacttgtg	4560
gcttttgaat	atcttccaca	gagggaagtt	taaaacccaa	acttccaaag	gttttaacta	4620
cctcaaaaaca	ctttcccatg	agtgtgatcc	acattgttag	gtgctgacct	agacagagat	4680
gaactgaggt	ccttggtttt	ttttgttcat	aatacaaagg	tgctaattaa	tagtatttca	4740
gatacttgaa	gaatgttgat	ggtgctagaa	gaatttgaga	agaaatactc	ctgtatttag	4800
ttgtatcgtg	tgggtgattt	tttaaaaaat	ttgatttagc	attcatattt	tccatcttat	4860
tcccaattaa	aagtatgcag	attatttgcc	caaagttgtc	ctcttcttca	gattcagcat	4920
ttgttctttg	ccagttctcat	tttcatcttc	ttccatggtt	ccacagaagc	tttgttctt	4980
gggcaagcag	aaaaattaaa	ttgtacctat	tttgtatatg	tgagatgttt	aaataaattg	5040
tgaaaaaaat	gaaataaagc	atgttttggtt	ttccaaaaga	acatat		5086

<211> 1366
 <212> PRT
 <213> Homo sapiens

<400> 38

Met	Leu	Ser	Phe	Val	Asp	Thr	Arg	Thr	Leu	Leu	Leu	Leu	Ala	Val	Thr
1				5					10					15	
Leu	Cys	Leu	Ala	Thr	Cys	Gln	Ser	Leu	Gln	Glu	Glu	Thr	Val	Arg	Lys
			20					25					30		
Gly	Pro	Ala	Gly	Asp	Arg	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Pro	Pro	Gly
		35					40					45			
Pro	Pro	Gly	Arg	Asp	Gly	Glu	Asp	Gly	Pro	Thr	Gly	Pro	Pro	Gly	Pro
	50					55					60				
Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Gly	Gly	Asn	Phe	Ala	Ala	Gln
65					70					75					80
Tyr	Asp	Gly	Lys	Gly	Val	Gly	Leu	Gly	Pro	Gly	Pro	Met	Gly	Leu	Met
			85						90				95		
Gly	Pro	Arg	Gly	Pro	Pro	Gly	Ala	Ala	Gly	Ala	Pro	Gly	Pro	Gln	Gly
			100						105				110		
Phe	Gln	Gly	Pro	Ala	Gly	Glu	Pro	Gly	Glu	Pro	Gly	Gln	Thr	Gly	Pro
		115					120					125			
Ala	Gly	Ala	Arg	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Lys	Ala	Gly	Glu	Asp
		130					135				140				
Gly	His	Pro	Gly	Lys	Pro	Gly	Arg	Pro	Gly	Glu	Arg	Gly	Val	Val	Gly
145					150					155					160
Pro	Gln	Gly	Ala	Arg	Gly	Phe	Pro	Gly	Thr	Pro	Gly	Leu	Pro	Gly	Phe
				165					170					175	
Lys	Gly	Ile	Arg	Gly	His	Asn	Gly	Leu	Asp	Gly	Leu	Lys	Gly	Gln	Pro
			180					185					190		
Gly	Ala	Pro	Gly	Val	Lys	Gly	Glu	Pro	Gly	Ala	Pro	Gly	Glu	Asn	Gly
		195					200					205			
Thr	Pro	Gly	Gln	Thr	Gly	Ala	Arg	Gly	Leu	Pro	Gly	Glu	Arg	Gly	Arg
	210					215						220			
Val	Gly	Ala	Pro	Gly	Pro	Ala	Gly	Ala	Arg	Gly	Ser	Asp	Gly	Ser	Val
225					230					235					240
Gly	Pro	Val	Gly	Pro	Ala	Gly	Pro	Ile	Gly	Ser	Ala	Gly	Pro	Pro	Gly
				245					250					255	
Phe	Pro	Gly	Ala	Pro	Gly	Pro	Lys	Gly	Glu	Ile	Gly	Ala	Val	Gly	Asn
			260					265					270		
Ala	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Glu	Val	Gly	Leu	Pro
		275					280					285			
Gly	Leu	Ser	Gly	Pro	Val	Gly	Pro	Pro	Gly	Asn	Pro	Gly	Ala	Asn	Gly
	290					295					300				
Leu	Thr	Gly	Ala	Lys	Gly	Ala	Ala	Gly	Leu	Pro	Gly	Val	Ala	Gly	Ala
305					310					315					320
Pro	Gly	Leu	Pro	Gly	Pro	Arg	Gly	Ile	Pro	Gly	Pro	Val	Gly	Ala	Ala
				325					330					335	
Gly	Ala	Thr	Gly	Ala	Arg	Gly	Leu	Val	Gly	Glu	Pro	Gly	Pro	Ala	Gly
			340					345					350		
Ser	Lys	Gly	Glu	Ser	Gly	Asn	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Pro
		355					360					365			
Gln	Gly	Pro	Pro	Gly	Pro	Ser	Gly	Glu	Glu	Gly	Lys	Arg	Gly	Pro	Asn
	370					375					380				
Gly	Glu	Ala	Gly	Ser	Ala	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Arg	Gly
385					390					395					400
Ser	Pro	Gly	Ser	Arg	Gly	Leu	Pro	Gly	Ala	Asp	Gly	Arg	Ala	Gly	Val
				405					410					415	
Met	Gly	Pro	Pro	Gly	Ser	Arg	Gly	Ala	Ser	Gly	Pro	Ala	Gly	Val	Arg
			420					425					430		

Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly
 435 440 445
 Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys
 450 455 460
 Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile
 465 470 475 480
 Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly
 485 490 495
 Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His
 500 505 510
 Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
 515 520 525
 Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly
 530 535 540
 Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
 545 550 555 560
 Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
 565 570 575
 Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
 580 585 590
 Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser
 595 600 605
 Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro
 610 615 620
 Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly
 625 630 635 640
 Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu
 645 650 655
 Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp
 660 665 670
 Gly Ala Arg Gly Ala His Gly Ala Val Gly Ala Pro Gly Pro Ala Gly
 675 680 685
 Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro
 690 695 700
 Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala
 705 710 715 720
 Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly
 725 730 735
 Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val
 740 745 750
 Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn
 755 760 765
 Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly
 770 775 780
 Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro
 785 790 795 800
 Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu
 805 810 815
 Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly
 820 825 830
 Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro
 835 840 845
 Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln
 850 855 860
 Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly
 865 870 875 880
 Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro
 885 890 895
 Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val

			900					905					910		
Gly	Ser	Pro	Gly	Val	Asn	Gly	Ala	Pro	Gly	Glu	Ala	Gly	Arg	Asp	Gly
		915					920					925			
Asn	Pro	Gly	Asn	Asp	Gly	Pro	Pro	Gly	Arg	Asp	Gly	Gln	Pro	Gly	His
	930					935					940				
Lys	Gly	Glu	Arg	Gly	Tyr	Pro	Gly	Asn	Ile	Gly	Pro	Val	Gly	Ala	Ala
945					950					955					960
Gly	Ala	Pro	Gly	Pro	His	Gly	Pro	Val	Gly	Pro	Ala	Gly	Lys	His	Gly
				965					970					975	
Asn	Arg	Gly	Glu	Thr	Gly	Pro	Ser	Gly	Pro	Val	Gly	Pro	Ala	Gly	Ala
			980					985					990		
Val	Gly	Pro	Arg	Gly	Pro	Ser	Gly	Pro	Gln	Gly	Ile	Arg	Gly	Asp	Lys
		995					1000					1005			
Gly	Glu	Pro	Gly	Glu	Lys	Gly	Pro	Arg	Gly	Leu	Pro	Gly	Leu	Lys	Gly
	1010					1015					1020				
His	Asn	Gly	Leu	Gln	Gly	Leu	Pro	Gly	Ile	Ala	Gly	His	His	Gly	Asp
1025					1030					1035					1040
Gln	Gly	Ala	Pro	Gly	Ser	Val	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Pro	Ala
				1045					1050					1055	
Gly	Pro	Ser	Gly	Pro	Ala	Gly	Lys	Asp	Gly	Arg	Thr	Gly	His	Pro	Gly
			1060					1065					1070		
Thr	Val	Gly	Pro	Ala	Gly	Ile	Arg	Gly	Pro	Gln	Gly	His	Gln	Gly	Pro
		1075					1080					1085			
Ala	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Val	Ser
	1090					1095					1100				
Gly	Gly	Gly	Tyr	Asp	Phe	Gly	Tyr	Asp	Gly	Asp	Phe	Tyr	Arg	Ala	Asp
1105					1110					1115					1120
Gln	Pro	Arg	Ser	Ala	Pro	Ser	Leu	Arg	Pro	Lys	Asp	Tyr	Glu	Val	Asp
				1125					1130					1135	
Ala	Thr	Leu	Lys	Ser	Leu	Asn	Asn	Gln	Ile	Glu	Thr	Leu	Leu	Thr	Pro
			1140					1145					1150		
Glu	Gly	Ser	Arg	Lys	Asn	Pro	Ala	Arg	Thr	Cys	Arg	Asp	Leu	Arg	Leu
		1155					1160					1165			
Ser	His	Pro	Glu	Trp	Ser	Ser	Gly	Tyr	Tyr	Trp	Ile	Asp	Pro	Asn	Gln
	1170					1175					1180				
Gly	Cys	Thr	Met	Asp	Ala	Ile	Lys	Val	Tyr	Cys	Asp	Phe	Ser	Thr	Gly
1185					1190					1195					1200
Glu	Thr	Cys	Ile	Arg	Ala	Gln	Pro	Glu	Asn	Ile	Pro	Ala	Lys	Asn	Trp
				1205					1210					1215	
Tyr	Arg	Ser	Ser	Lys	Asp	Lys	Lys	His	Val	Trp	Leu	Gly	Glu	Thr	Ile
			1220					1225					1230		
Asn	Ala	Gly	Ser	Gln	Phe	Glu	Tyr	Asn	Val	Glu	Gly	Val	Thr	Ser	Lys
		1235					1240					1245			
Glu	Met	Ala	Thr	Gln	Leu	Ala	Phe	Met	Arg	Leu	Leu	Ala	Asn	Tyr	Ala

<210> 39
 <211> 2235
 <212> DNA
 <213> Homo sapiens

<400> 39
 atggctgtgc tgcctggccc tctgcagctg ctgggagtg tgccttaccat ttccctgagt 60
 tccatcaggc tcattcaggc tgggtgcctac tatgggatca agccgctgcc acctcaaatt 120
 cctcctcaga tgcaccaca aattccacaa taccagcccc tgggtcagca agtacctcac 180
 atgccttttg ccaaagatgg cctcgccatg ggcaaggaga tgcccactt gcagtatggc 240
 aaagagtatc cacacctacc ccaatatatg aaggaaattc aaccggcgcc aagaatgggc 300
 aaggaagccg ttcccaagaa aggcaaagaa ataccattag ccagtttacg aggggaacaa 360
 ggtccccgtg gagagcctgg cccaagagga ccacctgggc cccctggttt accagggtcat 420
 gggatacctg gaattaaagg aaaaccaggg ccacagggat atccaggagt tggaaagcca 480
 ggtatgcctg gaatgccagg gaagccagga gccatgggca tgcctggggc aaaaggagaa 540
 attggacaga aaggggaaat tgggcctatg gggatcccag gaccacaagg acctccaggg 600
 cctcatggac ttcttgcat tgggaagcca ggtgggccag ggttaccagg gcaaccagga 660
 ccaaagggtg atcgaggacc caaaggacta ccaggacctc aaggccttcg gggctctaaa 720
 ggagacaagg gcttcgggat gccaggtag ccagggtgaa aggggcctcc agggatgac 780
 ggctccccg gccctgttg actgccagga gtgggcaaac caggagtgc aggcttccct 840
 gggccccagg gccccctgg aaagccagg gctccaggag aaccgggtcg acaaggccct 900
 attggggtag cgggggttca aggacctct gggatacccg gaattggaaa gccaggccag 960
 gatgggatcc caggccagcc aggatattcca ggtggcaaag gggagcaagg actgccaggg 1020
 ctaccagggg cccaggcct tccagggtatt gggaaaccag gcttcccagg acctcaaagg 1080
 gaccggggca tgggaggtgt tcctggggct cttggacca gaggggagaa aggaccaata 1140
 ggttccccg gaataggggg ttctccagga gagccaggcc tgcctggaat ccagggtcct 1200
 atggggcctc cagggtgctat tggttttcct ggacccaaag gagaagggtg gattgtaggg 1260
 ccacaggggc caccagggtc caagggtgag ccagggttc aaggcttccc aggaaagcca 1320
 ggtttccttg gtgaagtagg gctcctggc atgaggggtt tcccagggtc cataggcccc 1380
 aagggggaac atggggcaaaa aggtgtacca ggactccctg gtgttccagg gcttctcgga 1440
 cctaaggag aaccaggaat cccaggggat cagggtttac agggccccc aggtatccca 1500
 gggattggg gccctagtgg cccatttga ccacctggga ttccaggccc caaaggggag 1560
 cctggcctcc caggggcccc tgggttccct ggtataggga aaccgggagt ggcaggactt 1620
 catggcccc cagggaagcc tgggtgccctt ggtcctcaag gccagcctg ccttccagga 1680
 cccccaggc ctccaggacc tccaggacct ccagctgtga tgccccctac accaccacct 1740
 caggagagt atctgccaga tatgggctg ggaattgat gcgtaaaacc ccccatgct 1800
 acgggggcta agaaaggcaa gaatggagg ccagcctatg agatgcctgc atttaccgoc 1860
 gagctaaccg caccctttcc accggtgggg ggcccagtga agtttaacaa actgctgtat 1920
 aacggcagac agaactacaa cccgcagaca ggcattctca cctgtgaggt ccctggtgtc 1980
 tactactttg cataccacgt tctactgcaag ggggggaacg tgtgggttgc tctattcaag 2040
 aacaacgagc ccgtgatgta cacgtacgac gagtacaaaa agggcttcct ggaccaggca 2100
 tctgggagtg cagtgtgtgt gctcaggccc ggagaccggg tgttcctcca gatgccctca 2160
 gaacaggctg caggactgta tgccgggcag tatgtccact cctccttttc aggatattta 2220
 ttgtatccca tgtaa 2235

<210> 40
 <211> 744
 <212> PRT
 <213> Homo sapiens

<400> 40
 Met Ala Val Leu Pro Gly Pro Leu Gln Leu Leu Gly Val Leu Leu Thr
 1 5 10 15
 Ile Ser Leu Ser Ser Ile Arg Leu Ile Gln Ala Gly Ala Tyr Tyr Gly
 20 25 30
 Ile Lys Pro Leu Pro Pro Gln Ile Pro Pro Gln Met Pro Pro Gln Ile
 35 40 45

Pro	Gln	Tyr	Gln	Pro	Leu	Gly	Gln	Gln	Val	Pro	His	Met	Pro	Leu	Ala	50	55	60
Lys	Asp	Gly	Leu	Ala	Met	Gly	Lys	Glu	Met	Pro	His	Leu	Gln	Tyr	Gly	65	70	75
Lys	Glu	Tyr	Pro	His	Leu	Pro	Gln	Tyr	Met	Lys	Glu	Ile	Gln	Pro	Ala	85	90	95
Pro	Arg	Met	Gly	Lys	Glu	Ala	Val	Pro	Lys	Lys	Gly	Lys	Glu	Ile	Pro	100	105	110
Leu	Ala	Ser	Leu	Arg	Gly	Glu	Gln	Gly	Pro	Arg	Gly	Glu	Pro	Gly	Pro	115	120	125
Arg	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Pro	Gly	His	Gly	Ile	Pro	Gly	130	135	140
Ile	Lys	Gly	Lys	Pro	Gly	Pro	Gln	Gly	Tyr	Pro	Gly	Val	Gly	Lys	Pro	145	150	155
Gly	Met	Pro	Gly	Met	Pro	Gly	Lys	Pro	Gly	Ala	Met	Gly	Met	Pro	Gly	165	170	175
Ala	Lys	Gly	Glu	Ile	Gly	Gln	Lys	Gly	Glu	Ile	Gly	Pro	Met	Gly	Ile	180	185	190
Pro	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Pro	His	Gly	Leu	Pro	Gly	Ile	Gly	195	200	205
Lys	Pro	Gly	Gly	Pro	Gly	Leu	Pro	Gly	Gln	Pro	Gly	Pro	Lys	Gly	Asp	210	215	220
Arg	Gly	Pro	Lys	Gly	Leu	Pro	Gly	Pro	Gln	Gly	Leu	Arg	Gly	Pro	Lys	225	230	235
Gly	Asp	Lys	Gly	Phe	Gly	Met	Pro	Gly	Ala	Pro	Gly	Val	Lys	Gly	Pro	245	250	255
Pro	Gly	Met	His	Gly	Leu	Pro	Gly	Pro	Val	Gly	Leu	Pro	Gly	Val	Gly	260	265	270
Lys	Pro	Gly	Val	Thr	Gly	Phe	Pro	Gly	Pro	Gln	Gly	Pro	Leu	Gly	Lys	275	280	285
Pro	Gly	Ala	Pro	Gly	Glu	Pro	Gly	Arg	Gln	Gly	Pro	Ile	Gly	Val	Pro	290	295	300
Gly	Val	Gln	Gly	Pro	Pro	Gly	Ile	Pro	Gly	Ile	Gly	Lys	Pro	Gly	Gln	305	310	315
Asp	Gly	Ile	Pro	Gly	Gln	Pro	Gly	Phe	Pro	Gly	Gly	Lys	Gly	Glu	Gln	325	330	335
Gly	Leu	Pro	Gly	Leu	Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gly	Ile	Gly	Lys	340	345	350
Pro	Gly	Phe	Pro	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Met	Gly	Gly	Val	Pro	355	360	365
Gly	Ala	Leu	Gly	Pro	Arg	Gly	Glu	Lys	Gly	Pro	Ile	Gly	Ser	Pro	Gly	370	375	380
Ile	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Ile	Pro	Gly	Pro	385	390	395
Met	Gly	Pro	Pro	Gly	Ala	Ile	Gly	Phe	Pro	Gly	Pro	Lys	Gly	Glu	Gly	405	410	415
Gly	Ile	Val	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Glu	Pro	Gly	420	425	430
Leu	Gln	Gly	Phe	Pro	Gly	Lys	Pro	Gly	Phe	Leu	Gly	Glu	Val	Gly	Pro	435	440	445
Pro	Gly	Met	Arg	Gly	Phe	Pro	Gly	Pro	Ile	Gly	Pro	Lys	Gly	Glu	His	450	455	460
Gly	Gln	Lys	Gly	Val	Pro	Gly	Leu	Pro	Gly	Val	Pro	Gly	Leu	Leu	Gly	465	470	475
Pro	Lys	Gly	Glu	Pro	Gly	Ile	Pro	Gly	Asp	Gln	Gly	Leu	Gln	Gly	Pro	485	490	495
Pro	Gly	Ile	Pro	Gly	Ile	Gly	Gly	Pro	Ser	Gly	Pro	Ile	Gly	Pro	Pro	500	505	510
Gly	Ile	Pro	Gly	Pro	Lys	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Pro	Pro	Gly			

	515		520		525
Phe	Pro Gly Ile Gly Lys	Pro Gly Val Ala Gly	Leu His Gly Pro Pro		
	530	535	540		
Gly	Lys Pro Gly Ala Leu	Gly Pro Gln Gly Gln	Pro Gly Leu Pro Gly		
545	550	555	560		
Pro	Pro Gly Pro Pro Gly	Pro Pro Gly Pro Pro	Ala Val Met Pro Pro		
	565	570	575		
Thr	Pro Pro Pro Gln Gly	Glu Tyr Leu Pro Asp	Met Gly Leu Gly Ile		
	580	585	590		
Asp	Gly Val Lys Pro Pro	His Ala Thr Gly Ala	Lys Lys Gly Lys Asn		
	595	600	605		
Gly	Gly Pro Ala Tyr Glu	Met Pro Ala Phe Thr	Ala Glu Leu Thr Ala		
	610	615	620		
Pro	Phe Pro Pro Val Gly	Gly Pro Val Lys Phe	Asn Lys Leu Leu Tyr		
625	630	635	640		
Asn	Gly Arg Gln Asn Tyr	Asn Pro Gln Thr Gly	Ile Phe Thr Cys Glu		
	645	650	655		
Val	Pro Gly Val Tyr Tyr	Phe Ala Tyr His Val	His Cys Lys Gly Gly		
	660	665	670		
Asn	Val Trp Val Ala Leu	Phe Lys Asn Asn Glu	Pro Val Met Tyr Thr		
	675	680	685		
Tyr	Asp Glu Tyr Lys Lys	Gly Phe Leu Asp Gln	Ala Ser Gly Ser Ala		
	690	695	700		
Val	Leu Leu Leu Arg Pro	Gly Asp Arg Val Phe	Leu Gln Met Pro Ser		
705	710	715	720		
Glu	Gln Ala Ala Gly Leu	Tyr Ala Gly Gln Tyr	Val His Ser Ser Phe		
	725	730	735		
Ser	Gly Tyr Leu Leu Tyr	Pro Met			
	740				

<210> 41

<211> 5064

<212> DNA

<213> Homo sapiens

<400> 41

gagaaggagg	ccttcaggtc	caaggcaaagg	gggaacttct	gtcgtgggaa	cgaaaaagaa	60
agaggattta	caggggtggg	ggacagaggg	gcagcaggaa	ccagaaggga	gacagtggcg	120
gtcgcaccgg	ggccgatccg	agagttcccc	ttagagaacg	gagctcacgg	gcggggaggc	180
ctcacctgct	agtaggacgc	agaaagacag	aaggcgaagg	agacccccctg	ccgtagccat	240
cttgccctctc	tgctgagcgg	aagcccccg	tcggctcctg	tctgttagcg	gcctctctag	300
gctaccactg	acaccgctctc	tgtggccccg	agcctaagag	accggaagtt	cgtgtttcca	360
ggcgcttccg	gaaaccgcgg	gagagggctg	ctgacgtgga	ggcgtccgaa	gggcagcagg	420
gtgtgtcggg	gctcggatta	agacatcgga	gtcggagacc	tgagagatgt	taaccaaatt	480
cgagaccaag	agcgcgcggg	tcaaagggct	cagctttcac	cccaaaagac	cttggatcct	540
gactagttta	cataatgggg	tcatccagtt	atgggactat	cggatgtgca	ctctcattga	600
caagtttgat	gaacatgatg	gtccagtgcg	aggcattgac	ttccataagc	agcagccact	660
gttcgtctct	ggaggagatg	actataagat	taaggtttgg	aattacaagc	ttcggcgctg	720
tcttttcaca	ttgcttgggc	acttagatta	tattcgcacc	acgttttttc	atcatgaata	780
tccctggatt	ctgagtgcc	ccgatgatca	gaccatccga	gtgtggaatt	ggcaatctag	840
aacctgtgtt	tgtgtgttaa	cagggcacaa	ccattatgtg	atgtgtgctc	agttccaccc	900
cacagaagac	ttggtagtat	cagccagcct	ggaccagact	gtgcgcgttt	gggatatttc	960
tggctctgag	aaaaaaaaacc	tgtcccctgg	tgcggtggaa	tcggatgtga	gaggaataac	1020
tgggggtgat	ctattttggaa	ctacagatgc	agtggatgaag	catgtactag	agggtcacga	1080
tcgtggagta	aactgggctg	ccttccaccc	cactatgccc	cttattgtat	ctggggcaga	1140
tgatcgtcaa	gtgaagatct	ggcgcgatgaa	tgaatcaaag	gcatgggagg	ttgataacctg	1200
ccggggccat	tacaacaatg	tatcttgtgc	cgtcttccac	cctcgccaag	agttgatcct	1260
cagcaattct	gaggacaaga	gtattcgagt	ctgggatatg	tctaagcgga	ctgggggttca	1320

gactttccgc	agagaccatg	atogttttctg	ggtcctagct	gctcacccta	acottaacct	1380
ctttgcagca	ggccatgatg	gtgggtatgat	tgtgtttaag	ctggaacggg	aacggccagc	1440
ctatgctggt	catggcaata	tgctacacta	tgtaaggac	cgattcttac	gacagctgga	1500
tttcaacagc	tccaaagatg	tagctgtgat	gcagttgcgg	agtgggtcca	agtttccagt	1560
attcaatatg	tcatacaatc	cagcagaaaa	tgcatcctg	ctttgtacaa	gagctagcaa	1620
tctagagaat	agtacctatg	acctgtacac	catccctaaa	gatgctgact	cccagaatcc	1680
tgatgcgcct	gaagggaaac	gatoctcagg	cctgacagcc	gtttgggtcg	ctcgaaatcg	1740
gtttgctgtc	ctagatcgga	tgcattoctg	tctgatcaag	aatctgaaga	atgagatcac	1800
caaaaaggta	caggtgcccc	actgtgatga	gatcttctat	gctggcacag	gcaatctcct	1860
gcttcgagat	gcggaactcta	tcacactctt	tgacgtacag	cagaagcgga	ctctggcatc	1920
tgtgaagatt	tctaaagtga	aatacgttat	ctggtcagca	gacatgtcac	atgtagcact	1980
actagccaaa	cacgcatttg	tgatctgtaa	cgcgaactg	gatgctttat	gtaacattca	2040
tgagaacatt	cgtgtcaaga	gtggggcctg	ggatgagagt	ggggtattta	tctataccac	2100
aagcaaccac	atcaaatatg	ctgtcaccac	tggggaccac	gggatcattc	gaactctgga	2160
tttaccatc	tatgtcacac	gggtgaagg	caacaatgta	tactgcctag	acagggagtg	2220
tcgtccccgg	gtactcacca	ttgatccac	tgagttcaaa	ttcaagctgg	ccctgatcaa	2280
cagaaaatat	gatgaggtac	tgacatggt	gaggaatgcc	aaactagttg	gccagtctat	2340
tattgcttat	ctccagaaga	agggctatcc	tgaagtggca	ctgcattttg	tcaaggatga	2400
gaaaactcgc	tttagtctgg	cactggagtg	tggaaacatt	gagattgctc	tgggaagcagc	2460
caaagcactg	gatgacaaga	actgctggga	aaagctggga	gaagtggccc	tgctgcagg	2520
gaaccaccag	attgtggaaa	tgtgctatca	gcgtaccaa	aactttgaca	aagtttctct	2580
cctgtatctt	atcactggca	acttagaaaa	acctcgcaag	atgatgaaga	ttgctgagat	2640
cagaaaggac	atgagtggcc	actatcagaa	tgccctatac	ctgggtgatg	tgtcagagcg	2700
tgtgcggatc	ctgaagaact	gtggacagaa	gtccctggcc	tatctcacag	ctgctaccca	2760
tggcttagat	gaagaagctg	agagcctaaa	ggagacattt	gaccagaga	aggagacaat	2820
cccagacatt	gaccctaattg	ccaagctgct	ccagccacct	gcacctatca	tgccattgga	2880
taccaattgg	cctttattga	ctgtatccaa	aggatttttt	gaaggcacca	ttgccagcaa	2940
agggaaggga	ggagcactgg	ctgctgacat	tgacattgac	actggttgga	cagagggctg	3000
gggagagatg	gcagagctgc	agttggatga	agatgggttt	gtggaggcta	cagaaggttt	3060
gggggatgat	gctcttggca	agggacagga	agaaggaggt	ggctgggatg	tagaagaaga	3120
tctggagctc	cctcctgagc	tggatatatc	ccctggggca	gctgggtggg	ctgaagatgg	3180
tttctttgtg	cccccaacca	agggaacaag	tccaactcag	atctggtgta	ataactctca	3240
gcttccagtt	gatcacatcc	tggcaggctc	tttcgaaaca	gccatgcggc	tccttcatga	3300
ccaagtaggg	gtaatccagt	ttggccctca	caagcaactg	ttcctacaga	catacgcccg	3360
aggccgcaca	acctatcagg	ctctgccctg	cctaccctcc	atgtatggct	atcctaatac	3420
caactggaag	gatgcagggc	tgaagaatgg	tgtaccagct	gtgggcctga	agcttaatat	3480
cctcatccaa	cggttgcagc	tgtgctacca	gctcaccaca	gttggcaaat	ttgaggaggc	3540
tgtggaaaaa	ttccgttcca	tccttctcag	tgtgtcactt	cttgttgttg	acaataaaca	3600
agagattgca	gaggcccagc	agctcatcac	catttgccgt	gagtacattg	tgggtttgtc	3660
cgtggagaca	gaaaggaaga	agctgoccaa	agagactcta	gaacagcaga	agcgcatctg	3720
tgagatggca	gcctattttca	cccactcaaa	cctgcagcct	gtgcacatga	tcctggtgct	3780
gcgtacagcc	ctcaatctgt	tcttcaagct	caagaacttc	aagacagctg	ccacctttgc	3840
tcggcgcccta	ctagaactcg	ggcccaagcc	tgaggtggcc	caacagaccc	gaaaaatcct	3900
gtctgcctgt	gagaagaatc	ccacagatgc	ctaccagctc	aattatgaca	tgacacaacc	3960
ctttgacatt	tgtgctgcat	catatcggcc	catctaccgt	ggaaagccag	tagaaaagtg	4020
tccactcagt	ggggcctgct	attccctgga	gttcaaaagg	caaactctga	gggtcaccac	4080
agtgcagag	attggcaaag	atgtgatttg	tttaaggatc	agtcctctgc	agtttctgta	4140
aggccccctt	tgtgtgcatg	ggtcagtcac	catatgttcc	ccccagagaa	tgtgtctata	4200
tcctccttct	aacagcacct	tccccctgca	gctactcttc	agatctggct	ctctgtaccc	4260
taaaacctag	tatctttttc	tcttctatgg	aaaatccgaa	ggtctaaact	tgactttttt	4320
gaggtcttct	caacttgact	acagttgtgc	tcataattgt	ccttgccctt	ccagcttaat	4380
tatttttaagg	aacaaatgaa	aactctgggc	tgggtggagt	ggctcatacc	tgtaatccca	4440
gcactttggg	aggctacggg	gggcagatca	tctgaggcca	ggagttcgag	acctgcctgg	4500
ccaacatggc	aacaccccg	ctctaataaa	aatataaaaa	ttagcctggc	atggtagcat	4560
gcgcctatag	tcccagctgc	tcaggaggct	gaggcatgag	aatcgcttga	acctaggagg	4620
tggaggttgc	attcaactga	gatcatacca	cttcattcca	gcctgggtga	cagagcaaga	4680
ctctgtctca	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaggaaaac	tctgtgatgg	4740
acatttgttt	agtaaatccc	ttcagtattt	atccctcctt	tccccacagc	agctttcttt	4800
cctgtcaact	agaaaggagc	aggatgtaat	aaatacattt	tggtgtgact	aggccacacc	4860

```

aactcttaat catctcccat tttccttaga catttaaatt tcaaggcagg taccctctgt 4920
gtactcagaa atttgaagaa gttatttggt tttccaaaat gcacactgcg gggtattgat 4980
ttgttcttta caactattgt tctcatattt ctcacactaa ataatctct atgagagctt 5040
cttgaaaaaa aaaaaaaaaa agcg 5064

```

<210> 42

<211> 1224

<212> PRT

<213> Homo sapiens

<400> 42

```

Met Leu Thr Lys Phe Glu Thr Lys Ser Ala Arg Val Lys Gly Leu Ser
 1          5          10          15
Phe His Pro Lys Arg Pro Trp Ile Leu Thr Ser Leu His Asn Gly Val
 20          25          30
Ile Gln Leu Trp Asp Tyr Arg Met Cys Thr Leu Ile Asp Lys Phe Asp
 35          40          45
Glu His Asp Gly Pro Val Arg Gly Ile Asp Phe His Lys Gln Gln Pro
 50          55          60
Leu Phe Val Ser Gly Gly Asp Asp Tyr Lys Ile Lys Val Trp Asn Tyr
 65          70          75          80
Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile
 85          90          95
Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser
100          105          110
Asp Asp Gln Thr Ile Arg Val Trp Asn Trp Gln Ser Arg Thr Cys Val
115          120          125
Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His
130          135          140
Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg
145          150          155          160
Val Trp Asp Ile Ser Gly Leu Arg Lys Lys Asn Leu Ser Pro Gly Ala
165          170          175
Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr
180          185          190
Thr Asp Ala Val Val Lys His Val Leu Glu Gly His Asp Arg Gly Val
195          200          205
Asn Trp Ala Ala Phe His Pro Thr Met Pro Leu Ile Val Ser Gly Ala
210          215          220
Asp Asp Arg Gln Val Lys Ile Trp Arg Met Asn Glu Ser Lys Ala Trp
225          230          235          240
Glu Val Asp Thr Cys Arg Gly His Tyr Asn Asn Val Ser Cys Ala Val
245          250          255
Phe His Pro Arg Gln Glu Leu Ile Leu Ser Asn Ser Glu Asp Lys Ser
260          265          270
Ile Arg Val Trp Asp Met Ser Lys Arg Thr Gly Val Gln Thr Phe Arg
275          280          285
Arg Asp His Asp Arg Phe Trp Val Leu Ala Ala His Pro Asn Leu Asn
290          295          300
Leu Phe Ala Ala Gly His Asp Gly Gly Met Ile Val Phe Lys Leu Glu
305          310          315          320
Arg Glu Arg Pro Ala Tyr Ala Val His Gly Asn Met Leu His Tyr Val
325          330          335
Lys Asp Arg Phe Leu Arg Gln Leu Asp Phe Asn Ser Ser Lys Asp Val
340          345          350
Ala Val Met Gln Leu Arg Ser Gly Ser Lys Phe Pro Val Phe Asn Met
355          360          365
Ser Tyr Asn Pro Ala Glu Asn Ala Val Leu Leu Cys Thr Arg Ala Ser
370          375          380

```

Asn	Leu	Glu	Asn	Ser	Thr	Tyr	Asp	Leu	Tyr	Thr	Ile	Pro	Lys	Asp	Ala	385	390	395	400
Asp	Ser	Gln	Asn	Pro	Asp	Ala	Pro	Glu	Gly	Lys	Arg	Ser	Ser	Gly	Leu	405	410	415	
Thr	Ala	Val	Trp	Val	Ala	Arg	Asn	Arg	Phe	Ala	Val	Leu	Asp	Arg	Met	420	425	430	
His	Ser	Leu	Leu	Ile	Lys	Asn	Leu	Lys	Asn	Glu	Ile	Thr	Lys	Lys	Val	435	440	445	
Gln	Val	Pro	Asn	Cys	Asp	Glu	Ile	Phe	Tyr	Ala	Gly	Thr	Gly	Asn	Leu	450	455	460	
Leu	Leu	Arg	Asp	Ala	Asp	Ser	Ile	Thr	Leu	Phe	Asp	Val	Gln	Gln	Lys	465	470	475	480
Arg	Thr	Leu	Ala	Ser	Val	Lys	Ile	Ser	Lys	Val	Lys	Tyr	Val	Ile	Trp	485	490	495	
Ser	Ala	Asp	Met	Ser	His	Val	Ala	Leu	Leu	Ala	Lys	His	Ala	Ile	Val	500	505	510	
Ile	Cys	Asn	Arg	Lys	Leu	Asp	Ala	Leu	Cys	Asn	Ile	His	Glu	Asn	Ile	515	520	525	
Arg	Val	Lys	Ser	Gly	Ala	Trp	Asp	Glu	Ser	Gly	Val	Phe	Ile	Tyr	Thr	530	535	540	
Thr	Ser	Asn	His	Ile	Lys	Tyr	Ala	Val	Thr	Thr	Gly	Asp	His	Gly	Ile	545	550	555	560
Ile	Arg	Thr	Leu	Asp	Leu	Pro	Ile	Tyr	Val	Thr	Arg	Val	Lys	Gly	Asn	565	570	575	
Asn	Val	Tyr	Cys	Leu	Asp	Arg	Glu	Cys	Arg	Pro	Arg	Val	Leu	Thr	Ile	580	585	590	
Asp	Pro	Thr	Glu	Phe	Lys	Phe	Lys	Leu	Ala	Leu	Ile	Asn	Arg	Lys	Tyr	595	600	605	
Asp	Glu	Val	Leu	His	Met	Val	Arg	Asn	Ala	Lys	Leu	Val	Gly	Gln	Ser	610	615	620	
Ile	Ile	Ala	Tyr	Leu	Gln	Lys	Lys	Gly	Tyr	Pro	Glu	Val	Ala	Leu	His	625	630	635	640
Phe	Val	Lys	Asp	Glu	Lys	Thr	Arg	Phe	Ser	Leu	Ala	Leu	Glu	Cys	Gly	645	650	655	
Asn	Ile	Glu	Ile	Ala	Leu	Glu	Ala	Ala	Lys	Ala	Leu	Asp	Asp	Lys	Asn	660	665	670	
Cys	Trp	Glu	Lys	Leu	Gly	Glu	Val	Ala	Leu	Leu	Gln	Gly	Asn	His	Gln	675	680	685	
Ile	Val	Glu	Met	Cys	Tyr	Gln	Arg	Thr	Lys	Asn	Phe	Asp	Lys	Val	Ser	690	695	700	
Phe	Leu	Tyr	Leu	Ile	Thr	Gly	Asn	Leu	Glu	Lys	Leu	Arg	Lys	Met	Met	705	710	715	720
Lys	Ile	Ala	Glu	Ile	Arg	Lys	Asp	Met	Ser	Gly	His	Tyr	Gln	Asn	Ala	725	730	735	
Leu	Tyr	Leu	Gly	Asp	Val	Ser	Glu	Arg	Val	Arg	Ile	Leu	Lys	Asn	Cys	740	745	750	
Gly	Gln	Lys	Ser	Leu	Ala	Tyr	Leu	Thr	Ala	Ala	Thr	His	Gly	Leu	Asp	755	760	765	
Glu	Glu	Ala	Glu	Ser	Leu	Lys	Glu	Thr	Phe	Asp	Pro	Glu	Lys	Glu	Thr	770	775	780	
Ile	Pro	Asp	Ile	Asp	Pro	Asn	Ala	Lys	Leu	Leu	Gln	Pro	Pro	Ala	Pro	785	790	795	800
Ile	Met	Pro	Leu	Asp	Thr	Asn	Trp	Pro	Leu	Leu	Thr	Val	Ser	Lys	Gly	805	810	815	
Phe	Phe	Glu	Gly	Thr	Ile	Ala	Ser	Lys	Gly	Lys	Gly	Gly	Ala	Leu	Ala	820	825	830	
Ala	Asp	Ile	Asp	Ile	Asp	Thr	Val	Gly	Thr	Glu	Gly	Trp	Gly	Glu	Asp	835	840	845	
Ala	Glu	Leu	Gln	Leu	Asp	Glu	Asp	Gly	Phe	Val	Glu	Ala	Thr	Glu	Gly				

850		855		860
Leu Gly Asp Asp Ala Leu Gly Lys Gly Gln Glu Gly Gly Gly Trp				
865		870		875
Asp Val Glu Glu Asp Leu Glu Leu Pro Pro Glu Leu Asp Ile Ser Pro				
		885		890
Gly Ala Ala Gly Gly Ala Glu Asp Gly Phe Phe Val Pro Pro Thr Lys				
		900		905
Gly Thr Ser Pro Thr Gln Ile Trp Cys Asn Asn Ser Gln Leu Pro Val				
		915		920
Asp His Ile Leu Ala Gly Ser Phe Glu Thr Ala Met Arg Leu Leu His				
		930		935
Asp Gln Val Gly Val Ile Gln Phe Gly Pro Tyr Lys Gln Leu Phe Leu				
		945		950
Gln Thr Tyr Ala Arg Gly Arg Thr Thr Tyr Gln Ala Leu Pro Cys Leu				
		965		970
Pro Ser Met Tyr Gly Tyr Pro Asn Arg Asn Trp Lys Asp Ala Gly Leu				
		980		985
Lys Asn Gly Val Pro Ala Val Gly Leu Lys Leu Asn Asp Leu Ile Gln				
		995		1000
Arg Leu Gln Leu Cys Tyr Gln Leu Thr Thr Val Gly Lys Phe Glu Glu				
		1010		1015
Ala Val Glu Lys Phe Arg Ser Ile Leu Leu Ser Val Pro Leu Leu Val				
		1025		1030
Val Asp Asn Lys Gln Glu Ile Ala Glu Ala Gln Gln Leu Ile Thr Ile				
		1045		1050
Cys Arg Glu Tyr Ile Val Gly Leu Ser Val Glu Thr Glu Arg Lys Lys				
		1060		1065
Leu Pro Lys Glu Thr Leu Glu Gln Lys Arg Ile Cys Glu Met Ala				
		1075		1080
Ala Tyr Phe Thr His Ser Asn Leu Gln Pro Val His Met Ile Leu Val				
		1090		1095
Leu Arg Thr Ala Leu Asn Leu Phe Phe Lys Leu Lys Asn Phe Lys Thr				
		1105		1110
Ala Ala Thr Phe Ala Arg Arg Leu Leu Glu Leu Gly Pro Lys Pro Glu				
		1125		1130
Val Ala Gln Gln Thr Arg Lys Ile Leu Ser Ala Cys Glu Lys Asn Pro				
		1140		1145
Thr Asp Ala Tyr Gln Leu Asn Tyr Asp Met His Asn Pro Phe Asp Ile				
		1155		1160
Cys Ala Ala Ser Tyr Arg Pro Ile Tyr Arg Gly Lys Pro Val Glu Lys				
		1170		1175
Cys Pro Leu Ser Gly Ala Cys Tyr Ser Pro Glu Phe Lys Gly Gln Ile				
		1185		1190
Cys Arg Val Thr Thr Val Thr Glu Ile Gly Lys Asp Val Ile Gly Leu				
		1205		1210
Arg Ile Ser Pro Leu Gln Phe Arg				
		1220		

<210> 43

<211> 266

<212> DNA

<213> Homo sapiens

<400> 43

```

atgcccaagt gtcccaagtg caacaaggag gtgtacttcg ccgagagggt gacctctctg 60
ggcaaggact ggcacgagcc ctgcctgaag tgcgagaaat gtgggaagac gctgacctct 120
gggggccacg ctgagcacga aggcaaacc tactgcaacc acccctgcta cgcagccatg 180
tttgggccta aaggcttttg gcggggcgga gccgagagcc acactttcaa gtaaaccagg 240

```

tggtggagac ccattccttgg ctgctt

266

<210> 44

<211> 77

<212> PRT

<213> Homo sapiens

<400> 44

Met	Pro	Lys	Cys	Pro	Lys	Cys	Asn	Lys	Glu	Val	Tyr	Phe	Ala	Glu	Arg
1				5					10					15	
Val	Thr	Ser	Leu	Gly	Lys	Asp	Trp	His	Arg	Pro	Cys	Leu	Lys	Cys	Glu
			20					25				30			
Lys	Cys	Gly	Lys	Thr	Leu	Thr	Ser	Gly	Gly	His	Ala	Glu	His	Glu	Gly
		35					40				45				
Lys	Pro	Tyr	Cys	Asn	His	Pro	Cys	Tyr	Ala	Ala	Met	Phe	Gly	Pro	Lys
	50					55					60				
Gly	Phe	Gly	Arg	Gly	Gly	Ala	Glu	Ser	His	Thr	Phe	Lys			
65					70					75					

<210> 45

<211> 2312

<212> DNA

<213> Homo sapiens

<400> 45

tccagtgaag	gagccgcccc	gccgacagcc	ccgagacgac	agcccggcgc	gtcccgggtcc	60
ccacctccga	ccaccgccag	cgctccaggc	cccgcgctcc	ccgctcgccg	ccaccgcgcc	120
ctccgctccg	cccgagtgcc	caaccatgac	cgccgcagct	atgggccccg	tccgcgtcgc	180
cttcgtggtc	ctcctcgccc	tctgcagccg	gccggccgtc	ggccagaact	gcagcgggcc	240
gtgccgggtgc	ccggacgagc	cgccgcgcgc	ctgcccgccg	ggcgtgagcc	tccgtgctgga	300
cggctgcggc	tgtgtccgcg	tctgcgccc	gcagctgggc	gagctgtgca	ccgagcgcga	360
cccctgcgac	ccgcacaagg	gcctcttctg	tgacttcggc	tccccggcca	accgcaagat	420
cggcgtgtgc	accgccaagg	atggtgctcc	ctgcatcttc	ggtggtagcg	tgtaccgcag	480
cggagagtcc	ttccagagca	gctgcaagta	ccagtgcacg	tgccctggacg	gggcgggtggg	540
ctgcatgccc	ctgtgcagca	tggacgttcg	tctgcccagc	cctgactgcc	ccttcccagag	600
gagggtaag	ctgcccggga	aatgctgcga	ggagtgggtg	tgtgacgagc	ccaaggacca	660
aaccgtgggt	gggcctgccc	tgcgggctta	ccgactggaa	gacacgtttg	gcccagacc	720
aactatgatt	agagccaact	gcctggtcca	gaccacagag	tggagcgcc	gttccaagac	780
ctgtgggatg	ggcatctcca	cccgggttac	caatgacaac	gcctcctgca	ggctagagaa	840
gcagagccgc	ctgtgcatgg	tcaggccttg	cgaagctgac	ctggaagaga	acattaagaa	900
gggcaaaaag	tgcattccgta	ctcccaaaat	ctccaagcct	atcaagtttg	agctttcttg	960
ctgcaccagc	atgaagacat	accgagctaa	attctgtgga	gtatgtaccg	acggccgatg	1020
ctgcaccccc	cacagaacca	ccaccctgcc	ggtggagtcc	aagtgccttg	acggcgaggt	1080
catgaagaag	aacatgatgt	tcattcaagac	ctgtgctctg	cattacaact	gtcccggaga	1140
caatgacatc	tttgaatcgc	tgtactacag	gaagatgtac	ggagacatgg	catgaagcca	1200
gagagtgaag	gacattaaat	cattagactg	gaacttgaac	tgattcacat	ctcatttttc	1260
cgtaaaaatg	atttcagtag	cacaagttat	ttaaatctgt	ttttctaact	gggggaaaag	1320
attcccaccc	aattcaaaac	attgtgccat	gtcaaacaac	tagtctatct	tcccagaca	1380
ctggtttgaa	gaatgttaag	acttgacagt	ggaactacat	tagtacacag	caccagaatg	1440
tatattaagg	tgtggcttta	ggagcagtg	gagggtagca	gcagaaaggt	tagtatcatc	1500
agatagctct	tatacgagta	atatgcctgc	tatttgaagt	gtaattgaga	aggaaaattt	1560
tagcgtgctc	actgacctgc	ctgtagcccc	agtgcagct	aggatgtgca	ttctccagcc	1620
atcaagagac	tgagtcaagt	tgttccttaa	gtcagaacag	cagactcagc	tctgacattc	1680
tgattcgaat	gacactgttc	aggaatcgga	atcctgtcga	ttagactgga	cagcttgtgtg	1740
caagtgaatt	tcctgtaaca	agccagattt	tttaaaattt	atattgtaaa	tattgtgtgt	1800
gtgtgtgtgt	gtgtatatat	atatatatat	gtacagttaa	ctaagttaaa	ttaaagtgtgt	1860
ttgtgccttt	ttattttttgt	ttttaatgct	ttgatatttc	aatgttagcc	tcaattttctg	1920
aacaccatag	gtagaatgta	aagcttgtct	gatcgttcaa	agcatgaaat	ggatacttat	1980

```

atggaaattc tctcagatag aatgacagtc cgtcaaaaaca gattgtttgc aaaggggagg 2040
catcagtgtc cttggcaggc tgattttctag gtaggaaatg tggtagctca cgctcacttt 2100
taatgaacaa atggccttta ttaaaaactg agtgactcta tatagctgat cagttttttc 2160
acctggaagc atttgtttct actttgatat gactgttttt cggacagttt atttgttgag 2220
agtgtgacca aaagttacat gtttgcacct ttctagttga aaataaagta tattttttct 2280
aaaaaaaaa aaaaacgaca gcaacggaat tc 2312

```

<210> 46

<211> 349

<212> PRT

<213> Homo sapiens

<400> 46

```

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
 1          5          10          15
Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
 20          25          30
Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
 35          40          45
Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
 50          55          60
Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
 65          70          75          80
Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85          90          95
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 100         105         110
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115         120         125
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
 130         135         140
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
 145         150         155         160
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
 165         170         175
Pro Ala Leu Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
 180         185         190
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
 195         200         205
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
 210         215         220
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
 225         230         235         240
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
 245         250         255
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
 260         265         270
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
 275         280         285
Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
 290         295         300
Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
 305         310         315         320
Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
 325         330         335
Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340         345

```


<210> 47
 <211> 3025
 <212> DNA
 <213> Homo sapiens

<400> 47

```

gcacgagcag gcagttcaga ttaaagaagc taattgatca agaaatcaag tctcaggagg 60
agaaggagca agaaaaggag aaaaggggtc ccaccctgaa agaggagctg accaagctga 120
agtcttttgc tttgatgggtg gtggatgaac agcaaaggct gacggcacag ctcacccttc 180
aaagacagaa aatccaagag ctgaccacaa atgcaaagga aacacatacc aaactagccc 240
ttgctgaagc cagagttcag gaggaagagc agaaggcaac cagactagag aaggaaactgc 300
aaacgcagac cacaaagttt caccaagacc aagacacaat tatggcgaag ctcaccaatg 360
aggacagtca aaatcgccag cttcaacaaa agctggcagc actcagccgg cagattgatg 420
agttagaaga gacaaacagg tctttacgaa aagcagaaga ggagctgcaa gatataaaag 480
aaaaaatcag taagggagaa tatggaaacg ctggtatcat ggctgaagtg gaagagctca 540
taaaaatgga ggagcagtgc agagatctca ataagaggct tgaaaggagg acgttacaga 600
gtaaagactt taaactagag gttgaaaaac tcagtaaaag aattatggct ctggaaaagt 660
tagaagacgc tttcaacaaa agcaaacaag aatgctactc tctgaaatgc aatttagaaa 720
aagaaaggat gaccacaaag cagttgtctc aagaactgga gagtttaaaa gtaaggatca 780
aagactaga agccattgaa agtcggctag aaaagacaga attcactcta aaagaggatt 840
taactaaact gaaaacatta actgtgatgt ttgtagatga acggaaaaca atgagtgaag 900
aattaaagaa aactgaagat aaattacaag ctgottcttc tcagcttcaa gtggagcaaa 960
ataaagtaac aacagttact gagaagttaa ttgaggaaac taaaagggcg ctcaagttca 1020
aaaccgatgt agaagaaaag atgtacagcg taaccaagga gagagatgat ttaaaaaaca 1080
aattgaaagc ggaagaagag aaaggaaatg atctcctgtc aagagttaat atgttgaaaa 1140
ataggcttca atcattggaa gcaatttgaga aagatttctc aaaaaacaaa ttaaatcaag 1200
actctgggaa atccacaaca gcattacacc aagaaaacaa taagattaag gagctctctc 1260
aagaagtgga aagactgaaa ctgaagctaa aggacatgaa agccattgag gatgacctca 1320
tgaaaacaga agatgaatat gagactctag aacgaaggta tgctaatagaa cgagacaaag 1380
ctcaattttt atctaaagag ctagaacatg ttaaaatgga acttgctaag tacaagttag 1440
cagaaaagac agagaccagc catgaacaat ggcttttcaa aaggcttcaa gaagaagaag 1500
ctaagtcagg gcacctctca agagaagtgg atgcattaaa agagaaaatt catgaataca 1560
tggaactga agacctataa tgtcacctcc agggagatca ctcagtctgc aaaaaaaaaa 1620
taaatcaaca agaaaacagg aacagagatt taggaagaga gattgaaaac ctcactaagg 1680
agttagagag gtaccggcat ttcagtaaga gcctcaggcc tagtctcaat ggaagaagaa 1740
tttccgatcc tcaagtattt tctaaagaag ttcagacaga agcagtagac aatgaaccac 1800
ctgattacaa gagctcatt cctctggaac gtgcagtcac caatggtcag ttatatgag 1860
agagtggaaa tcaagacgag gaccctaatt atgagggatc tgtgctgtcc ttcaaagtga 1920
gccagtctac tccatgtcct gttaacagaa agctatggat tccctggatg aaatccaagg 1980
agggccatct tcagaatgga aaaatgcaaa ctaaacccaa tgccaacttt gtgcaacctg 2040
gagatctagt cctaagccac acacctgggc agccacttca tataaagggtt actccagacc 2100
atgtacaaaa cacagccact cttgaaatca caagtccaac cacagagagt cctcactctt 2160
acacgagtac tgcaagtata ccgaactgtg gcacgocaaa gcaaaggata accatcctcc 2220
aaaacgcctc cataacacca gtaaagtcca aaacctctac cgaagacctc atgaatttag 2280
aacaaggcat gtccccaatt accatggcaa cctttgccag agcacagacc ccagagtctt 2340
gtggttctct aactccagaa aggacaatgt cctattcag gttttggctg tgactggttc 2400
agctagctct cctgagcagg gacgtccccc agaaccaaca gaaatcagtg ccaagcatgc 2460
gatattcaga gtctccccag accggcagtc atcatggcag tttcagcgtt caaacagcaa 2520
tagctcaagt gtgataacta ctgaggataa taaaatccac attcacttag gaagtcctta 2580
catgcaagct gtagccagcc cttcagcacc actgcaggat aaccgaactc aaggcttaat 2640
taacggggca ctaaacaaaa caaccaataa agtcaccagc agtattacta tcacaccaac 2700
agccacacct cttcctcgac aatcacaaat tacagtaagt aatatatata actgaccacg 2760
ctcacccctc tccagtcctat actgatattt ttgcaaggaa ctcaatcctt ttttaatcat 2820
ccctccatat cccccaagac tgactgaact ogtacttttg gaaggtttgt gcatgaacta 2880
tacaagagta tctgaaacta actgttgctt gcatgtcat atcgagtgtg cacttactgt 2940
atatcttttc atttacatac ttgtatggaa aatatttagt ctgcacttgt ataaatacat 3000
ctttatgtat ttgaaaaaaa aaaaaa

```

<210> 48

<211> 752
 <212> PRT
 <213> Homo sapiens

<400> 48

Met	Val	Val	Asp	Glu	Gln	Gln	Arg	Leu	Thr	Ala	Gln	Leu	Thr	Leu	Gln
1				5					10					15	
Arg	Gln	Lys	Ile	Gln	Glu	Leu	Thr	Thr	Asn	Ala	Lys	Glu	Thr	His	Thr
			20					25					30		
Lys	Leu	Ala	Leu	Ala	Glu	Ala	Arg	Val	Gln	Glu	Glu	Glu	Gln	Lys	Ala
		35					40					45			
Thr	Arg	Leu	Glu	Lys	Glu	Leu	Gln	Thr	Gln	Thr	Thr	Lys	Phe	His	Gln
	50					55					60				
Asp	Gln	Asp	Thr	Ile	Met	Ala	Lys	Leu	Thr	Asn	Glu	Asp	Ser	Gln	Asn
65					70					75				80	
Arg	Gln	Leu	Gln	Gln	Lys	Leu	Ala	Ala	Leu	Ser	Arg	Gln	Ile	Asp	Glu
				85				90						95	
Leu	Glu	Glu	Thr	Asn	Arg	Ser	Leu	Arg	Lys	Ala	Glu	Glu	Glu	Leu	Gln
			100					105						110	
Asp	Ile	Lys	Glu	Lys	Ile	Ser	Lys	Gly	Glu	Tyr	Gly	Asn	Ala	Gly	Ile
		115					120						125		
Met	Ala	Glu	Val	Glu	Glu	Leu	Ile	Lys	Met	Glu	Glu	Gln	Cys	Arg	Asp
	130					135						140			
Leu	Asn	Lys	Arg	Leu	Glu	Arg	Glu	Thr	Leu	Gln	Ser	Lys	Asp	Phe	Lys
145					150					155					160
Leu	Glu	Val	Glu	Lys	Leu	Ser	Lys	Arg	Ile	Met	Ala	Leu	Glu	Lys	Leu
				165				170						175	
Glu	Asp	Ala	Phe	Asn	Lys	Ser	Lys	Gln	Glu	Cys	Tyr	Ser	Leu	Lys	Cys
			180					185					190		
Asn	Leu	Glu	Lys	Glu	Arg	Met	Thr	Thr	Lys	Gln	Leu	Ser	Gln	Glu	Leu
	195					200						205			
Glu	Ser	Leu	Lys	Val	Arg	Ile	Lys	Glu	Leu	Glu	Ala	Ile	Glu	Ser	Arg
	210					215					220				
Leu	Glu	Lys	Thr	Glu	Phe	Thr	Leu	Lys	Glu	Asp	Leu	Thr	Lys	Leu	Lys
225					230					235					240
Thr	Leu	Thr	Val	Met	Phe	Val	Asp	Glu	Arg	Lys	Thr	Met	Ser	Glu	Lys
				245				250						255	
Leu	Lys	Lys	Thr	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Leu	Gln
			260					265						270	
Val	Glu	Gln	Asn	Lys	Val	Thr	Thr	Val	Thr	Glu	Lys	Leu	Ile	Glu	Glu
			275				280						285		
Thr	Lys	Arg	Ala	Leu	Lys	Ser	Lys	Thr	Asp	Val	Glu	Glu	Lys	Met	Tyr
	290					295					300				
Ser	Val	Thr	Lys	Glu	Arg	Asp	Asp	Leu	Lys	Asn	Lys	Leu	Lys	Ala	Glu
305					310					315					320
Glu	Glu	Lys	Gly	Asn	Asp	Leu	Leu	Ser	Arg	Val	Asn	Met	Leu	Lys	Asn
				325				330						335	
Arg	Leu	Gln	Ser	Leu	Glu	Ala	Ile	Glu	Lys	Asp	Phe	Leu	Lys	Asn	Lys
			340					345						350	
Leu	Asn	Gln	Asp	Ser	Gly	Lys	Ser	Thr	Thr	Ala	Leu	His	Gln	Glu	Asn
		355					360						365		
Asn	Lys	Ile	Lys	Glu	Leu	Ser	Gln	Glu	Val	Glu	Arg	Leu	Lys	Leu	Lys
	370					375					380				
Leu	Lys	Asp	Met	Lys	Ala	Ile	Glu	Asp	Asp	Leu	Met	Lys	Thr	Glu	Asp
385					390					395					400
Glu	Tyr	Glu	Thr	Leu	Glu	Arg	Arg	Tyr	Ala	Asn	Glu	Arg	Asp	Lys	Ala
				405				410						415	
Gln	Phe	Leu	Ser	Lys	Glu	Leu	Glu	His	Val	Lys	Met	Glu	Leu	Ala	Lys
			420					425						430	

Tyr	Lys	Leu	Ala	Glu	Lys	Thr	Glu	Thr	Ser	His	Glu	Gln	Trp	Leu	Phe
		435					440					445			
Lys	Arg	Leu	Gln	Glu	Glu	Glu	Ala	Lys	Ser	Gly	His	Leu	Ser	Arg	Glu
	450					455					460				
Val	Asp	Ala	Leu	Lys	Glu	Lys	Ile	His	Glu	Tyr	Met	Ala	Thr	Glu	Asp
465					470					475				480	
Leu	Ile	Cys	His	Leu	Gln	Gly	Asp	His	Ser	Val	Cys	Lys	Lys	Lys	Leu
			485						490					495	
Asn	Gln	Gln	Glu	Asn	Arg	Asn	Arg	Asp	Leu	Gly	Arg	Glu	Ile	Glu	Asn
			500					505					510		
Leu	Thr	Lys	Glu	Leu	Glu	Arg	Tyr	Arg	His	Phe	Ser	Lys	Ser	Leu	Arg
	515						520					525			
Pro	Ser	Leu	Asn	Gly	Arg	Arg	Ile	Ser	Asp	Pro	Gln	Val	Phe	Ser	Lys
	530					535					540				
Glu	Val	Gln	Thr	Glu	Ala	Val	Asp	Asn	Glu	Pro	Pro	Asp	Tyr	Lys	Ser
545					550					555					560
Leu	Ile	Pro	Leu	Glu	Arg	Ala	Val	Ile	Asn	Gly	Gln	Leu	Tyr	Glu	Glu
				565					570					575	
Ser	Glu	Asn	Gln	Asp	Glu	Asp	Pro	Asn	Asp	Glu	Gly	Ser	Val	Leu	Ser
			580					585					590		
Phe	Lys	Cys	Ser	Gln	Ser	Thr	Pro	Cys	Pro	Val	Asn	Arg	Lys	Leu	Trp
		595					600					605			
Ile	Pro	Trp	Met	Lys	Ser	Lys	Glu	Gly	His	Leu	Gln	Asn	Gly	Lys	Met
	610					615					620				
Gln	Thr	Lys	Pro	Asn	Ala	Asn	Phe	Val	Gln	Pro	Gly	Asp	Leu	Val	Leu
625					630					635					640
Ser	His	Thr	Pro	Gly	Gln	Pro	Leu	His	Ile	Lys	Val	Thr	Pro	Asp	His
				645					650					655	
Val	Gln	Asn	Thr	Ala	Thr	Leu	Glu	Ile	Thr	Ser	Pro	Thr	Thr	Glu	Ser
			660					665					670		
Pro	His	Ser	Tyr	Thr	Ser	Thr	Ala	Val	Ile	Pro	Asn	Cys	Gly	Thr	Pro
	675						680					685			
Lys	Gln	Arg	Ile	Thr	Ile	Leu	Gln	Asn	Ala	Ser	Ile	Thr	Pro	Val	Lys
	690					695					700				
Ser	Lys	Thr	Ser	Thr	Glu	Asp	Leu	Met	Asn	Leu	Glu	Gln	Gly	Met	Ser
705					710					715					720
Pro	Ile	Thr	Met	Ala	Thr	Phe	Ala	Arg	Ala	Gln	Thr	Pro	Glu	Ser	Cys
			725						730					735	
Gly	Ser	Leu	Thr	Pro	Glu	Arg	Thr	Met	Ser	Leu	Phe	Arg	Phe	Trp	Leu
			740					745					750		

<210> 49

<211> 1480

<212> DNA

<213> Homo sapiens

<400> 49

```

gcggagaaag ccagtgggaa cccagaccca taggagaccc gcgtccccgc tcggcctggc 60
caggccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120
cgctgctgat cgccacaccg tcttctggaa cagttcaaat cccaagttcc ggaatgagga 180
ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
tcaactctgtg gcagacgctg ccatggagca gtacatactg tacctgggtg agcatgagga 300
gtaccagctg tgccagcccc agtccaagga ccaagtccgc tggcagtgca accggcccag 360
tgccaagcat ggcccggaga agctgtctga gaagttccag cgcttcacac ctttcaccct 420
gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
tgaagaccgc tgcttgaggt tgaaggtgac tgtcagtggc aaaatcactc acagtcctca 540
ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgccgggttct 600
acatagcatc ggtcacagtg ctgccccacg cctcttccca cttgcctgga ctgtgctgct 660

```

```

ccttcacttt ctgctgctgc aaaccccggt aaggtgtatg ccacacctgg ccttaaagag 720
ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttcagagccc 780
ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaaacgg 840
gtcagtatta aggtttttcaa ccggaaggag gccaaaccagc ccgacagtgc catccccacc 900
ttcacctcgg agggacggag aaagaagtgg agacagtcct ttcccaccat tcctgccttt 960
aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020
aagggggcac gtggatgggc aaagcttgct aaagatgcc cctccaggag agagccagga 1080
tgcccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140
caggagaggc agcatgcttg ggctgaccca gcattctcca gcaagacctc atctgtggag 1200
ctgccacaga gaagtttgta gccaggctact gcattctctc ccattcctggg gcagcactcc 1260
ccagagctgt gccagcaggg gggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgcccatg tgtacattct gcctagagt tagcctaaag ggcaggggcc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaaat aaagcaatgt gttttttcgg 1480

```

<210> 50

<211> 205

<212> PRT

<213> Homo sapiens

<400> 50

```

Met Glu Phe Leu Trp Ala Pro Leu Leu Gly Leu Cys Cys Ser Leu Ala
 1           5           10          15
Ala Ala Asp Arg His Thr Val Phe Trp Asn Ser Ser Asn Pro Lys Phe
 20          25          30
Arg Asn Glu Asp Tyr Thr Ile His Val Gln Leu Asn Asp Tyr Val Asp
 35          40          45
Ile Ile Cys Pro His Tyr Glu Asp His Ser Val Ala Asp Ala Ala Met
 50          55          60
Glu Gln Tyr Ile Leu Tyr Leu Val Glu His Glu Glu Tyr Gln Leu Cys
 65          70          75          80
Gln Pro Gln Ser Lys Asp Gln Val Arg Trp Gln Cys Asn Arg Pro Ser
 85          90          95
Ala Lys His Gly Pro Glu Lys Leu Ser Glu Lys Phe Gln Arg Phe Thr
100          105          110
Pro Phe Thr Leu Gly Lys Glu Phe Lys Glu Gly His Ser Tyr Tyr Tyr
115          120          125
Ile Ser Lys Pro Ile His Gln His Glu Asp Arg Cys Leu Arg Leu Lys
130          135          140
Val Thr Val Ser Gly Lys Ile Thr His Ser Pro Gln Ala His Val Asn
145          150          155          160
Pro Gln Glu Lys Arg Leu Ala Ala Asp Asp Pro Glu Val Arg Val Leu
165          170          175
His Ser Ile Gly His Ser Ala Ala Pro Arg Leu Phe Pro Leu Ala Trp
180          185          190
Thr Val Leu Leu Leu Pro Leu Leu Leu Gln Thr Pro
195          200          205

```

<210> 51

<211> 15952

<212> DNA

<213> Homo sapiens

<400> 51

```

ccagccgtgt gtgatgagtg gccacacctt gcctcctctt cccgtcccag gcaccaacag 60
cacagagcag gccagtgtac ccagagccat ggcagccacg ctgggagccg gcacgcccc 120
caggccccag gccaggagca tagctggggt gtatgtggag gcctcgggcc aggcccagag 180
tgtctacgcc gccatggagc agggcctcct gcctgctggg ctcgggcagg ctctgctaga 240

```

ggccagagca	gccactgggg	gcctggtgga	cctcgcccg	ggccagctgc	tcctgtgtc	300
caagccctg	cagcagggtc	tggtggggct	ggagctgaag	gagaagctgc	tggccgctga	360
gcgtgccact	acgggctatc	ctgaccccta	cggcggtgag	aagctggccc	tctttcaggc	420
catcggaag	gaggttgtgg	acagggccct	ggggcagagc	tggctggagg	tccaactggc	480
cactgggggc	ctgggtggacc	ccgcccaggg	agtgtctgtg	gcccctgagc	cagcctgcca	540
ccagggcctc	ctggaccggg	agacatggca	caagctgtca	gagcttgagc	ctggcacagg	600
tgacctgcgc	ttcctcaacc	ccaacacgct	ggagcggctg	acataccacc	agctgctgga	660
aaggtgtgtg	cgtgcccccg	ggtcggggct	agccttgctg	ccctcaaga	tcaccttccg	720
ctccatgggc	ggggcggtga	gtgcagctga	gctgctggag	gtgggcatcc	tggacgagca	780
ggctgtgcag	ggtctgcggg	agggcaggct	ggccgcagtg	gacgtgagtg	cacgtgccga	840
ggcgcggcgc	tacctggagg	gtaccggcac	cgtggccggg	gttgtcctgc	tggccgaagg	900
ccacaagaag	agctttttcc	aggetgccac	cgagcacctg	ctcccaatgg	gcaccgcgct	960
gccactccta	gaggcccagg	ctgccaccca	caccctggtg	gaccccatca	caggccagcg	1020
gctgtgggta	gacgaggcag	tcagggcggg	cctggtcagc	ccagagctcc	atgagcagct	1080
cctggtggct	gagcaggccg	tgacagggca	ccacgacccc	ttcagtggct	cccaaattcc	1140
ccttttccag	gccatgaaga	aggggctagt	ggacaggcca	ctagcactgc	ggctcttgga	1200
tggccagctg	gccacaggcg	ggctgggtctg	tccagcacgc	aggctccggc	tggccctgga	1260
ggccgccttg	cgtgcggct	gcctggatga	agacactcag	cggcagctct	cgcaggctgg	1320
cagcttctca	gacggcacgc	acggcgccct	gcgctatgaa	cagctgctgg	ccctctgtgt	1380
caccgaccca	gagaccgggc	ttgccttctc	gccactctca	gggggacccc	ggggagggga	1440
gccccaggga	cccccatcca	tcaagtacag	cactcggcag	gccctgagca	cggccacagc	1500
caccgtctct	gtggggaagt	tccggggccg	gcccgtgtcc	ctctgggagc	tgctcttctc	1560
tgaggccatc	tcctcagagc	agagggcgat	gctggcccag	cagtaccagg	aagggaacct	1620
ctccgtggag	aagctggccg	ctgagctgag	cgccaccctt	gagcaggctg	cagccactgc	1680
cagggtcacc	tttcttgggc	tgagggacac	cgtgacacca	ggagagctgc	tgaaagccga	1740
gatcatcgac	caggacctgt	acgagcgggt	ggagcatgga	caggccacag	ccaaggatgt	1800
gggcagcctg	gcctcggcgc	agaggtacct	gcagggtacg	ggctgcattg	ctggcctgct	1860
gctccttggc	tcccaggaac	gcctgagcat	ctatgaggcc	cgatgcaagg	ggctcctccg	1920
gcccggcact	gcctcatcc	ttctggaggc	acaagctgcc	acaggcttca	tcctgacccc	1980
aaaagcaaac	aaggggcact	ccgttgagga	ggcactgagg	gctgctgtca	ttgggocctg	2040
tgtgttcgcg	aagctgctgt	cggtgagcgc	cgctgtcact	ggctacactg	acccctacac	2100
cgggcagcag	atctccctct	tccaggccat	gcagaagggc	ctcatcgtcc	gggagcacgg	2160
catccgcctg	ctggaggccc	agatcgccac	gggcggcgtc	atcgaccccg	tgacacagca	2220
ccgcgtgccc	gtggacgtgg	cctaccggcg	cggctacttc	gatcagatgc	tgaacttgat	2280
cctgttgga	ccttctgacg	acaccaaggg	cttcttcgac	cccaacacgc	acgagaacct	2340
cacgtacctg	cagcttctgg	agcgtgtgt	gcgtgacccc	gagacgggcc	tgtacctcct	2400
gccactcagc	agcacgcagt	ccccgctggt	ggacatggcc	accagcagg	ccttccagaa	2460
cctgctgctc	tccgtgaagt	atggacgggt	tcaggggcag	agggctctccg	cgtgggagct	2520
gatcaactct	gagtacttca	gcgaggggcg	caggaggcag	ctgctgcgtc	gctaccggca	2580
gcgcgaggtc	acgctggggc	aggtggcaaa	gctgctggag	gcggagacgc	agagacaggc	2640
ggacatcatg	ctgcccgcac	tgccggagccg	ggtcaccgtc	caccagctcc	tggaggcccg	2700
tatcattgac	cagcagctgt	tggaccaagt	gctggccggg	acaatcagcc	cggaggccct	2760
cctactcatg	gacggcgctc	gcaggtaoct	gtcggccctg	ggagctgtgg	gcggtgtgcg	2820
gctgctgccc	tctggccagc	ggctcagcct	ctaccaggcc	atgaggcaga	agctgctggg	2880
gcccagggtg	gccttgcccc	tgctggaggc	ccaggcgccc	accggaacca	tcattggacct	2940
tcacagccca	gagagcctct	cgggtgatga	ggccgtgcgc	aggggtgtgg	tggggccgga	3000
gctgtatggc	aggctgaagc	gggtgaggg	tgccattgct	ggcttcagag	accccttctc	3060
tgggaagcag	gtgtctgtgt	tccaggccat	gaagaaaggt	ctcatccctt	gggagcaagc	3120
tggccgcctc	ctggaggctc	aagtggccac	aggagggatc	attgacccca	ccagccacca	3180
ccacctcccc	atgccagtgg	ccattcagcg	tggctatgtt	gaccaggaga	tggagacagc	3240
cttgtccagc	tcctccgaga	ccttccccac	accggacggc	caggggcgca	cgagctatgc	3300
ccagctcctg	gaggagtgcc	ccagggatga	gacttctggc	cttcacctcc	tggccctgcc	3360
agaaagtgtc	cctgcccctc	ccaccgagga	gcaggctccag	aggagcctgc	aggccgtgcc	3420
gggggccaag	gatggcacat	ccctctggga	cctgctcagc	tcctgccact	tcaccgagga	3480
gcaacggagg	ggcctgtctg	aggacgtgac	ggaggggagg	accactgtgc	cacagctgct	3540
agcctctgtg	cagctgtggg	tacaggagac	caagcttctg	gcccaggccc	gcgtcatggt	3600
gcccggccca	cggggtgagg	tacccgctgt	ctggctgctg	gatgctggca	tcatacccca	3660
ggagaccctt	gaggccctgg	ctcagggcac	gcagtgcgcc	gcccaggctc	ccgagcagcc	3720
ggcgggtgaag	gcctgcctgt	ggggcacagg	ctgcgtggcc	ggtgtgctgc	tacagccctc	3780

tggggccaag	gccagcatcg	cccaggccgt	gagggatggc	ctcctgcccc	caggcctggg	3840
ccagaggctg	ctggaagccc	aggtggcatc	tggcttcctt	gttgaccccc	tgaacaacca	3900
gagactgtca	gtggaggacg	cggtaaggt	cggcctggtg	ggcagggagc	tgagttagca	3960
gctcgggcag	gccgagagg	cggcggccgg	gtaccagat	ccctactcta	gggcctccct	4020
ctctctgtgg	caggccatgg	agaaggggt	cgtgccacag	aacgaggggt	tgccccctct	4080
gcaggtgcag	ctggccacag	gggggtgtgt	ggaccctgtc	cacgggggtg	acctgcccc	4140
ggcggcagcc	tgcagactcg	gccttctgga	cacacagacg	agccaggtgc	tgactgcagt	4200
tgacaaggac	aacaagttct	tctttgaccc	cagtgcgcgg	gaccaggtga	cctaccagca	4260
gctcagggag	cgctgcgtgt	gcgactccga	gaccggattg	ttgctgttgc	cactgccttc	4320
agacacagtg	cttgaggttg	acgaccacac	cgcgggtggc	ctgagggcca	tgaaggtgcc	4380
cgtcagcaca	gggaggttta	aggggtgtag	cgtgtcactc	tgggacctgc	tgctctccga	4440
atacgttggc	gctgacaagc	ggcgggagct	ggtggcactc	tgtcgggtctg	ggagggtctg	4500
ggccctgcgg	caggtggtca	gcgcagtcac	cgccctggtc	gaggctgcag	agaggcagcc	4560
cctgcaggcc	accttcagag	ggctccggaa	gcaggtgtca	gccagggacc	tgttcagggc	4620
gcagctgata	agcaggaaga	cgctggacga	gctgagccag	gggacaacga	ctgtgaagga	4680
ggtggcggag	atggacagcg	tgaagcggtc	cctggaggga	ggcaacttca	ttgccgggggt	4740
ccttatccag	ggcaccacag	agaggatgag	catcccagag	gccctgagga	ggcacatcct	4800
gcggcctggc	acagccctgg	tgctgctgga	ggcacaggca	gctaccggct	tcatacatcga	4860
ccccgcggag	aaccggaagc	tgaccgtgga	ggaggcgttc	aaagcaggaa	tgttcgggaa	4920
agaaacctac	gtgaagctgc	tgctggccga	gcgcgcgctc	accggctaca	ccgaccctta	4980
taccgggcag	cagatctccc	tcttcaggc	catgcagaag	gacctcatcg	tccgggagca	5040
cggcatccgc	ctgctggagg	cccagatcgc	cacgggcggc	atcatcgacc	ccgtgcacag	5100
ccaccgcgtg	cccgctggacg	tggcctaccg	ctgcggctac	ttcgacgagg	agatgaaccg	5160
catcctggcg	gacccacagc	acgacaccaa	gggcttcttc	gacccaaca	cgcacgagaa	5220
cctcacgtac	ctgcagcttc	tggagcgcgt	tgtggaggac	cccagagcgg	gcctgtacct	5280
gctacaaatc	ataaagaaaag	gagaaaacta	cgtgtacatc	aatgaggcca	cgagacacgt	5340
gttgcaatcc	agaactgcga	aaatgcgcgt	ggggaggttt	gctgaccagg	tggtctcttt	5400
ctgggacctg	ctgtcctctc	catacttcac	agaggacagg	aagcgggagc	tcataccagga	5460
gtatggagcc	cagagtgggg	gcctggagaa	attgctggaa	atcatcacca	cgacaattga	5520
agaaacagag	acgcaaaacc	aaggcatcaa	agtggcggcc	atcagagggg	aggtgacagc	5580
tgcagacctg	ttcaactcca	gggtcatcga	tcagaagacc	ctgcacacac	ttcgtgtggg	5640
gaggactggg	ggacaggcac	tcagcacgct	ggagtgtgtg	aagccctatc	tggaaaggcag	5700
cgactgcatt	gcgggggtca	cgggtgccctc	caccagggag	gtcatgagcc	tccatgaggc	5760
cagcaggaag	gagctcatcc	ctgcagcatt	tgcgacttgg	ctgctggagg	cgcaggccgc	5820
caccgggttc	ctcctggacc	cctgcacccg	ccagaagctc	tctgtggatg	aggctgtgga	5880
tgtgggcctg	gtgaacgagg	agctgcggga	gaggtcctg	aaggctgaaa	gagctgccac	5940
gggctacagg	gatccggcca	caggagacac	gatcccgctg	ttccaggcca	tgcagaagca	6000
gctcatcgag	aaggcggagg	cactgaggct	gctggagggtg	caggtggcca	cgggggggtgt	6060
catcgacca	cagcaccacc	accggctccc	actggaaaca	gcctacagac	ggggctgtct	6120
gcacaaggac	atctatgcgc	tcatttccga	ccagaagcac	atgaggaaac	ggtttgtgga	6180
cccgaacacg	caagagaagg	tctcgtaccg	agagctgcag	gagaggtgcc	gcccacaaga	6240
ggacacgggc	tgggtgctgt	tcccagtgaa	caaggctgca	cgggactccg	agcacatcga	6300
tgacgagacg	agaagggcc	tggaggcaga	gcaagtggaa	atcacagtgg	gaaggttcag	6360
aggccagaaa	ccaacactgt	gggcactact	gaattccgaa	tacgtgacag	aggagaagaa	6420
gctccagctg	gtgaggatgt	atagaacaca	caccagacgg	gcactgcaga	cggtagcgca	6480
gctcatctta	gagttgatcg	agaagcagga	aaccagcaac	aaacacctgt	ggttccaagg	6540
aattagacga	cagatcacag	cttctgaact	cctcagctca	gccataatca	cggaggaaat	6600
gctccaggac	ctggaaaacg	gacggagcac	gacgcaagag	ctcatggagg	acgaccgcgt	6660
caagcgctac	ctggagggca	ccagctgcat	cgcgggcgtc	ctgggtgccg	ccaaggacca	6720
gcccggccgc	caggagaaga	tgagcatcta	ccaggccatg	tggaaaggcg	tgctgcggcc	6780
cggcacggcc	ctgggtgctgc	tggaggcgca	ggcggccacc	ggcttcgtca	tgcaccccg	6840
gcgcaacctg	aggtgtgcgg	tggaggagcc	cgtgcccgcg	ggcgtggtgg	gcagcgagat	6900
ccaggagaag	ctgctgtcgg	ccgagcgcg	cgtcaccggc	tacaccgacc	cctacaccgg	6960
cgacgagatc	tccctcttcc	aggccatgca	gaaggacctc	atcgtccggg	agcacggcat	7020
ccgcctgctg	gaggcccaga	tcgccacggg	cgcgctatc	gaccccgctg	acagccacgg	7080
cgtgcccgtg	gacgtggcct	accggcgcg	ctacttcgac	gaggagatga	accgtgtcct	7140
ggccgacccc	agcgacgaca	ccaagggttt	cttcgacccc	aacacgcacg	agaacctcac	7200
gtacgtgcag	ctgctgcgcc	gctgcgtgcc	cgacccggac	accgggctct	acatgctgca	7260
gctggcaggc	cggggctccg	ccgtgcacca	gctgagcgag	gagctgcgct	gtgccctgcg	7320

cgacgccccg	gtgacgccag	gctcggggcg	cctccagggc	cagagcgtct	ccgtctggga	7380
gctcctcttc	taccgcgagg	tgtccgagga	ccggcgccag	gacctgctga	gcagataaccg	7440
ggcgggcaacg	ctgaccgtgg	aggagctgga	cgccaccctc	acctcgctgc	tggcccaggc	7500
ccaggccccag	gcccggggccg	aggccgaggc	cgggagcccg	cgcccagacc	cccgggaggc	7560
cctgcgtgcg	gccaccatgg	aggtcaaggt	gggcgcctc	cgggggcgcg	cggtgcccgt	7620
gtgggaactg	ctggcgctccg	gctacgtgag	cagggcccgcc	cgggaggagc	tgctggccga	7680
gttttgctcg	gggaccctgg	acttgcccgc	gctgaccgcg	cggtgaccgc	ccatcatcga	7740
ggaggccgag	gaagcccccg	gggcccggcc	gcagctccag	gacgccaggc	gcggcccgcg	7800
ggagccaggg	ccagccgggc	gaggggacgg	cgactcgggg	cgctcccagc	gagagggccca	7860
gggggagggc	gagaccaggg	aggccgcgcg	cgccgcgcgc	gcccgcgcgc	gccaggagca	7920
gacctgcgt	gatgccacca	tggaggtgca	gcgcgggcag	ttccaggggc	ggccggtctc	7980
cgtgtgggac	gtcctcttct	cctcgtacct	gagcgaggcc	cgccagagacg	agctcctggc	8040
ccagcacgcg	gcccggcgccc	tgggcctgcc	cgacctcgtc	gcgctcctca	cccgggtcat	8100
cgaggagacg	gaggagcggc	tcagcaaggt	gtccttcgcg	ggcctgaggc	gccagggtgtc	8160
cgcctccgag	ctgcacacgt	ccgggatcct	gggccccgag	acctgcggg	acctggccca	8220
gggcactaag	acgctgcagg	aggtgacgga	gatggactcg	gtcaagcgct	acctggaggg	8280
caccagctgc	atcgcgggcg	tcctggtgcc	cgccaaggac	cagcccggcc	gccaggagaa	8340
gatgagcatc	taccaggcca	tgtggaaggg	cgtgctgcgg	cccggcacgg	ccctggtgct	8400
gctggaggcg	caggcgggcca	ccggtctcgt	catcgacccc	gtgcgcaacc	tgaggctgtc	8460
ggtggaggag	gcccgtggcg	cgggcggtgt	gggcggcgag	atccaggaga	agctgctgtc	8520
ggcggagcgc	gcccgtcacccg	gctacaccga	cccctacacc	gggcagcaga	tctcctctct	8580
ccaggccatg	cagaaggacc	tcctcgtccg	ggagcacggc	atccgcctgc	tggaggccca	8640
gatcgccacg	ggcgcggtca	tcgaccccg	gcacagccac	cgcggtgccc	tggacgtggc	8700
ctaccggcgc	ggctacttcg	acgaggagat	gaaccgtgtc	ctggccgacc	ccagcgacga	8760
caccaagggt	ttcttcgacc	ccaacacgca	cgagaacctc	acgtacgtgc	agctgctgcg	8820
ccgctgcgtg	cccgacccgg	acaccgggct	ctacatgctg	cagctggcag	gccggggctc	8880
cgccgtgcac	cagctgagcg	aggagctgcg	ctgtgccctg	cgcgacgccc	gcgtgacgcc	8940
aggctcgggc	gcccctccagg	gccagagcgt	ctccgtctgg	gagctcctct	tctaccgcga	9000
ggtgtccgag	gaccgcgcgc	aggacctgct	gagcagatac	cgggcgggga	cgctgacctg	9060
ggaggagctg	ggcgccaccc	tcacctcgct	gctggcccag	gcccaggccc	aggcccgggc	9120
cgaggccgag	gcccgggagcc	cgcgcccaga	cccccgggag	gcccgtgcgtg	cgccaccat	9180
ggaggtcaag	gtgggcccgc	tcggggggcg	cgcggtgccc	gtgtgggacg	tgctggcgctc	9240
cggctaactg	agcggggccg	cccgggagga	gctgctggcc	gagtttggt	cggggacct	9300
ggacttgccc	gcgctgaccc	gcccgtgac	cgccatcatc	gaggaggccg	aggaggcccc	9360
cggggcccgcg	ccgcagctcc	aggacgctg	gcgcggccc	cgggagccag	ggccagccgg	9420
gcgaggggac	ggcgactcgg	ggcgctccca	gcgagagggc	cagggggagg	gcgagaccga	9480
ggaggccgcg	gcccgcgcgc	ccgcgcgcgc	ccgcaggag	cagacctgc	gtgatgccac	9540
catggagggtg	cagcgcgggc	agttccaggg	gcggccggtc	tcctgtgtgg	acgtcctctt	9600
ctcctcgtac	ctgagcgagg	cccgcgcgga	cgagctcctg	gcccagcacg	cgcccgggcg	9660
cctgggcctg	cccgaacctg	tcgcccgtct	cacccggttc	atcgaggaga	cgaggagcg	9720
gctcagcaag	gtgtccttcc	gcggcctgag	gcgcagggtg	tcgcctccg	agctgcacac	9780
gtccgggatac	ctgggcccgc	agacctgcg	ggacctggcc	cagggcacta	agacgctgca	9840
ggaggtgacg	gagatggact	cggtaagcg	ctacctggag	ggcaccagct	gcatacgggg	9900
cgtcctggtg	cccgcgaagg	accagcccgg	ccgccaggag	aagatgagca	tctaccaggc	9960
catgtggaag	ggcgtgctgc	ggcccggcac	ggccctggtg	ctgctggagg	cgcaggcggc	10020
caccggcttc	gtcatcgacc	ccgtgcgcaa	cctgaggctg	tcggtggagg	aggccgtggc	10080
cgcgggcgctg	gtgggcggcg	agatccagga	gaagctgctg	tcggccgagc	gcgccgtcac	10140
cggctacacc	gacccctaca	ccgggcagca	gatctccctc	ttccaggcca	tgcagaagga	10200
cctcatcgte	cgggagcacg	gcataccgct	gctggaggcc	cagatcgcca	cgggcggcgt	10260
catcgacccc	gtgcacagcc	accgcgtgcc	cgtggacgtg	gcctaccggc	gcggctactt	10320
cgacgaggag	atgaacctg	tcctggccga	ccccagcgac	gacaccaagg	gtttcttcga	10380
ccccaacacg	cacgagaacc	tcacgtacgt	gcagctgctg	cgccgctgcg	tgcccgaacc	10440
ggacaccggg	ctctacatgc	tcgagctggc	aggccggggc	tcgcgcgtgc	accagctgag	10500
cgaggagctg	cgctgtgccc	tgcgcgacgc	ccgctgacg	ccaggctcgg	gcgcctcca	10560
gggcccagag	gtctcgtct	gggagctcct	cttctaccgc	gaggtgtccg	aggaccggcg	10620
ccaggacctg	ctgagcagat	accgggcggg	cacgtgacc	gtggaggagc	tgggcggcac	10680
cctcacctcg	ctgctggccc	aggcccaggc	ccaggcccgc	gccgaggccg	aggccgggag	10740
cccgcgccc	gacccccggg	aggccctgcg	tgcgccacc	atggagggtca	agggtggccg	10800
cctccggggg	cgcgcggtgc	ccgtgtggga	cgtgctggcg	tcgggctacg	tgagcggggc	10860

cgcccgagg	gagctgctgg	ccgagtttgg	ctcggggacc	ctggacttgc	ccgcgctgac	10920
ccgcccgtg	accgccatca	tcgaggaggc	cgaggaggcc	cccggggccc	ggccgcagct	10980
ccaggacgcc	tggcgcgggc	cgcgggagcc	agggccagcc	gggcgagggg	acggcgactc	11040
ggggcgctcc	cagcgagagg	gccaggggga	gggcgagacc	caggaggccg	ccgccgccgc	11100
cgccgcgcc	cgccgccagg	agcagaccct	gcgtgatgcc	accatggagg	tgcagcgcg	11160
gcagttccag	gggcggccgg	tctccgtgtg	ggacgtcctc	ttctcctcgt	acctgagcga	11220
ggcccgccga	gacgagctcc	tggcccagca	cgcgcccggc	gcctggggcc	tgcccgacct	11280
cgtcgccgtc	ctcaccgggg	tcacgcagga	gacggaggag	cggtccagca	aggtgtcctt	11340
ccgcgccctg	aggcgccagg	tgtccgcctc	cgagctgcac	acgtccggga	tcctggggccc	11400
cgagaccctg	cgggacctgg	cccagggcac	taagacgctg	caggagggtga	cggagatgga	11460
ctcgggtcaag	gcctacctgg	agggcaccag	ctgcctcgcg	ggcgctcctg	tggccgcaa	11520
ggaccagccc	ggccgcccagg	agaagatgag	catctaccag	gccaatgtga	agggcggtgt	11580
gcggcccggc	acggccctgg	tgtgtgtgga	ggcgaggcg	gccaacgggt	tcgtcatcga	11640
ccccgtgccc	aacctgaggc	tgtcggtgga	ggaggccgtg	ggcgggggcg	tgggtggcg	11700
cgagatccag	gagaagctgc	tgtcgccga	gcgcgccgtc	acgggtaca	ccgaccccta	11760
caccgggcag	cagatctccc	tcttccaggc	catgcagaag	gacctcatcg	tcggggagca	11820
cggcatccgc	ctgctggagg	cccagatcgc	cacgggcggc	gtcatcgacc	ccgtgcacag	11880
ccaccgcgtg	cccggtggacg	tggcctaccg	gcgcggctac	ttcgacgagg	agatgaaccg	11940
tgtcctggcc	gacccagcgc	acgacaccaa	gggttctctc	gaccccaaca	cgcacgagaa	12000
cctcacgtac	tgccagctgc	tgcccgctg	cgcccgccgc	ccggacaccg	ggctctatct	12060
gctgcagctg	gcaggccggg	gtcccgccgt	gcaccagctg	agcgaggagc	tgcgtctgtc	12120
cctgcgcgac	gcccgcgtga	cgccaggctc	ggcgccctc	caggggccaga	gcgtctccgt	12180
ctgggagctc	ctcttctacc	gcgagggtgc	cgaggaccgg	cgccaggacc	tgtgtgagcag	12240
ataccggggc	agcacgctga	ccgtggagga	gctgggcgcc	acctcacct	cgctgctggc	12300
ccaggcccag	gcccaggccc	gggcccaggc	cgaggccggg	agcccgccgc	cagacccccg	12360
ggaggccctg	cgtgcggcca	ccatggagg	caagggtggc	cgccctccggg	ggcgcgcggt	12420
gcccgtgtg	gacgtgctgg	cgtccggcta	cgtgagcagg	gcgcgccggg	aggagctgct	12480
ggccgagttt	ggctcgggga	ccctggactt	gcccgcgtg	acccgcggcg	tgaccgccat	12540
catcgaggag	cccgaggagg	ccccggggc	ccggcccgag	ctccaggagc	cctggcgcg	12600
cccgcgggag	ccagggccag	ccgggcccag	ggacggcgac	tcggggcgct	cccagcgaga	12660
gggcccagg	gagggcgaga	cccaggaggc	cgccgcccgc	accgcgcgcg	cccgccgcca	12720
ggagcagacc	ctgcgtgatg	ccaccatgga	ggtgcagcgc	gggcagttcc	aggggcggcc	12780
ggtctccgtg	tgggacgtcc	tcttctcctc	gtacctgagc	gaggcccgcc	gagacgagct	12840
cctggcccag	cacgcggccg	gcgccctggg	cctgcccgac	ctcgtcgccg	tcctcacccg	12900
ggtcatcgag	gagacggagg	agcggtcag	caagggtgtc	ttccgcggcc	tgaggcgcca	12960
ggtgtccgcc	tcogagctgc	acacgtccgg	gatcctgggc	cccagacccc	tgcgggacct	13020
ggcccagggc	actaagacgc	tgcaggaggt	gacggagatg	gactcgggtc	agcgctacct	13080
ggagggcacc	agctgcacgc	cgggcgctcc	ggtgcccgcc	aaggaccagc	ccggccggcc	13140
ggagaagatg	agcatctacc	aggccatgtg	gaagggcgtg	ctgcggcccg	gcacggccct	13200
ggtgtgtgtg	gaggcgaggg	cgccaccggg	cttcgtcatc	gaccccgctg	gcaacctgag	13260
gctgtcggtg	gaggaggccg	tggccgcggg	cgtgggtggc	ggcgagatcc	aggagaagct	13320
gctgtcgggc	gagcgcgccg	tcaccggcta	caccgacccc	tacaccgggc	agcagatctc	13380
cctcttccag	gccatgcaga	aggacctcat	cgtccgggag	cacggcatcc	gcctgctgga	13440
ggcccagatc	gccacggggc	gcgtcatcga	ccccgtgcac	agccaccggc	tgcctgtgga	13500
cgtggccctac	cggcgcggtc	acttcgacga	ggagatgaac	cgtgtcctgg	ccgaccccag	13560
cgacgacacc	aagggttctc	tcgaccccaa	cacgcacgag	aacctcacgt	acgtgcagct	13620
gctgcgcgcg	tgcgtgcccg	acccggacac	cgggtctctac	atgctgcagc	tggcaggccg	13680
gggctccgcc	gtgcaccagc	tgagcgagga	gctgcgtgtg	gcctgcgcg	acgcccgcgt	13740
gacgccaggc	tcgggcgccc	tcaggggcca	gagcgtctcc	gtctgggagc	tcctcttcta	13800
ccgcgaggtg	tcogaggacc	ggcgccagga	cctgctgagc	agataccggg	cgggcacgct	13860
gaccgtggag	gagctggggc	ccacctcac	ctcgtgctg	gcccaggccc	aggcccaggc	13920
ccgggcccag	gcogaggccg	ggagcccgcg	cccagacccc	cgggaggccc	tgcgtgcggc	13980
caccatggag	gtcaagggtg	gocgcctccg	ggggcgcgcg	gtgcccgtgt	gggacgtgct	14040
ggcgtccggc	tacgtgagcg	gggcccggcg	ggaggagctg	ctggccgagt	ttggctcggg	14100
gacctgggac	ttgcccgcgc	tgacccggcg	gctgaccgcc	atcatcgagg	agggcgagga	14160
ggcccccggg	gcccggccgc	agctccagga	cgccgtggcg	ggcccgcggg	agccaggggc	14220
agccggggcga	ggggacggcg	actcggggcg	ctcccagcga	gaggggccagg	gggaggggcga	14280
gaccaggag	gcccgcggcg	ccgcgcggcg	cgcccgccgc	caggagcaga	ccctgcgtga	14340
tgccaccatg	gaggtgcagc	gcgggcagtt	ccaggggcg	ccggtctccg	tgtgggacgt	14400


```

cctctttctcc togtacctga gcgaggcccc ccgagacgag ctccctggccc agcacgcggc 14460
cgggcgccctg ggccctgcccg acctcgctcgc cgtccctcacc cgggtcatcg aggagacgga 14520
ggagcggtctc agcaaggtgt ccttccgcgg cctgaggcgc caggtgtccg cctccgagct 14580
gcacacgtcc gggatcctgg gccccgagac cctgcgggac ctggcccagg gcactaagac 14640
gctgcaggag gtgacggaga tggactcggg caagcgctac ctggagggca ccagctgcat 14700
cgcgggcgctc ctgggtgcccg ccaaggacca gcccgggcgc caggagaaga tgagcatcta 14760
ccaggccatg tgggaaggcg tgctgcggcc cggcacggcc ctgggtgctgc tggaggcgca 14820
ggcgggccacc ggcttcgtca tcgaccccgt gcgcaacctg aggctgtcgg tggaggaggc 14880
cgtggcccgcg ggcggtggtg gcggcgagat ccaggagaag ctgctgtcgg ccgagcgcg 14940
cgtcaccggc tacaccgacc cctacaccgg gcagcagatc tccctcttcc aggccatgca 15000
gaaggacctc atcgctcggg agcacggcat ccgcctgctg gaggcccaga tcgccacggg 15060
cggcgctcatc gaccccgctg acagccaccg cgtgcccggt gacgtggcct accggcgcg 15120
ctacttcgac gaggagatga accgcgtcct ggccgacccc agcgacgaca ccaagggctt 15180
cttcgacccc aacacgcacg agaacctcac gtacctgcag cttctgcaga gggccaccct 15240
ggaccctgag acggggctcc tatttcttct tctctctcta cagtgactgg gcttcctccg 15300
tgcagttttc tgcaactctg gagaagttga ggcatacttg tgtgtctggg ttgttttttt 15360
ttttttttgt cattctttta tttgttgtt ttaccattc gttatctgtg gaaaacgttt 15420
taagttgtca tgtgacagaa acttttccct tgtccatcga ggtgtttcat aagttttttg 15480
gtgtgttttc tgggtcgtct atgtgtcata tggttttact tttctctcct ttttcgtttt 15540
cagaacattt ttctgtctgt tttggattca ctgcttccat tttacagaat gtcactcttt 15600
agactctcag tccatcatgc cattgggtac tcttgttgca gtgtaatttt tattacatgc 15660
ggttattttc ctaacgatgt gctattcacg ttcattctca aactcatttt ccatcagcca 15720
gtgtctacta tttagtgcc tggctctatt tcggtcctcc tccccgggct ttccttggt 15780
gctgtgctgg ccaaaagcat gggctttatt ctctccattg gctgctgctc caccttagag 15840
gtgtgacctc actagcgttg actgagcgag tctgttgtgg agaagaactt tttgtagtaa 15900
tttactagga aaaattctga acaagtaaaa tatgaaggaa aaaaaaaaaa aa 15952

```

<210> 52

<211> 5065

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Ala Ala Thr Leu Gly Ala Gly Thr Pro Pro Arg Pro Gln Ala Arg
1 5 10 15
Ser Ile Ala Gly Val Tyr Val Glu Ala Ser Gly Gln Ala Gln Ser Val
20 25 30
Tyr Ala Ala Met Glu Gln Gly Leu Leu Pro Ala Gly Leu Gly Gln Ala
35 40 45
Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Leu Val Asp Leu Ala Arg
50 55 60
Gly Gln Leu Leu Pro Val Ser Lys Ala Leu Gln Gln Gly Leu Val Gly
65 70 75 80
Leu Glu Leu Lys Glu Lys Leu Leu Ala Ala Glu Arg Ala Thr Thr Gly
85 90 95
Tyr Pro Asp Pro Tyr Gly Gly Glu Lys Leu Ala Leu Phe Gln Ala Ile
100 105 110
Gly Lys Glu Val Val Asp Arg Ala Leu Gly Gln Ser Trp Leu Glu Val
115 120 125
Gln Leu Ala Thr Gly Gly Leu Val Asp Pro Ala Gln Gly Val Leu Val
130 135 140
Ala Pro Glu Pro Ala Cys His Gln Gly Leu Leu Asp Arg Glu Thr Trp
145 150 155 160
His Lys Leu Ser Glu Leu Glu Pro Gly Thr Gly Asp Leu Arg Phe Leu
165 170 175
Asn Pro Asn Thr Leu Glu Arg Leu Thr Tyr His Gln Leu Leu Glu Arg
180 185 190
Cys Val Arg Ala Pro Gly Ser Gly Leu Ala Leu Leu Pro Leu Lys Ile
195 200 205

```

Thr	Phe	Arg	Ser	Met	Gly	Gly	Ala	Val	Ser	Ala	Ala	Glu	Leu	Leu	Glu
	210					215					220				
Val	Gly	Ile	Leu	Asp	Glu	Gln	Ala	Val	Gln	Gly	Leu	Arg	Glu	Gly	Arg
225					230					235					240
Leu	Ala	Ala	Val	Asp	Val	Ser	Ala	Arg	Ala	Glu	Val	Arg	Arg	Tyr	Leu
				245					250					255	
Glu	Gly	Thr	Gly	Ser	Val	Ala	Gly	Val	Val	Leu	Leu	Pro	Glu	Gly	His
			260					265					270		
Lys	Lys	Ser	Phe	Phe	Gln	Ala	Ala	Thr	Glu	His	Leu	Leu	Pro	Met	Gly
		275					280					285			
Thr	Ala	Leu	Pro	Leu	Leu	Glu	Ala	Gln	Ala	Ala	Thr	His	Thr	Leu	Val
	290					295					300				
Asp	Pro	Ile	Thr	Gly	Gln	Arg	Leu	Trp	Val	Asp	Glu	Ala	Val	Arg	Ala
305					310					315					320
Gly	Leu	Val	Ser	Pro	Glu	Leu	His	Glu	Gln	Leu	Leu	Val	Ala	Glu	Gln
				325					330					335	
Ala	Val	Thr	Gly	His	His	Asp	Pro	Phe	Ser	Gly	Ser	Gln	Ile	Pro	Leu
			340					345					350		
Phe	Gln	Ala	Met	Lys	Lys	Gly	Leu	Val	Asp	Arg	Pro	Leu	Ala	Leu	Arg
	355						360					365			
Leu	Leu	Asp	Ala	Gln	Leu	Ala	Thr	Gly	Gly	Leu	Val	Cys	Pro	Ala	Arg
	370					375					380				
Arg	Leu	Arg	Leu	Pro	Leu	Glu	Ala	Ala	Leu	Arg	Cys	Gly	Cys	Leu	Asp
385					390					395					400
Glu	Asp	Thr	Gln	Arg	Gln	Leu	Ser	Gln	Ala	Gly	Ser	Phe	Ser	Asp	Gly
				405					410					415	
Thr	His	Gly	Gly	Leu	Arg	Tyr	Glu	Gln	Leu	Leu	Ala	Leu	Cys	Val	Thr
			420					425					430		
Asp	Pro	Glu	Thr	Gly	Leu	Ala	Phe	Leu	Pro	Leu	Ser	Gly	Gly	Pro	Arg
		435					440					445			
Gly	Gly	Glu	Pro	Gln	Gly	Pro	Pro	Phe	Ile	Lys	Tyr	Ser	Thr	Arg	Gln
	450					455					460				
Ala	Leu	Ser	Thr	Ala	Thr	Ala	Thr	Val	Ser	Val	Gly	Lys	Phe	Arg	Gly
465					470					475					480
Arg	Pro	Val	Ser	Leu	Trp	Glu	Leu	Leu	Phe	Ser	Glu	Ala	Ile	Ser	Ser
				485					490					495	
Glu	Gln	Arg	Ala	Met	Leu	Ala	Gln	Gln	Tyr	Gln	Glu	Gly	Thr	Leu	Ser
			500					505					510		
Val	Glu	Lys	Leu	Ala	Ala	Glu	Leu	Ser	Ala	Thr	Leu	Glu	Gln	Ala	Ala
		515						520				525			
Ala	Thr	Ala	Arg	Val	Thr	Phe	Ser	Gly	Leu	Arg	Asp	Thr	Val	Thr	Pro
	530					535					540				
Gly	Glu	Leu	Leu	Lys	Ala	Glu	Ile	Ile	Asp	Gln	Asp	Leu	Tyr	Glu	Arg
545					550					555					560
Leu	Glu	His	Gly	Gln	Ala	Thr	Ala	Lys	Asp	Val	Gly	Ser	Leu	Ala	Ser
				565					570					575	
Ala	Gln	Arg	Tyr	Leu	Gln	Gly	Thr	Gly	Cys	Ile	Ala	Gly	Leu	Leu	Leu
			580					585					590		
Pro	Gly	Ser	Gln	Glu	Arg	Leu	Ser	Ile	Tyr	Glu	Ala	Arg	Cys	Lys	Gly
		595					600					605			
Leu	Leu	Arg	Pro	Gly	Thr	Ala	Leu	Ile	Leu	Leu	Glu	Ala	Gln	Ala	Ala
	610					615					620				
Thr	Gly	Phe	Ile	Ile	Asp	Pro	Lys	Ala	Asn	Lys	Gly	His	Ser	Val	Glu
625					630					635					640
Glu	Ala	Leu	Arg	Ala	Ala	Val	Ile	Gly	Pro	Asp	Val	Phe	Ala	Lys	Leu
				645					650					655	
Leu	Ser	Ala	Glu	Arg	Ala	Val	Thr	Gly	Tyr	Thr	Asp	Pro	Tyr	Thr	Gly
			660					665					670		
Gln	Gln	Ile	Ser	Leu	Phe	Gln	Ala	Met	Gln	Lys	Gly	Leu	Ile	Val	Arg

675				680				685							
Glu	His	Gly	Ile	Arg	Leu	Leu	Glu	Ala	Gln	Ile	Ala	Thr	Gly	Gly	Val
	690					695					700				
Ile	Asp	Pro	Val	His	Ser	His	Arg	Val	Pro	Val	Asp	Val	Ala	Tyr	Arg
705					710					715					720
Arg	Gly	Tyr	Phe	Asp	Gln	Met	Leu	Asn	Leu	Ile	Leu	Leu	Asp	Pro	Ser
				725				730						735	
Asp	Asp	Thr	Lys	Gly	Phe	Phe	Asp	Pro	Asn	Thr	His	Glu	Asn	Leu	Thr
			740					745					750		
Tyr	Leu	Gln	Leu	Leu	Glu	Arg	Cys	Val	Arg	Asp	Pro	Glu	Thr	Gly	Leu
		755					760					765			
Tyr	Leu	Leu	Pro	Leu	Ser	Ser	Thr	Gln	Ser	Pro	Leu	Val	Asp	Ser	Ala
770						775					780				
Thr	Gln	Gln	Ala	Phe	Gln	Asn	Leu	Leu	Leu	Ser	Val	Lys	Tyr	Gly	Arg
785					790					795					800
Phe	Gln	Gly	Gln	Arg	Val	Ser	Ala	Trp	Glu	Leu	Ile	Asn	Ser	Glu	Tyr
				805					810					815	
Phe	Ser	Glu	Gly	Arg	Arg	Arg	Gln	Leu	Leu	Arg	Arg	Tyr	Arg	Gln	Arg
			820					825					830		
Glu	Val	Thr	Leu	Gly	Gln	Val	Ala	Lys	Leu	Leu	Glu	Ala	Glu	Thr	Gln
		835					840					845			
Arg	Gln	Ala	Asp	Ile	Met	Leu	Pro	Ala	Leu	Arg	Ser	Arg	Val	Thr	Val
850						855					860				
His	Gln	Leu	Leu	Glu	Ala	Gly	Ile	Ile	Asp	Gln	Gln	Leu	Leu	Asp	Gln
865					870					875					880
Val	Leu	Ala	Gly	Thr	Ile	Ser	Pro	Glu	Ala	Leu	Leu	Leu	Met	Asp	Gly
				885					890					895	
Val	Arg	Arg	Tyr	Leu	Cys	Gly	Leu	Gly	Ala	Val	Gly	Gly	Val	Arg	Leu
			900					905					910		
Leu	Pro	Ser	Gly	Gln	Arg	Leu	Ser	Leu	Tyr	Gln	Ala	Met	Arg	Gln	Lys
		915					920					925			
Leu	Leu	Gly	Pro	Arg	Val	Ala	Leu	Ala	Leu	Leu	Glu	Ala	Gln	Ala	Ala
	930					935					940				
Thr	Gly	Thr	Ile	Met	Asp	Pro	His	Ser	Pro	Glu	Ser	Leu	Ser	Val	Asp
945					950					955					960
Glu	Ala	Val	Arg	Arg	Gly	Val	Val	Gly	Pro	Glu	Leu	Tyr	Gly	Arg	Leu
				965					970					975	
Lys	Arg	Ala	Glu	Gly	Ala	Ile	Ala	Gly	Phe	Arg	Asp	Pro	Phe	Ser	Gly
			980					985					990		
Lys	Gln	Val	Ser	Val	Phe	Gln	Ala	Met	Lys	Lys	Gly	Leu	Ile	Pro	Trp
		995					1000					1005			
Glu	Gln	Ala	Ala	Arg	Leu	Leu	Glu	Ala	Gln	Val	Ala	Thr	Gly	Gly	Ile
	1010					1015					1020				
Ile	Asp	Pro	Thr	Ser	His	His	His	Leu	Pro	Met	Pro	Val	Ala	Ile	Gln
1025					1030					1035					1040
Arg	Gly	Tyr	Val	Asp	Gln	Glu	Met	Glu	Thr	Ala	Leu	Ser	Ser	Ser	Ser
				1045					1050					1055	
Glu	Thr	Phe	Pro	Thr	Pro	Asp	Gly	Gln	Gly	Arg	Thr	Ser	Tyr	Ala	Gln
			1060					1065					1070		
Leu	Leu	Glu	Glu	Cys	Pro	Arg	Asp	Glu	Thr	Ser	Gly	Leu	His	Leu	Leu
		1075					1080					1085			
Pro	Leu	Pro	Glu	Ser	Ala	Pro	Ala	Leu	Pro	Thr	Glu	Glu	Gln	Val	Gln
	1090					1095					1100				
Arg	Ser	Leu	Gln	Ala	Val	Pro	Gly	Ala	Lys	Asp	Gly	Thr	Ser	Leu	Trp
1105					1110					1115					1120
Asp	Leu	Leu	Ser	Ser	Cys	His	Phe	Thr	Glu	Glu	Gln	Arg	Arg	Gly	Leu
				1125					1130					1135	
Leu	Glu	Asp	Val	Gln	Glu	Gly	Arg	Thr	Thr	Val	Pro	Gln	Leu	Leu	Ala
			1140					1145					1150		

Ser Val Gln Arg Trp Val Gln Glu Thr Lys Leu Leu Ala Gln Ala Arg
 1155 1160 1165
 Val Met Val Pro Gly Pro Arg Gly Glu Val Pro Ala Val Trp Leu Leu
 1170 1175 1180
 Asp Ala Gly Ile Ile Thr Gln Glu Thr Leu Glu Ala Leu Ala Gln Gly
 1185 1190 1195 1200
 Thr Gln Ser Pro Ala Gln Val Ala Glu Gln Pro Ala Val Lys Ala Cys
 1205 1210 1215
 Leu Trp Gly Thr Gly Cys Val Ala Gly Val Leu Leu Gln Pro Ser Gly
 1220 1225 1230
 Ala Lys Ala Ser Ile Ala Gln Ala Val Arg Asp Gly Leu Leu Pro Thr
 1235 1240 1245
 Gly Leu Gly Gln Arg Leu Leu Glu Ala Gln Val Ala Ser Gly Phe Leu
 1250 1255 1260
 Val Asp Pro Leu Asn Asn Gln Arg Leu Ser Val Glu Asp Ala Val Lys
 1265 1270 1275 1280
 Val Gly Leu Val Gly Arg Glu Leu Ser Glu Gln Leu Gly Gln Ala Glu
 1285 1290 1295
 Arg Ala Ala Ala Gly Tyr Pro Asp Pro Tyr Ser Arg Ala Ser Leu Ser
 1300 1305 1310
 Leu Trp Gln Ala Met Glu Lys Gly Leu Val Pro Gln Asn Glu Gly Leu
 1315 1320 1325
 Pro Leu Leu Gln Val Gln Leu Ala Thr Gly Gly Val Val Asp Pro Val
 1330 1335 1340
 His Gly Val His Leu Pro Gln Ala Ala Ala Cys Arg Leu Gly Leu Leu
 1345 1350 1355 1360
 Asp Thr Gln Thr Ser Gln Val Leu Thr Ala Val Asp Lys Asp Asn Lys
 1365 1370 1375
 Phe Phe Phe Asp Pro Ser Ala Arg Asp Gln Val Thr Tyr Gln Gln Leu
 1380 1385 1390
 Arg Glu Arg Cys Val Cys Asp Ser Glu Thr Gly Leu Leu Leu Leu Pro
 1395 1400 1405
 Leu Pro Ser Asp Thr Val Leu Glu Val Asp Asp His Thr Ala Val Ala
 1410 1415 1420
 Leu Arg Ala Met Lys Val Pro Val Ser Thr Gly Arg Phe Lys Gly Cys
 1425 1430 1435 1440
 Ser Val Ser Leu Trp Asp Leu Leu Leu Ser Glu Tyr Val Gly Ala Asp
 1445 1450 1455
 Lys Arg Arg Glu Leu Val Ala Leu Cys Arg Ser Gly Arg Ala Ala Ala
 1460 1465 1470
 Leu Arg Gln Val Val Ser Ala Val Thr Ala Leu Val Glu Ala Ala Glu
 1475 1480 1485
 Arg Gln Pro Leu Gln Ala Thr Phe Arg Gly Leu Arg Lys Gln Val Ser
 1490 1495 1500
 Ala Arg Asp Leu Phe Arg Ala Gln Leu Ile Ser Arg Lys Thr Leu Asp
 1505 1510 1515 1520
 Glu Leu Ser Gln Gly Thr Thr Thr Val Lys Glu Val Ala Glu Met Asp
 1525 1530 1535
 Ser Val Lys Arg Ser Leu Glu Gly Gly Asn Phe Ile Ala Gly Val Leu
 1540 1545 1550
 Ile Gln Gly Thr Gln Glu Arg Met Ser Ile Pro Glu Ala Leu Arg Arg
 1555 1560 1565
 His Ile Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala Gln Ala
 1570 1575 1580
 Ala Thr Gly Phe Ile Ile Asp Pro Ala Glu Asn Arg Lys Leu Thr Val
 1585 1590 1595 1600
 Glu Glu Ala Phe Lys Ala Gly Met Phe Gly Lys Glu Thr Tyr Val Lys
 1605 1610 1615
 Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro Tyr Thr

Leu Trp Ala Leu Leu Asn Ser Glu Tyr Val Thr Glu Glu Lys Lys Leu
 2100 2105 2110
 Gln Leu Val Arg Met Tyr Arg Thr His Thr Arg Arg Ala Leu Gln Thr
 2115 2120 2125
 Val Ala Gln Leu Ile Leu Glu Leu Ile Glu Lys Gln Glu Thr Ser Asn
 2130 2135 2140
 Lys His Leu Trp Phe Gln Gly Ile Arg Arg Gln Ile Thr Ala Ser Glu
 2145 2150 2155 2160
 Leu Leu Ser Ser Ala Ile Ile Thr Glu Glu Met Leu Gln Asp Leu Glu
 2165 2170 2175
 Thr Gly Arg Ser Thr Thr Gln Glu Leu Met Glu Asp Asp Arg Val Lys
 2180 2185 2190
 Arg Tyr Leu Glu Gly Thr Ser Cys Ile Ala Gly Val Leu Val Pro Ala
 2195 2200 2205
 Lys Asp Gln Pro Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln Ala Met
 2210 2215 2220
 Trp Lys Gly Val Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala
 2225 2230 2235 2240
 Gln Ala Ala Thr Gly Phe Val Ile Asp Pro Val Arg Asn Leu Arg Leu
 2245 2250 2255
 Ser Val Glu Glu Pro Val Pro Ala Gly Val Val Gly Ser Glu Ile Gln
 2260 2265 2270
 Glu Lys Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro
 2275 2280 2285
 Tyr Thr Gly Gln Gln Ile Ser Leu Phe Gln Ala Met Gln Lys Asp Leu
 2290 2295 2300
 Ile Val Arg Glu His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala Thr
 2305 2310 2315 2320
 Gly Gly Val Ile Asp Pro Val His Ser His Arg Val Pro Val Asp Val
 2325 2330 2335
 Ala Tyr Arg Arg Gly Tyr Phe Asp Glu Glu Met Asn Arg Val Leu Ala
 2340 2345 2350
 Asp Pro Ser Asp Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr His Glu
 2355 2360 2365
 Asn Leu Thr Tyr Val Gln Leu Leu Arg Arg Cys Val Pro Asp Pro Asp
 2370 2375 2380
 Thr Gly Leu Tyr Met Leu Gln Leu Ala Gly Arg Gly Ser Ala Val His
 2385 2390 2395 2400
 Gln Leu Ser Glu Glu Leu Arg Cys Ala Leu Arg Asp Ala Arg Val Thr
 2405 2410 2415
 Pro Gly Ser Gly Ala Leu Gln Gly Gln Ser Val Ser Val Trp Glu Leu
 2420 2425 2430
 Leu Phe Tyr Arg Glu Val Ser Glu Asp Arg Arg Gln Asp Leu Leu Ser
 2435 2440 2445
 Arg Tyr Arg Ala Gly Thr Leu Thr Val Glu Glu Leu Gly Ala Thr Leu
 2450 2455 2460
 Thr Ser Leu Leu Ala Gln Ala Gln Ala Gln Ala Arg Ala Glu Ala Glu
 2465 2470 2475 2480
 Ala Gly Ser Pro Arg Pro Asp Pro Arg Glu Ala Leu Arg Ala Ala Thr
 2485 2490 2495
 Met Glu Val Lys Val Gly Arg Leu Arg Gly Arg Ala Val Pro Val Trp
 2500 2505 2510
 Asp Val Leu Ala Ser Gly Tyr Val Ser Arg Ala Ala Arg Glu Glu Leu
 2515 2520 2525
 Leu Ala Glu Phe Gly Ser Gly Thr Leu Asp Leu Pro Ala Leu Thr Arg
 2530 2535 2540
 Arg Leu Thr Ala Ile Ile Glu Glu Ala Glu Glu Ala Pro Gly Ala Arg
 2545 2550 2555 2560
 Pro Gln Leu Gln Asp Ala Arg Arg Gly Pro Arg Glu Pro Gly Pro Ala

										2565											2570											2575
Gly	Arg	Gly	Asp	Gly	Asp	Ser	Gly	Arg	Ser	Gln	Arg	Glu	Gly	Gln	Gly																	
										2580											2585											2590
Glu	Gly	Glu	Thr	Gln	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Arg	Arg																	
										2595											2600											2605
Gln	Glu	Gln	Thr	Leu	Arg	Asp	Ala	Thr	Met	Glu	Val	Gln	Arg	Gly	Gln																	
										2610											2615											2620
Phe	Gln	Gly	Arg	Pro	Val	Ser	Val	Trp	Asp	Val	Leu	Phe	Ser	Ser	Tyr																	
										2625											2630											2635
Leu	Ser	Glu	Ala	Arg	Arg	Asp	Glu	Leu	Leu	Ala	Gln	His	Ala	Ala	Gly																	
										2645											2650											2655
Ala	Leu	Gly	Leu	Pro	Asp	Leu	Val	Ala	Val	Leu	Thr	Arg	Val	Ile	Glu																	
										2660											2665											2670
Glu	Thr	Glu	Glu	Arg	Leu	Ser	Lys	Val	Ser	Phe	Arg	Gly	Leu	Arg	Arg																	
										2675											2680											2685
Gln	Val	Ser	Ala	Ser	Glu	Leu	His	Thr	Ser	Gly	Ile	Leu	Gly	Pro	Glu																	
										2690											2695											2700
Thr	Leu	Arg	Asp	Leu	Ala	Gln	Gly	Thr	Lys	Thr	Leu	Gln	Glu	Val	Thr																	
										2705											2710											2715
Glu	Met	Asp	Ser	Val	Lys	Arg	Tyr	Leu	Glu	Gly	Thr	Ser	Cys	Ile	Ala																	
										2725											2730											2735
Gly	Val	Leu	Val	Pro	Ala	Lys	Asp	Gln	Pro	Gly	Arg	Gln	Glu	Lys	Met																	
										2740											2745											2750
Ser	Ile	Tyr	Gln	Ala	Met	Trp	Lys	Gly	Val	Leu	Arg	Pro	Gly	Thr	Ala																	
										2755											2760											2765
Leu	Val	Leu	Leu	Glu	Ala	Gln	Ala	Ala	Thr	Gly	Phe	Val	Ile	Asp	Pro																	
										2770											2775											2780
Val	Arg	Asn	Leu	Arg	Leu	Ser	Val	Glu	Glu	Ala	Val	Ala	Ala	Gly	Val																	
										2785											2790											2795
Val	Gly	Gly	Glu	Ile	Gln	Glu	Lys	Leu	Leu	Ser	Ala	Glu	Arg	Ala	Val																	
										2805											2810											2815
Thr	Gly	Tyr	Thr	Asp	Pro	Tyr	Thr	Gly	Gln	Gln	Ile	Ser	Leu	Phe	Gln																	
										2820											2825											2830
Ala	Met	Gln	Lys	Asp	Leu	Ile	Val	Arg	Glu	His	Gly	Ile	Arg	Leu	Leu																	
										2835											2840											2845
Glu	Ala	Gln	Ile	Ala	Thr	Gly	Gly	Val	Ile	Asp	Pro	Val	His	Ser	His																	
										2850											2855											2860
Arg	Val	Pro	Val	Asp	Val	Ala	Tyr	Arg	Arg	Gly	Tyr	Phe	Asp	Glu	Glu																	
										2865											2870											2875
Met	Asn	Arg	Val	Leu	Ala	Asp	Pro	Ser	Asp	Asp	Thr	Lys	Gly	Phe	Phe																	
										2885											2890											2895
Asp	Pro	Asn	Thr	His	Glu	Asn	Leu	Thr	Tyr	Val	Gln	Leu	Leu	Arg	Arg																	
										2900											2905											2910
Cys	Val	Pro	Asp	Pro	Asp	Thr	Gly	Leu	Tyr	Met	Leu	Gln	Leu	Ala	Gly																	
										2915											2920											2925
Arg	Gly	Ser	Ala	Val	His	Gln	Leu	Ser	Glu	Glu	Leu	Arg	Cys	Ala	Leu																	
										2930											2935											2940
Arg	Asp	Ala	Arg	Val	Thr	Pro	Gly	Ser	Gly	Ala	Leu	Gln	Gly	Gln	Ser																	
										2945											2950											2955
Val	Ser	Val	Trp	Glu	Leu	Leu	Phe	Tyr	Arg	Glu	Val	Ser	Glu	Asp	Arg																	
										2965											2970											2975
Arg	Gln	Asp	Leu	Leu	Ser	Arg	Tyr	Arg	Ala	Gly	Thr	Leu	Thr	Val	Glu																	
										2980											2985											2990
Glu	Leu	Gly	Ala	Thr	Leu	Thr	Ser	Leu	Leu	Ala	Gln	Ala	Gln	Ala	Gln																	
										2995											3000											3005
Ala	Arg	Ala	Glu	Ala	Glu	Ala	Gly	Ser	Pro	Arg	Pro	Asp	Pro	Arg	Glu																	
										3010											3015											3020
Ala	Leu	Arg	Ala	Ala	Thr	Met	Glu	Val	Lys	Val	Gly	Arg	Leu	Arg	Gly																	
										3025											3030											3035

Arg Ala Val Pro Val Trp Asp Val Leu Ala Ser Gly Tyr Val Ser Gly
 3045 3050 3055
 Ala Ala Arg Glu Glu Leu Leu Ala Glu Phe Gly Ser Gly Thr Leu Asp
 3060 3065 3070
 Leu Pro Ala Leu Thr Arg Arg Leu Thr Ala Ile Ile Glu Glu Ala Glu
 3075 3080 3085
 Glu Ala Pro Gly Ala Arg Pro Gln Leu Gln Asp Ala Trp Arg Gly Pro
 3090 3095 3100
 Arg Glu Pro Gly Pro Ala Gly Arg Gly Asp Gly Asp Ser Gly Arg Ser
 3105 3110 3115 3120
 Gln Arg Glu Gly Gln Gly Glu Gly Glu Thr Gln Glu Ala Ala Ala Ala
 3125 3130 3135
 Ala Ala Ala Ala Arg Arg Gln Glu Gln Thr Leu Arg Asp Ala Thr Met
 3140 3145 3150
 Glu Val Gln Arg Gly Gln Phe Gln Gly Arg Pro Val Ser Val Trp Asp
 3155 3160 3165
 Val Leu Phe Ser Ser Tyr Leu Ser Glu Ala Arg Arg Asp Glu Leu Leu
 3170 3175 3180
 Ala Gln His Ala Ala Gly Ala Leu Gly Leu Pro Asp Leu Val Ala Val
 3185 3190 3195 3200
 Leu Thr Arg Val Ile Glu Glu Thr Glu Glu Arg Leu Ser Lys Val Ser
 3205 3210 3215
 Phe Arg Gly Leu Arg Arg Gln Val Ser Ala Ser Glu Leu His Thr Ser
 3220 3225 3230
 Gly Ile Leu Gly Pro Glu Thr Leu Arg Asp Leu Ala Gln Gly Thr Lys
 3235 3240 3245
 Thr Leu Gln Glu Val Thr Glu Met Asp Ser Val Lys Arg Tyr Leu Glu
 3250 3255 3260
 Gly Thr Ser Cys Ile Ala Gly Val Leu Val Pro Ala Lys Asp Gln Pro
 3265 3270 3275 3280
 Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln Ala Met Trp Lys Gly Val
 3285 3290 3295
 Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala Gln Ala Ala Thr
 3300 3305 3310
 Gly Phe Val Ile Asp Pro Val Arg Asn Leu Arg Leu Ser Val Glu Glu
 3315 3320 3325
 Ala Val Ala Ala Gly Val Val Gly Gly Glu Ile Gln Glu Lys Leu Leu
 3330 3335 3340
 Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro Tyr Thr Gly Gln
 3345 3350 3355 3360
 Gln Ile Ser Leu Phe Gln Ala Met Gln Lys Asp Leu Ile Val Arg Glu
 3365 3370 3375
 His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala Thr Gly Gly Val Ile
 3380 3385 3390
 Asp Pro Val His Ser His Arg Val Pro Val Asp Val Ala Tyr Arg Arg
 3395 3400 3405
 Gly Tyr Phe Asp Glu Glu Met Asn Arg Val Leu Ala Asp Pro Ser Asp
 3410 3415 3420
 Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr His Glu Asn Leu Thr Tyr
 3425 3430 3435 3440
 Val Gln Leu Leu Arg Arg Cys Val Pro Asp Pro Asp Thr Gly Leu Tyr
 3445 3450 3455
 Met Leu Gln Leu Ala Gly Arg Gly Ser Ala Val His Gln Leu Ser Glu
 3460 3465 3470
 Glu Leu Arg Cys Ala Leu Arg Asp Ala Arg Val Thr Pro Gly Ser Gly
 3475 3480 3485
 Ala Leu Gln Gly Gln Ser Val Ser Val Trp Glu Leu Leu Phe Tyr Arg
 3490 3495 3500
 Glu Val Ser Glu Asp Arg Arg Gln Asp Leu Leu Ser Arg Tyr Arg Ala

3505		3510		3515		3520
Gly Thr Leu Thr	Val Glu Glu Leu Gly	Ala Thr Leu Thr Ser Leu Leu				
	3525	3530		3535		
Ala Gln Ala Gln	Ala Gln Ala Arg Ala Glu Ala Glu Ala Gly Ser Pro					
	3540	3545		3550		
Arg Pro Asp Pro Arg	Glu Ala Leu Arg Ala Ala Thr Met Glu Val Lys					
	3555	3560		3565		
Val Gly Arg Leu Arg Gly	Arg Ala Val Pro Val Trp Asp Val Leu Ala					
	3570	3575		3580		
Ser Gly Tyr Val Ser Gly	Ala Ala Arg Glu Glu Leu Leu Ala Glu Phe					
3585	3590	3595		3600		
Gly Ser Gly Thr Leu Asp	Leu Pro Ala Leu Thr Arg Arg Leu Thr Ala					
	3605	3610		3615		
Ile Ile Glu Glu Ala Glu	Glu Ala Pro Gly Ala Arg Pro Gln Leu Gln					
	3620	3625		3630		
Asp Ala Trp Arg Gly Pro	Arg Glu Pro Gly Pro Ala Gly Arg Gly Asp					
	3635	3640		3645		
Gly Asp Ser Gly Arg Ser	Gln Arg Glu Gly Gln Gly Glu Gly Glu Thr					
	3650	3655		3660		
Gln Glu Ala Ala Ala Ala	Ala Ala Ala Ala Arg Arg Gln Glu Gln Thr					
3665	3670	3675		3680		
Leu Arg Asp Ala Thr Met	Glu Val Gln Arg Gly Gln Phe Gln Gly Arg					
	3685	3690		3695		
Pro Val Ser Val Trp Asp	Val Leu Phe Ser Ser Tyr Leu Ser Glu Ala					
	3700	3705		3710		
Arg Arg Asp Glu Leu Leu	Ala Gln His Ala Ala Gly Ala Leu Gly Leu					
	3715	3720		3725		
Pro Asp Leu Val Ala Val	Leu Thr Arg Val Ile Glu Glu Thr Glu Glu					
	3730	3735		3740		
Arg Leu Ser Lys Val Ser	Phe Arg Gly Leu Arg Arg Gln Val Ser Ala					
3745	3750	3755		3760		
Ser Glu Leu His Thr Ser	Gly Ile Leu Gly Pro Glu Thr Leu Arg Asp					
	3765	3770		3775		
Leu Ala Gln Gly Thr Lys	Thr Leu Gln Glu Val Thr Glu Met Asp Ser					
	3780	3785		3790		
Val Lys Arg Tyr Leu Glu	Gly Thr Ser Cys Ile Ala Gly Val Leu Val					
	3795	3800		3805		
Pro Ala Lys Asp Gln Pro	Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln					
	3810	3815		3820		
Ala Met Trp Lys Gly Val	Leu Arg Pro Gly Thr Ala Leu Val Leu Leu					
3825	3830	3835		3840		
Glu Ala Gln Ala Ala Thr	Gly Phe Val Ile Asp Pro Val Arg Asn Leu					
	3845	3850		3855		
Arg Leu Ser Val Glu Glu	Ala Val Ala Ala Gly Val Val Gly Gly Glu					
	3860	3865		3870		
Ile Gln Glu Lys Leu Leu	Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr					
	3875	3880		3885		
Asp Pro Tyr Thr Gly Gln	Gln Ile Ser Leu Phe Gln Ala Met Gln Lys					
	3890	3895		3900		
Asp Leu Ile Val Arg Glu	His Gly Ile Arg Leu Leu Glu Ala Gln Ile					
3905	3910	3915		3920		
Ala Thr Gly Gly Val Ile	Asp Pro Val His Ser His Arg Val Pro Val					
	3925	3930		3935		
Asp Val Ala Tyr Arg Arg	Gly Tyr Phe Asp Glu Glu Met Asn Arg Val					
	3940	3945		3950		
Leu Ala Asp Pro Ser Asp	Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr					
	3955	3960		3965		
His Glu Asn Leu Thr Tyr	Val Gln Leu Leu Arg Arg Cys Val Pro Asp					
	3970	3975		3980		

Pro Asp Thr Gly Leu Tyr Met Leu Gln Leu Ala Gly Arg Gly Ser Ala
 3985 3990 3995 4000
 Val His Gln Leu Ser Glu Glu Leu Arg Cys Ala Leu Arg Asp Ala Arg
 4005 4010 4015
 Val Thr Pro Gly Ser Gly Ala Leu Gln Gly Gln Ser Val Ser Val Trp
 4020 4025 4030
 Glu Leu Leu Phe Tyr Arg Glu Val Ser Glu Asp Arg Arg Gln Asp Leu
 4035 4040 4045
 Leu Ser Arg Tyr Arg Ala Ser Thr Leu Thr Val Glu Glu Leu Gly Ala
 4050 4055 4060
 Thr Leu Thr Ser Leu Leu Ala Gln Ala Gln Ala Gln Ala Arg Ala Glu
 4065 4070 4075 4080
 Ala Glu Ala Gly Ser Pro Arg Pro Asp Pro Arg Glu Ala Leu Arg Ala
 4085 4090 4095
 Ala Thr Met Glu Val Lys Val Gly Arg Leu Arg Gly Arg Ala Val Pro
 4100 4105 4110
 Val Trp Asp Val Leu Ala Ser Gly Tyr Val Ser Arg Ala Ala Arg Glu
 4115 4120 4125
 Glu Leu Leu Ala Glu Phe Gly Ser Gly Thr Leu Asp Leu Pro Ala Leu
 4130 4135 4140
 Thr Arg Arg Leu Thr Ala Ile Ile Glu Glu Ala Glu Glu Ala Pro Gly
 4145 4150 4155 4160
 Ala Arg Pro Gln Leu Gln Asp Ala Trp Arg Gly Pro Arg Glu Pro Gly
 4165 4170 4175
 Pro Ala Gly Arg Gly Asp Gly Asp Ser Gly Arg Ser Gln Arg Glu Gly
 4180 4185 4190
 Gln Gly Glu Gly Glu Thr Gln Glu Ala Ala Ala Thr Ala Ala Ala
 4195 4200 4205
 Arg Arg Gln Glu Gln Thr Leu Arg Asp Ala Thr Met Glu Val Gln Arg
 4210 4215 4220
 Gly Gln Phe Gln Gly Arg Pro Val Ser Val Trp Asp Val Leu Phe Ser
 4225 4230 4235 4240
 Ser Tyr Leu Ser Glu Ala Arg Arg Asp Glu Leu Leu Ala Gln His Ala
 4245 4250 4255
 Ala Gly Ala Leu Gly Leu Pro Asp Leu Val Ala Val Leu Thr Arg Val
 4260 4265 4270
 Ile Glu Glu Thr Glu Glu Arg Leu Ser Lys Val Ser Phe Arg Gly Leu
 4275 4280 4285
 Arg Arg Gln Val Ser Ala Ser Glu Leu His Thr Ser Gly Ile Leu Gly
 4290 4295 4300
 Pro Glu Thr Leu Arg Asp Leu Ala Gln Gly Thr Lys Thr Leu Gln Glu
 4305 4310 4315 4320
 Val Thr Glu Met Asp Ser Val Lys Arg Tyr Leu Glu Gly Thr Ser Cys
 4325 4330 4335
 Ile Ala Gly Val Leu Val Pro Ala Lys Asp Gln Pro Gly Arg Gln Glu
 4340 4345 4350
 Lys Met Ser Ile Tyr Gln Ala Met Trp Lys Gly Val Leu Arg Pro Gly
 4355 4360 4365
 Thr Ala Leu Val Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Val Ile
 4370 4375 4380
 Asp Pro Val Arg Asn Leu Arg Leu Ser Val Glu Glu Ala Val Ala Ala
 4385 4390 4395 4400
 Gly Val Val Gly Gly Glu Ile Gln Glu Lys Leu Leu Ser Ala Glu Arg
 4405 4410 4415
 Ala Val Thr Gly Tyr Thr Asp Pro Tyr Thr Gly Gln Gln Ile Ser Leu
 4420 4425 4430
 Phe Gln Ala Met Gln Lys Asp Leu Ile Val Arg Glu His Gly Ile Arg
 4435 4440 4445
 Leu Leu Glu Ala Gln Ile Ala Thr Gly Gly Val Ile Asp Pro Val His

4450	4455	4460
Ser His Arg Val Pro Val Asp Val Ala Tyr Arg Arg Gly Tyr Phe Asp		
4465	4470	4475
Glu Glu Met Asn Arg Val Leu Ala Asp Pro Ser Asp Asp Thr Lys Gly		4480
	4485	4490
Phe Phe Asp Pro Asn Thr His Glu Asn Leu Thr Tyr Val Gln Leu Leu		4495
	4500	4505
Arg Arg Cys Val Pro Asp Pro Asp Thr Gly Leu Tyr Met Leu Gln Leu		4510
	4515	4520
Ala Gly Arg Gly Ser Ala Val His Gln Leu Ser Glu Glu Leu Arg Cys		4525
	4530	4535
Ala Leu Arg Asp Ala Arg Val Thr Pro Gly Ser Gly Ala Leu Gln Gly		4540
4545	4550	4555
Gln Ser Val Ser Val Trp Glu Leu Leu Phe Tyr Arg Glu Val Ser Glu		4560
	4565	4570
Asp Arg Arg Gln Asp Leu Leu Ser Arg Tyr Arg Ala Gly Thr Leu Thr		4575
	4580	4585
Val Glu Glu Leu Gly Ala Thr Leu Thr Ser Leu Leu Ala Gln Ala Gln		4590
	4595	4600
Ala Gln Ala Arg Ala Glu Ala Glu Ala Gly Ser Pro Arg Pro Asp Pro		4605
	4610	4615
Arg Glu Ala Leu Arg Ala Ala Thr Met Glu Val Lys Val Gly Arg Leu		4620
4625	4630	4635
Arg Gly Arg Ala Val Pro Val Trp Asp Val Leu Ala Ser Gly Tyr Val		4640
	4645	4650
Ser Gly Ala Ala Arg Glu Glu Leu Leu Ala Glu Phe Gly Ser Gly Thr		4655
	4660	4665
Leu Asp Leu Pro Ala Leu Thr Arg Arg Leu Thr Ala Ile Ile Glu Glu		4670
	4675	4680
Ala Glu Glu Ala Pro Gly Ala Arg Pro Gln Leu Gln Asp Ala Trp Arg		4685
	4690	4695
Gly Pro Arg Glu Pro Gly Pro Ala Gly Arg Gly Asp Gly Asp Ser Gly		4700
4705	4710	4715
Arg Ser Gln Arg Glu Gly Gln Gly Glu Gly Glu Thr Gln Glu Ala Ala		4720
	4725	4730
Ala Ala Ala Ala Ala Arg Arg Gln Glu Gln Thr Leu Arg Asp Ala		4735
	4740	4745
Thr Met Glu Val Gln Arg Gly Gln Phe Gln Gly Arg Pro Val Ser Val		4750
	4755	4760
Trp Asp Val Leu Phe Ser Ser Tyr Leu Ser Glu Ala Arg Arg Asp Glu		4765
	4770	4775
Leu Leu Ala Gln His Ala Ala Gly Ala Leu Gly Leu Pro Asp Leu Val		4780
4785	4790	4795
Ala Val Leu Thr Arg Val Ile Glu Glu Thr Glu Glu Arg Leu Ser Lys		4800
	4805	4810
Val Ser Phe Arg Gly Leu Arg Arg Gln Val Ser Ala Ser Glu Leu His		4815
	4820	4825
Thr Ser Gly Ile Leu Gly Pro Glu Thr Leu Arg Asp Leu Ala Gln Gly		4830
	4835	4840
Thr Lys Thr Leu Gln Glu Val Thr Glu Met Asp Ser Val Lys Arg Tyr		4845
	4850	4855
Leu Glu Gly Thr Ser Cys Ile Ala Gly Val Leu Val Pro Ala Lys Asp		4860
4865	4870	4875
Gln Pro Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln Ala Met Trp Lys		4880
	4885	4890
Gly Val Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala Gln Ala		4895
	4900	4905
Ala Thr Gly Phe Val Ile Asp Pro Val Arg Asn Leu Arg Leu Ser Val		4910
	4915	4920
		4925

Glu Glu Ala Val Ala Ala Gly Val Val Gly Gly Glu Ile Gln Glu Lys
 4930 4935 4940
 Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro Tyr Thr
 4945 4950 4955 4960
 Gly Gln Gln Ile Ser Leu Phe Gln Ala Met Gln Lys Asp Leu Ile Val
 4965 4970 4975
 Arg Glu His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala Thr Gly Gly
 4980 4985 4990
 Val Ile Asp Pro Val His Ser His Arg Val Pro Val Asp Val Ala Tyr
 4995 5000 5005
 Arg Arg Gly Tyr Phe Asp Glu Glu Met Asn Arg Val Leu Ala Asp Pro
 5010 5015 5020
 Ser Asp Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr His Glu Asn Leu
 5025 5030 5035 5040
 Thr Tyr Leu Gln Leu Leu Gln Arg Ala Thr Leu Asp Pro Glu Thr Gly
 5045 5050 5055
 Leu Leu Phe Leu Ser Leu Ser Leu Gln
 5060 5065

<210> 53
 <211> 1664
 <212> DNA
 <213> Homo sapiens

<400> 53
 tcatggccgg ctctactcct gaaggtgcac ctgcaatcct cgccgataag aggcagcagt 60
 tcggaagccg gttcctgagc gatccggcgc gggctctcca ccacaatgcc tgttgattat 120
 gagatcaatg cccacaaata ctggaatgac ttctacaaaa tccacgaaaa tgggtttttc 180
 aaggatagac attggctttt taccgaattc cctgagctgg cacctagcca aaatcaaaat 240
 catttgaagg attggttctt ggagaacaag agtgaagtat gtgaatgtag aaacaatgag 300
 gatggacctg gtttaataat ggaagaacag cacaagtgtt cttcgaagag ccttgaacat 360
 aaaacacaga cacctcctgt ggaggagaat gtaactcaga aaattagtga cctggaaatt 420
 tgtgctgatg agtttctctg atcctcagcc acctaccgaa tactggagggt tggctgtggt 480
 gtgggaaaca cagtctttcc aattttacaa acgaacaatg acccaggact ctttgtttat 540
 tgcgtgattt tttcttcac agctatagaa ctggtccaga caaattcaga atatgatcct 600
 tctcgggtgt ttgoccttgt tcacgacctg tgtgatgaag agaagagtta ccagtgccc 660
 aagggcagtc ttgatattat cattctcata tttgttcttt cagcaattgt tccagacaag 720
 atgcagaagg ctatcaacag gctgagcagg cttctgaaac ctggggggat ggtacttctg 780
 cgagattacg gccgctatga catggctcag cttcggttta aaaaagggtca gtgtctatct 840
 ggaaatttct atgtgagagg tgatggaacc agagtttact tcttcacaca agaggaactg 900
 gacacgcttt tcaccactgc tggactggaa aaagttcaga acctggtgga ccgccgactg 960
 caggtgaacc gagggaagca actgacaatg taccgggttt ggattcagtg caaatactgc 1020
 aagccccttc tgtccagcac cagctaagag gcacctgctg ccaacacgat gcaagcccgt 1080
 tgtgtttccg agcttttttt aaaaaaaaaat ttgtagcacc gggcatgggt catgcctgta 1140
 atcccagcca ctccaggaggc tgaggcaggg aggatccatt gagcccagga gtccagcctg 1200
 ggcaaaatag cgagagaccc tgaatctgaa agtaatgata aaataaaaaag aatataaatg 1260
 aggtctcggt gatgctggac aattcaagaa ttcagacttg aaccttaaac ctaggaaaag 1320
 ttacttttga tcaggattct aacaattatg cttcatattt gtgaagtcct ttaaaacata 1380
 attttctcaa gttctttctt tgagacctca atctgtctta gcatttttga actaataact 1440
 gaaattttat tcaaaggaat tgtaaacctt aaaccaccaa tttattttcca tgtgaaaaag 1500
 tggtatatat gacaagtgtt ttttgattgt aattgcgtta aatcttttga gagtgtaaat 1560
 gccgggctag gcaattgcag ttaatacata caggggttag tgaagggtt attaatgtgt 1620
 aggggaagca agctgggaag aatcagatca gatattttcc tgac 1664

<210> 54
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 54
Met Pro Val Asp Tyr Glu Ile Asn Ala His Lys Tyr Trp Asn Asp Phe
1 5 10 15
Tyr Lys Ile His Glu Asn Gly Phe Phe Lys Asp Arg His Trp Leu Phe
20 25 30
Thr Glu Phe Pro Glu Leu Ala Pro Ser Gln Asn Gln Asn His Leu Lys
35 40 45
Asp Trp Phe Leu Glu Asn Lys Ser Glu Val Cys Glu Cys Arg Asn Asn
50 55 60
Glu Asp Gly Pro Gly Leu Ile Met Glu Glu Gln His Lys Cys Ser Ser
65 70 75 80
Lys Ser Leu Glu His Lys Thr Gln Thr Pro Pro Val Glu Glu Asn Val
85 90 95
Thr Gln Lys Ile Ser Asp Leu Glu Ile Cys Ala Asp Glu Phe Pro Gly
100 105 110
Ser Ser Ala Thr Tyr Arg Ile Leu Glu Val Gly Cys Gly Val Gly Asn
115 120 125
Thr Val Phe Pro Ile Leu Gln Thr Asn Asn Asp Pro Gly Leu Phe Val
130 135 140
Tyr Cys Cys Asp Phe Ser Ser Thr Ala Ile Glu Leu Val Gln Thr Asn
145 150 155 160
Ser Glu Tyr Asp Pro Ser Arg Cys Phe Ala Phe Val His Asp Leu Cys
165 170 175
Asp Glu Glu Lys Ser Tyr Pro Val Pro Lys Gly Ser Leu Asp Ile Ile
180 185 190
Ile Leu Ile Phe Val Leu Ser Ala Ile Val Pro Asp Lys Met Gln Lys
195 200 205
Ala Ile Asn Arg Leu Ser Arg Leu Leu Lys Pro Gly Gly Met Val Leu
210 215 220
Leu Arg Asp Tyr Gly Arg Tyr Asp Met Ala Gln Leu Arg Phe Lys Lys
225 230 235 240
Gly Gln Cys Leu Ser Gly Asn Phe Tyr Val Arg Gly Asp Gly Thr Arg
245 250 255
Val Tyr Phe Phe Thr Gln Glu Glu Leu Asp Thr Leu Phe Thr Thr Ala
260 265 270
Gly Leu Glu Lys Val Gln Asn Leu Val Asp Arg Arg Leu Gln Val Asn
275 280 285
Arg Gly Lys Gln Leu Thr Met Tyr Arg Val Trp Ile Gln Cys Lys Tyr
290 295 300
Cys Lys Pro Leu Leu Ser Ser Thr Ser
305 310

<210> 55
<211> 3334
<212> DNA
<213> Homo sapiens

<400> 55
gaaaaggaaa tcgcagctgt gattttctcct gaactggagc atctagataa aacccttccc 60
accatgaata atctcatcag ccaagataag cgtatcagct ctaaccctgt ggccaaaata 120
atataatggtg acccagtgac cttcctgccc cacctgcccc ggaaaagtgt ggtccattgc 180
tctaagattt ggagctgcag gaaaagaatt acagttgagt acctccagca cattgtggaa 240
cagaaaaatg gcaaagaaag agtgcccatc ctctggcatt tcctgcagaa ggaagcagag 300
ctgaggctgg taaagttcct gcctgagatt ttggccttgc aaagggatct agtgaagcag 360
ttccagaacg ttcagcaagt tgaatacagc tccatcagag gcttcctcag caagcacagc 420
tcagatgggt tgaggcagct gcttcacaac aggatcacag tctttctgtc cacatggaac 480
aaactgagga gatcgcttga gacgaacggt gagatcaacc taccctaaaga ctactgcagc 540

```

actgacttgg atctggacac tgagtttgag atcctcttgc cagccgacg gggcctgggc 600
ctctgtgcta cgcctctcgt cagctacttg attcgcctac acaatgaaat tgtctacgcc 660
gtggaaaaac tctccaagga aaacaacagc tattccgtgg atgcgcgca ggtcactgaa 720
ctgcatgtca tcagttatga agtggagcgg gacctgactc cactgattct ctccaactgc 780
cagtaccagg tggaggaggg cagagagacc gtgcaggagt tcgatctgga gaagattcag 840
cggcagatcg tcagccgctt cctccagggc aagccccggc tgagcctcaa ggaatacccc 900
actctggtgt acagacacga ctggaactat gaacatctct ttatggacat caagaacaaa 960
atggcacagg actccctccc cagctcggtc attagtcca tcagtggaca gctgcagtcc 1020
tacagcgatg cctgtgaagt gctgtctgtc gtagaagtca ctctgggggt tctgagcaca 1080
gctggtgggg atccaaacat gcagctgaat gtgtatactc aagacatcct gcaaattgggt 1140
gatcagacga ttcaogtgtt aaaggcctta aacagatgcc agttaaaaca caccattgcc 1200
ctctggcagt tctgtctctg tcataagctc gaacagctgc tgccgctgca caaagagcca 1260
tttggggaaa tcagttcaag gtacaaagcg gatctgagcc cggaaaatgc taagctcctc 1320
agcacattcc taaatcagac tggcctagac gccttctctg tagagctgca cgaaatgata 1380
atcttgaaac taaagaaccc ccaaacccaa accgaggagc gcttccgccc tcagtggagc 1440
ctgagagaca ctctcgtaag ttacatgcaa actaaagaaa gtgaaattct tctgaaatg 1500
gcatctcagt tcccagaaga gatactgctc gccagctgtg tctcagtgtg gaaaacagct 1560
gctgtgctga aatggaatcg agaaatgaga tagaattatt tctcagcta tctttggatg 1620
actttggaga gaagactcct ctctcctcgt ctgcccgtg gacttgatca tggactggtg 1680
cctttgcatt cagaaggaga gctgtcagcg tagcaccgaa ttcaagacca aggcgtgcta 1740
cctgagctga cagctttttg aaagccgagc tgtttctgaa ccatgtacat acatgttctg 1800
aaactttctc atcattttat gagtactgtt cattgagaga tgacaatgaa gattagatga 1860
aattggaaat aaaccaacat tgtttacatt ccaggagact tgtagctcag ccacacacgc 1920
agtaatgacc tgtgcccggt cgctcttggt actgccacc cctctttttt tttttcttct 1980
aattctgtac tcacaaaaga gaatctcatt ttcttctttc ttccattccc tttaaattctg 2040
agtactgtac atatatattct gggttcccac gatgatgtga aaaactacca gactgttttt 2100
tgtcttctca caaagacaag aaaaatcagg gcattttgtg agtgccctaa gatcaaaacta 2160
acaagatctg accctctccc ctacacagtga gccactgcc cacttcagag ggtaagagcc 2220
aaaagcctca ttgtgaaagg cactggactt ggaccaggga caccatcagg gccttggttt 2280
tctcacgcat aaaatggaga gtggattaat cgccaaagat tcttctgata tgacattttg 2340
aaattgtgag agaaactaga tgactgtaaa cttggtcaca ggccctgggtc tggcagttct 2400
ttgcggaact ttttctagca ttatgccaaa taaacatgca gtctcagtgt gctctcgcat 2460
gtatgaatat ctagtctctt ctgtggttct cagccaagac ataaaaacta ggactcagag 2520
cacatacaaa accagttatg tttcggaaag agggaaaaga gtccccgagc ccgcatcttg 2580
tgctgctttt ctactgacg tgttgccctt tttctttaca aaatctgctt tgatacttag 2640
gacctctctg gactaatttc tcttcctaga cagctcagca cagctattga tatgttagag 2700
gcagtatcct taataattcat tctaaatgag ttaacgactt aacttgaaat tgggcctaag 2760
gagtgagaac tacaaaaata caaaatgctt gtccaggact cagccatgca cacttgagc 2820
agcgcgggca ggaggcacgg aaggaaactgt gctccgttct cctcactgtc atgggtgccac 2880
cagtgtctga tgaagggcag agtgaccag actgcaggca gtaactgact tcacacagtc 2940
cctggcattt agtcatctgt gattgtttta tcactctgga ctgtgcagag ccacctgcca 3000
ccgagatctg cattccgact gcctatgaac ggggtgtggg gccggggggt ggcttgctga 3060
agtcttcaac ttgcaactcg agctcctttg atacctcaga gctggctgtc aggtggcagc 3120
tcacacccag actcactggc cacacctcag caggggggga gtcgagtgtc agtctctttc 3180
tgtgaaggct ttttttttcc tttggcctg gaatttttcc catttttatg aaggggtttt 3240
aaattgtttc attttgtgtg ctgtgcttca aagcctaac tgtcaaactc tgcattatct 3300
tgtttgtaca gaaatatact ggccctagcag aggc 3334

```

<210> 56
 <211> 509
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Asn Asn Leu Ile Ser Gln Asp Lys Arg Ile Ser Ser Asn Pro Val
 1 5 10 15
 Ala Lys Ile Ile Tyr Gly Asp Pro Val Thr Phe Leu Pro His Leu Pro
 20 25 30
 Arg Lys Ser Val Val His Cys Ser Lys Ile Trp Ser Cys Arg Lys Arg

<210> 57
 <211> 1760
 <212> DNA
 <213> Homo sapiens

<400> 57
 gcagcaggcc aagggggagg tgcgagcgtg gacctgggac ggggtctgggc ggctctcggt 60
 ggttggcacg ggttcgcaca cccattcaag cggcaggacg cacttgtctt agcagttctc 120
 gctgaccgcg ctagctgcgg cttctacgct cggcactct gagttcatca gcaaacgccc 180
 tggcgtctgt cctcaccatg cctagccttt gggaccgctt ctgctgctcg tccacctcct 240
 cttgcgccctc gtccttgccc cgaactccca ccccagatcg gccgcgcgcg tcagcctggg 300
 ggtcggcgac ccgggaggag gggtttgacc gctccacgag cctggagagc tcggactgcg 360
 agtccttgga cagcagcaac agtggcttcg ggccggagga agacacggct tacctggatg 420
 ggggtgtcgtt gcccgacttc gagctgctca gtgaccctga ggatgaacac ttgtgtgcca 480
 acctgatgca gctgctgcag gagagcctgg cccaggcgcg gctgggctct cgacgccctg 540
 cgcgccctgct gatgcctagc cagttagtaa gccagggtggg caaagaacta ctgcgcctgg 600
 cctacagcga gccgtgcggc ctgcgggggg cgctgctgga cgtctgcgtg gagcagggca 660
 agagctgcca cagcgtgggc cagctggcac tcgacccag cctggtgccc acctccagc 720
 tgacctctgt gctgcgcctg gactcacgac tctggcccaa gatccagggg ctgttttagct 780
 ccgccaactc tcccttcctc cctggcttca gccagtcctt gacgctgagc actggcttcc 840
 gagtcatcaa gaagaagctg tacagctcgg aacagctgct cattgaggag tgttgaactt 900
 caacctgagg gggccgacag tgccctccaa gacagagacg actgaacttt tgggggtggag 960
 actagaggca ggagctgagg gactgattcc agtggttgga aaactgaggc agccacctaa 1020
 ggtggagggtg ggggaatagt gtttcccagg aagctcattg agttgtgtgc ggggtggctgt 1080
 gcattgggga cacatacccc tcagtactgt agcatggaac aaaggcttag gggccaacaa 1140
 ggcttccagc tggatgtgtg tgtagcatgt accttattat ttttgttact gacagttaac 1200
 agtgggtgtga catccagaga gcagctgggc tgctcccgcc ccagcctggc ccagggtgaa 1260
 ggaagaggca cgtgctcctc agagcagccg gagggagggg ggaggtcgga ggtcgtggag 1320
 gtggtttgtg tatcttactg gtctgaaggg accaagtgtg tttgttgttt gttttgtatc 1380
 ttgtttttct gatcggagca tcactactga cctgtttagt gcagctatct tacagacgca 1440
 tgaatgtaag agtaggaagg ggtgggtgtc agggatcact tgggatcttt gacacttgaa 1500
 aaattacacc tggcagctgc gtttaagcct tccccatcg tgtactgcag agttgagctg 1560
 gcaggggagg ggtgagagg gtgggggctg gaaccctcc ccgggaggag tgccatctgg 1620
 gtcttccatc tagaactgtt tacatgaaga taagatactc actgttcatg aatacacttg 1680
 atgttcaagt attaagacct atgcaatatt ttttactttt ctaataaaca tgtttgttaa 1740
 aacaaaaaaaa aaaaaaaaaa 1760

<210> 58
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Pro Ser Leu Trp Asp Arg Phe Ser Ser Ser Ser Thr Ser Ser Ser
 1 5 10 15
 Pro Ser Ser Leu Pro Arg Thr Pro Thr Pro Asp Arg Pro Pro Arg Ser
 20 25 30
 Ala Trp Gly Ser' Ala Thr Arg Glu Glu Gly Phe Asp Arg Ser Thr Ser
 35 40 45
 Leu Glu Ser Ser Asp Cys Glu Ser Leu Asp Ser Ser Asn Ser Gly Phe
 50 55 60
 Gly Pro Glu Glu Asp Thr Ala Tyr Leu Asp Gly Val Ser Leu Pro Asp
 65 70 75 80
 Phe Glu Leu Leu Ser Asp Pro Glu Asp Glu His Leu Cys Ala Asn Leu
 85 90 95
 Met Gln Leu Leu Gln Glu Ser Leu Ala Gln Ala Arg Leu Gly Ser Arg
 100 105 110

Arg	Pro	Ala	Arg	Leu	Leu	Met	Pro	Ser	Gln	Leu	Val	Ser	Gln	Val	Gly
		115					120					125			
Lys	Glu	Leu	Leu	Arg	Leu	Ala	Tyr	Ser	Glu	Pro	Cys	Gly	Leu	Arg	Gly
	130					135					140				
Ala	Leu	Leu	Asp	Val	Cys	Val	Glu	Gln	Gly	Lys	Ser	Cys	His	Ser	Val
145					150					155					160
Gly	Gln	Leu	Ala	Leu	Asp	Pro	Ser	Leu	Val	Pro	Thr	Phe	Gln	Leu	Thr
			165						170					175	
Leu	Val	Leu	Arg	Leu	Asp	Ser	Arg	Leu	Trp	Pro	Lys	Ile	Gln	Gly	Leu
		180						185					190		
Phe	Ser	Ser	Ala	Asn	Ser	Pro	Phe	Leu	Pro	Gly	Phe	Ser	Gln	Ser	Leu
	195						200					205			
Thr	Leu	Ser	Thr	Gly	Phe	Arg	Val	Ile	Lys	Lys	Lys	Leu	Tyr	Ser	Ser
	210					215						220			
Glu	Gln	Leu	Leu	Ile	Glu	Glu	Cys								
225					230										

<210> 59

<211> 2012

<212> DNA

<213> Homo sapiens

<400> 59

tctgaagcga	atcagtgagg	agtggcctac	agtgggtcgg	ctaccgaata	caccttcacc	60
cacttgaaac	caggcacttt	gtacaaactc	cgagcatgct	gcatcagtag	cggcggacac	120
agccagtgtt	ctgaaagtct	ccctgttgcg	acactaagca	ttgcaccagg	tcaatgtcga	180
ccaccgaggg	ttttgggtag	accaaagcac	aaagaagtcc	acttagagtg	ggatgttcct	240
gcatcgaaaa	gtggctgtga	ggtctcagag	tacagcgtgg	agatgacgga	gcccgaagac	300
gtagcctcgg	aagtgtacca	tggcccagag	ctggagtgcg	ccgtcggcaa	cctgcttcct	360
ggaaccgtgt	atcgcttccg	ggtgagggct	ctgaatgatg	gagggtatgg	tccctattct	420
gatgtctcag	aaattaccac	tgctgcaggg	cctcctggac	aatgcaaagc	accttgtatt	480
tcttgtagac	ctgatggatg	tgtcttagtg	ggttgggaga	gtcctgatag	ttctgggtgct	540
gacatctcag	agtacaggtt	ggaatgggga	gaagatgaag	aatccttaga	actcatttat	600
catgggacag	acaccggttt	tgaataaaga	gacctgttgc	ctgctgcaca	gtattgctgt	660
agactacag	ccttcaatca	agcaggggca	gggccgtaca	gtgaacttgt	cctttgccag	720
acgcccagct	ctgcccctga	ccccgtctcc	actctctgtg	tcctggagga	ggagcccctt	780
gatgcctacc	ctgattcacc	ttctgcgtgc	cttgtagtga	actgggaaga	gccgtgcaat	840
aacggatctg	aaatccttgc	ttacaccatt	gatctaggag	acactagcat	taccgtgggc	900
aacaccacca	tgcattgtat	gaaagatctc	cttccagaaa	ccacctaccg	gacagaatt	960
caggctataa	atgaaattgg	agctggacca	tttagtcagt	tcattaaagc	aaaaactcgg	1020
ccattaccac	ccttgccctc	taggctagaa	tgtgctgctg	ctggctcctc	gagcctgaag	1080
ctaaaatggg	gagacagtaa	ctccaagaca	catgctgctg	aggacattgt	gtacacacta	1140
cagctggagg	acagaaacaa	gagggtttatt	tcaatctaca	gaggacccag	ccacacctac	1200
aaggtccaga	gactgacgga	attcacatgc	tactccttca	gaatccaggc	agcaagcgag	1260
gctggagaag	ggcccttctc	agaaacctat	accttcagca	caaccaaaag	tgtccccccc	1320
accatcaaa	cacctcgagt	aacacagtta	gaaggaaaat	catgtgaaat	tttatgggag	1380
acggtagcat	caatgaaagg	tgacctgttt	aactacattc	tgcagggtatt	ggttggaaga	1440
gaatctgagt	acaaacaggt	gtacaaggga	gaagaagcca	cattccaaat	ctcaggcctc	1500
cagaccaaca	cagactacag	gttccgcgta	tgtgcgtgtc	gtcgtgtgtt	agacacctct	1560
caggagctaa	gcggagcctt	cagcccctct	gcggcttttg	tattacaacg	aagtgaggtc	1620
atgcttacag	gggacatggg	gagcttagat	gatcccaaaa	tgaagagcat	gatgcctact	1680
gatgaacagt	ttgcagccat	cattgtgtct	ggctttgcaa	ctttgtccat	tttatttgcc	1740
tttatattac	agtacttctt	aatgaagtaa	acccaacaaa	actagaggta	tgaattaatg	1800
ctacacattt	taatacacac	atttattcag	atactcccct	ttttaaagcc	cttttgtttt	1860
ttgtttata	tactctgttt	tacagattta	gctagaaaaa	aaatgtcagt	gttttgggtg	1920
acctttttga	aatgcaaaa	taggaaaagg	ttaaactgga	tttttttttt	taaaaaaaaa	1980
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aa			2012

<210> 60
 <211> 495
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Thr Glu Pro Glu Asp Val Ala Ser Glu Val Tyr His Gly Pro Glu
 1 5 10 15
 Leu Glu Cys Thr Val Gly Asn Leu Leu Pro Gly Thr Val Tyr Arg Phe
 20 25 30
 Arg Val Arg Ala Leu Asn Asp Gly Tyr Gly Pro Tyr Ser Asp Val
 35 40 45
 Ser Glu Ile Thr Thr Ala Ala Gly Pro Pro Gly Gln Cys Lys Ala Pro
 50 55 60
 Cys Ile Ser Cys Thr Pro Asp Gly Cys Val Leu Val Gly Trp Glu Ser
 65 70 75 80
 Pro Asp Ser Ser Gly Ala Asp Ile Ser Glu Tyr Arg Leu Glu Trp Gly
 85 90 95
 Glu Asp Glu Glu Ser Leu Glu Leu Ile Tyr His Gly Thr Asp Thr Arg
 100 105 110
 Phe Glu Ile Arg Asp Leu Leu Pro Ala Ala Gln Tyr Cys Cys Arg Leu
 115 120 125
 Gln Ala Phe Asn Gln Ala Gly Ala Gly Pro Tyr Ser Glu Leu Val Leu
 130 135 140
 Cys Gln Thr Pro Ala Ser Ala Pro Asp Pro Val Ser Thr Leu Cys Val
 145 150 155 160
 Leu Glu Glu Glu Pro Leu Asp Ala Tyr Pro Asp Ser Pro Ser Ala Cys
 165 170 175
 Leu Val Leu Asn Trp Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu
 180 185 190
 Ala Tyr Thr Ile Asp Leu Gly Asp Thr Ser Ile Thr Val Gly Asn Thr
 195 200 205
 Thr Met His Val Met Lys Asp Leu Leu Pro Glu Thr Thr Tyr Arg Ile
 210 215 220
 Arg Ile Gln Ala Ile Asn Glu Ile Gly Ala Gly Pro Phe Ser Gln Phe
 225 230 235 240
 Ile Lys Ala Lys Thr Arg Pro Leu Pro Pro Leu Pro Pro Arg Leu Glu
 245 250 255
 Cys Ala Ala Ala Gly Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser
 260 265 270
 Asn Ser Lys Thr His Ala Ala Glu Asp Ile Val Tyr Thr Leu Gln Leu
 275 280 285
 Glu Asp Arg Asn Lys Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His
 290 295 300
 Thr Tyr Lys Val Gln Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg
 305 310 315 320
 Ile Gln Ala Ala Ser Glu Ala Gly Glu Gly Pro Phe Ser Glu Thr Tyr
 325 330 335
 Thr Phe Ser Thr Thr Lys Ser Val Pro Pro Thr Ile Lys Ala Pro Arg
 340 345 350
 Val Thr Gln Leu Glu Gly Asn Ser Cys Glu Ile Leu Trp Glu Thr Val
 355 360 365
 Pro Ser Met Lys Gly Asp Pro Val Asn Tyr Ile Leu Gln Val Leu Val
 370 375 380
 Gly Arg Glu Ser Glu Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr
 385 390 395 400
 Phe Gln Ile Ser Gly Leu Gln Thr Asn Thr Asp Tyr Arg Phe Arg Val
 405 410 415
 Cys Ala Cys Arg Arg Cys Leu Asp Thr Ser Gln Glu Leu Ser Gly Ala

<400>	61					
atcaaacaga	aatgactatt	gaaggccttgc	agcccacagt	ggagtatgtg	gttagtgtct	60
atgctcagaa	tccaagcgga	gagagtcagc	ctctggttca	gactgcagta	accaacattg	120
atcgccctaa	aggactggca	ttcactgatg	tggatgtcga	ttccatcaaa	attgcttggg	180
aaagcccaca	ggggcaagtt	tccaggtaca	gggtgacct	ctcgagccct	gaggatggaa	240
tccatgagct	attcccttga	cctgatgggt	aagaagacac	tgcagagctg	caaggcctca	300
gaccgggttc	tgagtacaca	gtcagtggtg	ttgccttgc	cgatgatag	gagagccagc	360
cctgatttgg	aaccagctcc	acagctattc	ctgcaccaac	tgacttgaag	ttcactcagg	420
tcacacccac	aagcctgagc	gccagtgga	caccacccaa	tgttcagctc	actggatata	480
gagtgcgggt	gacccccaa	gagaagaccg	gaccaatgaa	agaaatcaac	cttgctcctg	540
acagctcatc	cgtggttgta	tcaggactta	tgggtggccac	caaatatgaa	gtgagtgtct	600
atgctcttaa	ggacactttg	acaagcagac	cagctcaggg	tgttgtcacc	actctggaga	660
atgtcagccc	accaagaagg	gctcgtgtga	cagatgctac	tgagaccacc	atcaccatta	720
gctggagaac	caagactgag	acgatcactg	gcttccaagt	tgatgccgtt	ccagccaatg	780
gccagactcc	aatccagaga	accatcaagc	cagatgtcag	aagctacacc	atcacaggtt	840
tacaaccagg	cactgactac	aagatctacc	tgtatacctt	gaatgacaat	gctcggagct	900
cccctgtggt	catcgacgcc	tccactgcc	ttgatgcacc	atccaaacctg	cgtttccctgg	960
ccaccacacc	caattccttg	ctggtatcat	ggcagccgcc	acgtgccagg	attaccggct	1020
acatcatcaa	gtatgagaag	cctgggtctc	ctcccagaga	agtgtccct	cggccccgcc	1080
ctggtgtcac	agaggctact	attactggcc	tggaaaccggg	aaccgaatat	acaatttatg	1140
tcatttcccc	gaagaataat	cagaagagcg	agcccctgat	tggaaaggaaa	aagacagacg	1200
agcttgccta	actggttaacc	cttccacacc	ccaattctta	tggaccagag	atcttggatg	1260
ttccttccac	agttcaaaag	acccttttcg	tcaccacacc	tgggtatgac	actggaaatg	1320
gtattcagct	tcttggcagg	tctggtcagc	tacccagctgt	tgggcaacaa	atgatctttg	1380
aggaacatgg	ttttaggcgg	accacaccgc	ccacaacggc	cacccccata	aggcataggc	1440
caagaccata	ccgcgccaat	gtaggtgagg	aaatccaaat	tggtcacatt	cccagggaag	1500
atgtagacta	tcacctgtac	ccacacggtc	cggggctcaa	tccaaatgcc	tctacaggac	1560
aagaagctct	ctctcagaca	accatctcat	gggccccatt	ccaggacact	tctgagtaca	1620
tcattttcatg	tcatcctgtt	ggcactgatg	aagaacctt	acagttcagg	gttcctggaa	1680
cttctaccag	tgcagactg	acaggcctca	ccagaggtgc	cacctacaac	atcatagtgg	1740
aggcactgaa	agaccactag	aggcataagg	ttcgggaaga	ggttgttacc	gtgggcaact	1800
ctgtcaacga	aggcttgaac	caacctacgg	atgactcgtg	ctttgacccc	tacacagttt	1860
cccattatgc	cgttggagat	gagtgggaac	gaatgtctga	atcaggcttt	aaactgttgt	1920
gccagtgtt	aggctttgga	agtggtcatt	tcagatgtga	ttcatctaga	tggtgccatg	1980
acaatggtgt	gaactacaag	attggagaga	agtgggaccg	tcaggggagaa	aatggccaga	2040
tgatgagctg	cacatgtctt	gggaacggaa	aaggagaatt	caagtgtgac	cctcatgagg	2100
caacgtgtta	cgatgatggg	aagacatacc	acgtaggaga	acagtggcag	aaggaatatc	2160
tccgttgccat	ttgctcctgc	acatgctttg	gaggccagcg	gggtctgggc	tgtgacaact	2220
gcgcgagacc	tgggggtgaa	ccagctccc	aaggcactac	tggccagtcc	tacaaccagt	2280
attctcagag	ataccatcag	agaacaaaca	ctaattgttaa	ttgcccaatt	gagtgttca	2340
tgcctttaga	tgtacaggct	gacagagaag	attcccgaqa	qtaa		2384

<210> 62

<211> 793

<212> PRT

<213> Homo sapiens

<400> 62

Gln	Thr	Glu	Met	Thr	Ile	Glu	Gly	Leu	Gln	Pro	Thr	Val	Glu	Tyr	Val	1	5	10	15
Val	Ser	Val	Tyr	Ala	Gln	Asn	Pro	Ser	Gly	Glu	Ser	Gln	Pro	Leu	Val	20	25	30	
Gln	Thr	Ala	Val	Thr	Asn	Ile	Asp	Arg	Pro	Lys	Gly	Leu	Ala	Phe	Thr	35	40	45	
Asp	Val	Asp	Val	Asp	Ser	Ile	Lys	Ile	Ala	Trp	Glu	Ser	Pro	Gln	Gly	50	55	60	
Gln	Val	Ser	Arg	Tyr	Arg	Val	Thr	Tyr	Ser	Ser	Pro	Glu	Asp	Gly	Ile	65	70	75	80
His	Glu	Leu	Phe	Pro	Ala	Pro	Asp	Gly	Glu	Glu	Asp	Thr	Ala	Glu	Leu	85	90	95	
Gln	Gly	Leu	Arg	Pro	Gly	Ser	Glu	Tyr	Thr	Val	Ser	Val	Val	Ala	Leu	100	105	110	
His	Asp	Asp	Met	Glu	Ser	Gln	Pro	Leu	Ile	Gly	Thr	Gln	Ser	Thr	Ala	115	120	125	
Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	130	135	140	
Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	145	150	155	160
Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	165	170	175	
Leu	Ala	Pro	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	180	185	190	
Thr	Lys	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	195	200	205	
Arg	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	210	215	220	
Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	225	230	235	240
Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	245	250	255	
Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	260	265	270	
Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	275	280	285	
Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile	290	295	300	
Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn	Leu	Arg	Phe	Leu	Ala	305	310	315	320
Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp	Gln	Pro	Pro	Arg	Ala	Arg	325	330	335	
Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu	Lys	Pro	Gly	Ser	Pro	Pro	Arg	340	345	350	
Glu	Val	Val	Pro	Arg	Pro	Arg	Pro	Gly	Val	Thr	Glu	Ala	Thr	Ile	Thr	355	360	365	
Gly	Leu	Glu	Pro	Gly	Thr	Glu	Tyr	Thr	Ile	Tyr	Val	Ile	Ala	Leu	Lys	370	375	380	
Asn	Asn	Gln	Lys	Ser	Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Asp	Glu	385	390	395	400
Leu	Pro	Gln	Leu	Val	Thr	Leu	Pro	His	Pro	Asn	Leu	His	Gly	Pro	Glu	405	410	415	
Ile	Leu	Asp	Val	Pro	Ser	Thr	Val	Gln	Lys	Thr	Pro	Phe	Val	Thr	His	420	425	430	

Pro Gly Tyr Asp Thr Gly Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly
 435 440 445
 Gln Gln Pro Ser Val Gly Gln Gln Met Ile Phe Glu Glu His Gly Phe
 450 455 460
 Arg Arg Thr Thr Pro Pro Thr Thr Ala Thr Pro Ile Arg His Arg Pro
 465 470 475 480
 Arg Pro Tyr Pro Pro Asn Val Gly Glu Glu Ile Gln Ile Gly His Ile
 485 490 495
 Pro Arg Glu Asp Val Asp Tyr His Leu Tyr Pro His Gly Pro Gly Leu
 500 505 510
 Asn Pro Asn Ala Ser Thr Gly Gln Glu Ala Leu Ser Gln Thr Thr Ile
 515 520 525
 Ser Trp Ala Pro Phe Gln Asp Thr Ser Glu Tyr Ile Ile Ser Cys His
 530 535 540
 Pro Val Gly Thr Asp Glu Glu Pro Leu Gln Phe Arg Val Pro Gly Thr
 545 550 555 560
 Ser Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn
 565 570 575
 Ile Ile Val Glu Ala Leu Lys Asp Gln Gln Arg His Lys Val Arg Glu
 580 585 590
 Glu Val Val Thr Val Gly Asn Ser Val Asn Glu Gly Leu Asn Gln Pro
 595 600 605
 Thr Asp Asp Ser Cys Phe Asp Pro Tyr Thr Val Ser His Tyr Ala Val
 610 615 620
 Gly Asp Glu Trp Glu Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys
 625 630 635 640
 Gln Cys Leu Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg
 645 650 655
 Trp Cys His Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp
 660 665 670
 Arg Gln Gly Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn
 675 680 685
 Gly Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr Asp
 690 695 700
 Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu
 705 710 715 720
 Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg
 725 730 735
 Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr
 740 745 750
 Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr
 755 760 765
 Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu Asp Val
 770 775 780
 Gln Ala Asp Arg Glu Asp Ser Arg Glu
 785 790

<210> 63

<211> 7680

<212> DNA

<213> Homo sapiens

<400> 63

gaagagcaag aggcaggctc agcaaattggt tcagccccag tccccgggtgg ctgtcagtca 60
 aagcaagccc gggtgttatg acaatggaaa acactatcag ataaatcaac agtgggagcg 120
 gacctaccta ggtaattgtg ttggtttgtac ttgttatgga ggaagccgag gttttaactg 180
 cgaaagtaaa cctgaagctg aagagacttg ctttgacaag tacactggga acacttaccg 240
 agtgggtgac acttatgagc gtcctaaaga ctccatgatc tgggactgta cctgcacg 300

ggctgggcca	gggagaataa	gctgtaccat	cgcaaaccgc	tgccatgaag	ggggtcagtc	360
ctacaagatt	ggtgacacct	ggaggagacc	acatgagact	ggtgggttaca	tggttagagt	420
tgtgtgtctt	ggtaatggaa	aaggagaatg	gacctgcaag	cccatagctg	agaagtgttt	480
tgatcatgct	gctgggactt	cctatgtggt	cggagaaacg	tgggagaagc	cctaccaagg	540
ctggatgatg	gtagattgta	cttgccctggg	agaaggcagc	ggacgcatca	cttgcaacttc	600
tagaaataga	tgcaacgatc	aggacacaag	gacatccctat	agaattggag	acacctggag	660
caagaaggat	aatcgaggaa	acctgctcca	gtgcatctgc	acaggcaacg	gccgaggaga	720
gtggaagtgt	gagaggcaca	cctctgtgca	gaccacatcg	agcggatctg	gccccttcac	780
cgatgttcgt	gcagctgttt	accaaccgca	gcctcacccc	cagcctcctc	cctatggcca	840
ctgtgtcaca	gacagtgggtg	tgggtctactc	tgtgggggatg	cagtgggttga	agacacaagg	900
aaataagcaa	atgcttttgc	cgtgcctggg	caacggagtc	agctgccaag	agacagctgt	960
aaccagact	tacggtggca	acttaaatgg	agagccatgt	gtcttaccat	tcacctacaa	1020
tggcaggacg	ttctactcct	gcaccacgga	aggcgacacg	gacggacatc	tttgggtgcag	1080
cacaacttcg	aattatgagc	aggaccagaa	atactctttc	tgacagagcc	acaactgtttt	1140
ggttcagact	caaggaggaa	attccaatgg	tgccctgtgc	cacttccctc	tcctatacaa	1200
caaccacaat	tacactgatt	gcactttctga	gggcagaaga	gacaacatga	agtgggtgtg	1260
gaccacacag	aactatgatg	ccgaccagaa	gtttgggttc	tgccccatgg	ctgcccacga	1320
ggaaatctgc	acaaccaatg	aaggggtcat	gtaccgcatt	ggagatcagt	gggataagca	1380
gcatgacatg	ggtcacatga	tgaggtgcac	gtgtgttggg	aatgggtcgtg	gggaatggac	1440
atgcatttgc	tactcgcaac	ttcgagatca	gtgcattgtt	gatgacatca	cttacaatgt	1500
gaacgacaca	ttccacaagc	gtcatgaaga	ggggcacatg	ctgaactgta	catgcttcgg	1560
tcagggctcg	ggcaggtgga	agtgtgatcc	cgtcgacca	tgccaggatt	cagagactgg	1620
gacgttttat	caaattggag	attcatggga	gaagtatgtg	catgggtgtca	gataaccagt	1680
ctactgctat	ggcctgtggc	ttggggagtg	gcattgccaa	cctttacaga	cctatccaag	1740
ctcaagtgg	cctgtcgaag	tatttatcac	tgagactccg	agtcagccca	actcccaccc	1800
catccagtgg	aatgcaccac	agccatctca	catttccaag	tacattctca	ggtggagacc	1860
taaaaattct	gtaggccgtt	ggaaggaagc	taccatacca	ggccacttaa	actcctacac	1920
catcaaagtc	ctgaagcctg	gtgtgggtata	cgagggccag	ctcatcagca	tccagcagta	1980
cggccaccaa	gaagtgcac	gctttgactt	caccaccacc	agcaccagca	cacctgtgac	2040
cagcaacacc	gtgacaggag	agacgactcc	cttttctcct	cttgtggcca	cttctgatac	2100
tgtgaccgaa	atcacagcca	gtagctttgt	ggtctcctgg	gtctcagctt	ccgacacccg	2160
gtcgggattc	cgggtggaat	atgagctgag	tgaggaggga	gatgagccac	agtacctgga	2220
tcttccaagc	acagccactt	ctgtgaacat	ccctgacctg	cttcctggcc	gaaaatacat	2280
tgtaaatgtc	tatcagatat	ctgaggatgg	ggagcagagt	ttgatcctgt	ctacttcaca	2340
aacaacagcg	cctgatgccc	ctcctgaccc	gactgtggac	caagttgatg	acacctcaat	2400
tgttgttcgc	tggagcagac	cccaggctcc	catcacaggg	tacagaatag	tctatttcgcc	2460
atcagtagaa	ggtagcagca	cagaactcaa	ccttcctgaa	actgcaaact	ccgtcacccct	2520
cagtgaactt	caacctgggtg	ttcagtataa	catcactatc	tatgctgtgg	aagaaaaatca	2580
agaaagtaca	cctgtttgtca	ttcaacaaga	aaccactggc	accccacgct	cagatacagt	2640
gccctctccc	agggacctgc	agtttgtgga	agtgacagac	gtgaagggtca	ccatcatgtg	2700
gacaccgcct	gagagtgcag	tgaccggcta	ccgtgtggat	gtgatccccg	tcaacctgcc	2760
tggcgagcac	gggcagaggc	tgcccatcag	caggaaacac	tttgacagaag	tcaccgggct	2820
gtcccctggg	gtcacctatt	acttcaaagt	ctttgcagt	agccatggga	gggagagcaa	2880
gcctctgact	gctcaacaga	caaccaaact	ggatgctccc	actaacctcc	agtttgtcaa	2940
tgaactgat	tctactgtcc	tgggtgagatg	gactccacct	cgggcccaga	taacaggata	3000
ccgactgacc	gtgggcctta	cccgaagagg	ccagcccagg	cagtacaatg	tgggtccctc	3060
tgtctccaag	taccccttga	ggaatctgca	gcctgcattc	gagtacaccg	tatccctcgt	3120
ggccataaag	ggcaaccaag	agagccccaa	agccactgga	gtctttacca	cactgcagcc	3180
tgggagctct	attccacctt	acaacaccga	ggtgactgag	accaccatcg	tgatcacatg	3240
gacgcctgct	ccaagaattg	gttttaagct	gggtgtacga	ccaagccagg	gaggagaggc	3300
accacgagaa	gtgacttcag	actcaggaag	catcgttgtg	tccggcttga	ctccaggagt	3360
agaatacgtc	tacaccatcc	aagtccctgag	agatggacag	gaaagagatg	cgccaattgt	3420
aaacaaagt	gtgacaccat	tgtctccacc	aacaaaactg	catctggagg	caaaccctga	3480
acttgagtg	ctcacagtct	cctgggagag	gagcaccacc	ccagacatta	ctgggttatag	3540
aattaccaca	acccctacaa	acggccagca	gggaaattct	ttggaagaag	tggtccatgc	3600
tgatcagagc	tcctgcactt	ttgataacct	gagtcocggc	ctggagtaca	atgtcagtgt	3660
ttactactgtc	aaggatgaca	aggaaagtgt	ccctatctct	gataccatca	tcccagctgt	3720
tcctcctccc	actgacctgc	gattcaccaa	cattgggtcca	gacaccatgc	gtgtcacctg	3780
ggctccaccc	ccatccattg	atttaaccaa	cttcctgggtg	cgttactcac	ctgtgaaaaa	3840

tgaggaagat	gttgacagagt	tgtcaatttc	tccttcagac	aatgcagtg	tcttaacaaa	3900
tctcctgcct	ggtacagaat	atgtagttag	tgtctccagt	gtctacgaac	aacatgagag	3960
cacacctctt	agaggaagac	agaaaacagg	tcttgattcc	ccaactggca	ttgacttttc	4020
tgatattact	gccaaactctt	ttactgtgca	ctggattgct	cctcgagcca	ccatcactgg	4080
ctacaggatc	cgccatcatc	ccgagcactt	cagtgaggaga	cctcgagaag	atcgggtgcc	4140
ccactctcgg	aattccatca	ccctcaccaa	cctcactcca	ggcacagagt	atgtggtcag	4200
catcggtgct	cttaatggca	gagaggaaag	tcccttattg	attggccaac	aatcaacagt	4260
ttctgatgtt	ccgaggggacc	tggaagttgt	tgctgcgacc	cccaccagcc	tactgatcag	4320
ctgggatgct	cctgctgtca	cagttagata	ttacaggatc	acttacggag	aaacaggagg	4380
aaatagccct	gtccaggagt	tcactgtgcc	tgggagcaag	tctacagcta	ccatcagcgg	4440
ccttaaacct	ggagttgatt	ataccatcac	tgtgtatgct	gtcactggcc	gtggagacag	4500
ccccgcaagc	agcaagccaa	tttccattaa	ttaccgaaca	gaaattgaca	aaccatccca	4560
gatgcaagt	accgatgttc	aggacaacag	cattagtgtc	aagtggctgc	cttcaagtcc	4620
ccctgttact	ggttacagag	taaccaccac	tccccaaaat	ggaccaggac	caacaaaaac	4680
taaaactgca	ggtccagatc	aaacagaaat	gactattgaa	ggcttgcagc	ccacagtggg	4740
gtatgtggtt	agtgtctatg	ctcagaatcc	aagcggagag	agtcagcctc	tgggttcagac	4800
tgcagtaaac	aacattgatc	gccctaaagg	actggcattc	actgatgtgg	atgtcgattc	4860
catcaaaaat	gcttgggaaa	gcccacaggg	gcaagtttcc	aggtacaggg	tgacctactc	4920
gagccctgag	gatggaatcc	atgagctatt	ccctgcacct	gatggtgaag	aagacactgc	4980
agagctgcaa	ggcctcagac	cgggttctga	gtacacagtc	agtgtggttg	ccttgccacga	5040
tgatatggag	agccagcccc	tgattggaac	ccagtcacac	gctattctctg	caccaactga	5100
cctgaagtcc	actcaggtca	caccacaag	cctgagcgcc	cagtggacac	cacccaatgt	5160
tcagctcact	ggatatcgag	tgcggttgac	ccccaaagg	aagaccggac	caatgaaaga	5220
aatcaacctt	gctcctgaca	gctcatccgt	ggttgtatca	ggacttatgg	tggccaccaa	5280
atatgaagt	agtgtctatg	ctcttaagga	cactttgaca	agcagaccag	ctcagggtgt	5340
tgtcaccact	ctggagaatg	tcagcccacc	aagaagggct	cgtgtgacag	atgctactga	5400
gaccaccatc	accattagct	ggagaaccaa	gactgagacg	atcactggct	tccaagttga	5460
tgcgcttcca	gccaatggcc	agactccaat	ccagagaacc	atcaagccag	atgtcagaag	5520
ctacaccatc	acaggtttac	aaccaggcac	tgactacaag	atctacctgt	acacctgaa	5580
tgacaatgct	cggagctccc	ctgtggtcat	cgacgcctcc	actgccattg	atgcaaccatc	5640
caacctgcgt	ttcctggcca	ccacacccaa	ttccttgctg	gtatcatggc	agccgccacg	5700
tgccaggatt	accggctaca	tcatacaagta	tgagaagcct	gggtctcctc	ccagagaagt	5760
ggtccctcgg	ccccgcctcg	gtgtcacaga	ggctactatt	actggcctgg	aaccgggaac	5820
cgaatatata	atttatgtca	ttgccctgaa	gaataatcag	aagagcgagc	ccctgattgg	5880
aaggaaaaag	acagacgagc	ttccccaaact	ggtaaccctt	ccacacccca	atcttcatgg	5940
accagagatc	ttggatgttc	cttccacagt	tcaaaagacc	cctttctgtca	cccaccctgg	6000
glatgacact	ggaaatggta	ttcagcttcc	tggcacttct	ggtcagcaac	ccagtgttgg	6060
gcaacaaatg	atctttgagg	aacatgggtt	tgagcggacc	acacgcgcca	caacggccac	6120
cccataaagg	cataggccaa	gaccataccc	gccgaatgta	ggacaagaag	ctctctctca	6180
gacaaccatc	tcattgggccc	cattccagga	cacttctgag	tacatcattt	catgtcatcc	6240
tgttggcact	gatgaagaac	ccttacagtt	cagggttcc	ggaacttcta	ccagtgccac	6300
tctgacaggc	ctcaccagag	gtgccaccta	caacatcata	gtggaggcac	tgaaagacca	6360
gcagaggcat	aaggttcggg	aagaggttgt	taccgtgggc	aactctgtca	acgaaggctt	6420
gaaccaacct	acggatgact	cgtgctttga	cccctacaca	gtttcccat	atgccgttgg	6480
agatgagtgg	gaacgaatgt	ctgaatcagg	ctttaaactg	ttgtgccagt	gcttaggctt	6540
tggaaagtgg	catttccagat	gtgattcatc	tagatggtgc	catgacaatg	gtgtgaacta	6600
caagattgga	gagaagtggg	accgtcagg	agaaaatggc	cagatgatga	gctgcacatg	6660
tcttggaagc	ggaaaaggag	aattcaagt	tgacctcat	gaggcaacgt	gttacgatga	6720
tgggaagaca	taccacgtag	gagaacagt	gcagaaggaa	tatctcgggtg	ccatttgcctc	6780
ctgcacatgc	tttgagggcc	agcggggctg	gcgctgtgac	aactgccgca	gacctggggg	6840
tgaaccaggt	cccgaaggca	ctactggcca	gtcctacaac	cagtattctc	agagatacca	6900
tcagagaaca	aacactaatg	ttaattgccc	aattgagtgc	ttcatgcctt	tagatgtaca	6960
ggctgacaga	gaagattccc	gagagtaaat	catctttcca	atccagagga	acaagcatgt	7020
ctctcttgcca	agatccatct	aaactggagt	gatgttagca	gaccagcctt	agagttcttc	7080
tttctttctt	agccccctt	ctctggagga	agttctccag	cttcagctca	actcacagct	7140
tctccaagca	tcaccctggg	agtttctctg	gggttttctc	ataaatgagg	gctgcacatt	7200
gcctgttctg	cttcgaagta	ttcaataaccg	ctcagtattt	taaatgaagt	gattctaaaga	7260
tttggtttgg	gatcaatagg	aaagcatatg	cagccaacca	agatgcaaat	gttttgaaat	7320
gatatgacca	aaatttttaag	taggaaagtc	acccaaacac	ttctgctttc	acttaagtgt	7380

```

ctggcccgca atactgtagg aacaagcatg atcttggttac tgtgatattt taaatatcca 7440
cagtactcac tttttccaaa tgatcctagt aattgcctag aaatatcttt ctcttacctg 7500
ttatttatca atttttccca gtatttttat acggaaaaaa ttgtattgaa aacacttagt 7560
atgcagttga taagaggaat ttggtataat tatggtgggt gattattttt tatactgtat 7620
gtgccaaagc ttactactg tggaagaca actgttttaa taaaagattt acattccaca 7680

```

<210> 64

<211> 2328

<212> PRT

<213> Homo sapiens

<400> 64

```

Lys Ser Lys Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val
 1          5          10          15
Ala Val Ser Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr
          20          25          30
Gln Ile Asn Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val
          35          40          45
Cys Thr Cys Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro
 50          55          60
Glu Ala Glu Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg
65          70          75          80
Val Gly Asp Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys
          85          90          95
Thr Cys Ile Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn
          100          105          110
Arg Cys His Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg
          115          120          125
Arg Pro His Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly
          130          135          140
Asn Gly Lys Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe
          145          150          155          160
Asp His Ala Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys
          165          170          175
Pro Tyr Gln Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly
          180          185          190
Ser Gly Arg Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp
          195          200          205
Thr Arg Thr Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn
          210          215          220
Arg Gly Asn Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu
          225          230          235          240
Trp Lys Cys Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser
          245          250          255
Gly Pro Phe Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His
          260          265          270
Pro Gln Pro Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val
          275          280          285
Tyr Ser Val Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met
          290          295          300
Leu Cys Thr Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val
          305          310          315          320
Thr Gln Thr Tyr Gly Gly Asn Leu Asn Gly Glu Pro Cys Val Leu Pro
          325          330          335
Phe Thr Tyr Asn Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg
          340          345          350
Gln Asp Gly His Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp
          355          360          365

```


Gln	Lys	Tyr	Ser	Phe	Cys	Thr	Asp	His	Thr	Val	Leu	Val	Gln	Thr	Gln
370						375					380				
Gly	Gly	Asn	Ser	Asn	Gly	Ala	Leu	Cys	His	Phe	Pro	Phe	Leu	Tyr	Asn
385					390					395					400
Asn	His	Asn	Tyr	Thr	Asp	Cys	Thr	Ser	Glu	Gly	Arg	Arg	Asp	Asn	Met
				405					410					415	
Lys	Trp	Cys	Gly	Thr	Thr	Gln	Asn	Tyr	Asp	Ala	Asp	Gln	Lys	Phe	Gly
			420						425				430		
Phe	Cys	Pro	Met	Ala	Ala	His	Glu	Glu	Ile	Cys	Thr	Thr	Asn	Glu	Gly
			435				440						445		
Val	Met	Tyr	Arg	Ile	Gly	Asp	Gln	Trp	Asp	Lys	Gln	His	Asp	Met	Gly
	450					455					460				
His	Met	Met	Arg	Cys	Thr	Cys	Val	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Thr
465					470					475					480
Cys	Ile	Ala	Tyr	Ser	Gln	Leu	Arg	Asp	Gln	Cys	Ile	Val	Asp	Asp	Ile
				485					490					495	
Thr	Tyr	Asn	Val	Asn	Asp	Thr	Phe	His	Lys	Arg	His	Glu	Glu	Gly	His
			500					505					510		
Met	Leu	Asn	Cys	Thr	Cys	Phe	Gly	Gln	Gly	Arg	Gly	Arg	Trp	Lys	Cys
		515					520						525		
Asp	Pro	Val	Asp	Gln	Cys	Gln	Asp	Ser	Glu	Thr	Gly	Thr	Phe	Tyr	Gln
	530					535					540				
Ile	Gly	Asp	Ser	Trp	Glu	Lys	Tyr	Val	His	Gly	Val	Arg	Tyr	Gln	Cys
545					550					555					560
Tyr	Cys	Tyr	Gly	Arg	Gly	Ile	Gly	Glu	Trp	His	Cys	Gln	Pro	Leu	Gln
				565					570					575	
Thr	Tyr	Pro	Ser	Ser	Gly	Pro	Val	Glu	Val	Phe	Ile	Thr	Glu	Thr	
			580				585						590		
Pro	Ser	Gln	Pro	Asn	Ser	His	Pro	Ile	Gln	Trp	Asn	Ala	Pro	Gln	Pro
		595					600					605			
Ser	His	Ile	Ser	Lys	Tyr	Ile	Leu	Arg	Trp	Arg	Pro	Lys	Asn	Ser	Val
	610					615					620				
Gly	Arg	Trp	Lys	Glu	Ala	Thr	Ile	Pro	Gly	His	Leu	Asn	Ser	Tyr	Thr
625					630					635					640
Ile	Lys	Gly	Leu	Lys	Pro	Gly	Val	Val	Tyr	Glu	Gly	Gln	Leu	Ile	Ser
				645						650				655	
Ile	Gln	Gln	Tyr	Gly	His	Gln	Glu	Val	Thr	Arg	Phe	Asp	Phe	Thr	Thr
			660					665					670		
Thr	Ser	Thr	Ser	Thr	Pro	Val	Thr	Ser	Asn	Thr	Val	Thr	Gly	Glu	Thr
		675				680						685			
Thr	Pro	Phe	Ser	Pro	Leu	Val	Ala	Thr	Ser	Glu	Ser	Val	Thr	Glu	Ile
	690					695					700				
Thr	Ala	Ser	Ser	Phe	Val	Val	Ser	Trp	Val	Ser	Ala	Ser	Asp	Thr	Val
705					710					715					720
Ser	Gly	Phe	Arg	Val	Glu	Tyr	Glu	Leu	Ser	Glu	Glu	Gly	Asp	Glu	Pro
				725					730					735	
Gln	Tyr	Leu	Asp	Leu	Pro	Ser	Thr	Ala	Thr	Ser	Val	Asn	Ile	Pro	Asp
			740					745					750		
Leu	Leu	Pro	Gly	Arg	Lys	Tyr	Ile	Val	Asn	Val	Tyr	Gln	Ile	Ser	Glu
		755					760					765			
Asp	Gly	Glu	Gln	Ser	Leu	Ile	Leu	Ser	Thr	Ser	Gln	Thr	Thr	Ala	Pro
	770					775					780				
Asp	Ala	Pro	Pro	Asp	Pro	Thr	Val	Asp	Gln	Val	Asp	Asp	Thr	Ser	Ile
785					790					795					800
Val	Val	Arg	Trp	Ser	Arg	Pro	Gln	Ala	Pro	Ile	Thr	Gly	Tyr	Arg	Ile
				805					810					815	
Val	Tyr	Ser	Pro	Ser	Val	Glu	Gly	Ser	Ser	Thr	Glu	Leu	Asn	Leu	Pro
			820					825					830		
Glu	Thr	Ala	Asn	Ser	Val	Thr	Leu	Ser	Asp	Leu	Gln	Pro	Gly	Val	Gln

835					840					845					
Tyr	Asn	Ile	Thr	Ile	Tyr	Ala	Val	Glu	Glu	Asn	Gln	Glu	Ser	Thr	Pro
	850					855					860				
Val	Val	Ile	Gln	Gln	Glu	Thr	Thr	Gly	Thr	Pro	Arg	Ser	Asp	Thr	Val
865					870					875					880
Pro	Ser	Pro	Arg	Asp	Leu	Gln	Phe	Val	Glu	Val	Thr	Asp	Val	Lys	Val
				885					890					895	
Thr	Ile	Met	Trp	Thr	Pro	Pro	Glu	Ser	Ala	Val	Thr	Gly	Tyr	Arg	Val
			900					905					910		
Asp	Val	Ile	Pro	Val	Asn	Leu	Pro	Gly	Glu	His	Gly	Gln	Arg	Leu	Pro
		915					920					925			
Ile	Ser	Arg	Asn	Thr	Phe	Ala	Glu	Val	Thr	Gly	Leu	Ser	Pro	Gly	Val
	930					935					940				
Thr	Tyr	Tyr	Phe	Lys	Val	Phe	Ala	Val	Ser	His	Gly	Arg	Glu	Ser	Lys
945					950					955					960
Pro	Leu	Thr	Ala	Gln	Gln	Thr	Thr	Lys	Leu	Asp	Ala	Pro	Thr	Asn	Leu
				965					970					975	
Gln	Phe	Val	Asn	Glu	Thr	Asp	Ser	Thr	Val	Leu	Val	Arg	Trp	Thr	Pro
			980					985				990			
Pro	Arg	Ala	Gln	Ile	Thr	Gly	Tyr	Arg	Leu	Thr	Val	Gly	Leu	Thr	Arg
		995					1000					1005			
Arg	Gly	Gln	Pro	Arg	Gln	Tyr	Asn	Val	Gly	Pro	Ser	Val	Ser	Lys	Tyr
	1010					1015					1020				
Pro	Leu	Arg	Asn	Leu	Gln	Pro	Ala	Ser	Glu	Tyr	Thr	Val	Ser	Leu	Val
1025					1030					1035					1040
Ala	Ile	Lys	Gly	Asn	Gln	Glu	Ser	Pro	Lys	Ala	Thr	Gly	Val	Phe	Thr
				1045					1050					1055	
Thr	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Pro	Pro	Tyr	Asn	Thr	Glu	Val	Thr
			1060					1065					1070		
Glu	Thr	Thr	Ile	Val	Ile	Thr	Trp	Thr	Pro	Ala	Pro	Arg	Ile	Gly	Phe
		1075					1080					1085			
Lys	Leu	Gly	Val	Arg	Pro	Ser	Gln	Gly	Gly	Glu	Ala	Pro	Arg	Glu	Val
	1090					1095					1100				
Thr	Ser	Asp	Ser	Gly	Ser	Ile	Val	Val	Ser	Gly	Leu	Thr	Pro	Gly	Val
1105					1110					1115					1120
Glu	Tyr	Val	Tyr	Thr	Ile	Gln	Val	Leu	Arg	Asp	Gly	Gln	Glu	Arg	Asp
				1125					1130					1135	
Ala	Pro	Ile	Val	Asn	Lys	Val	Val	Thr	Pro	Leu	Ser	Pro	Pro	Thr	Asn
			1140					1145				1150			
Leu	His	Leu	Glu	Ala	Asn	Pro	Asp	Thr	Gly	Val	Leu	Thr	Val	Ser	Trp
		1155					1160					1165			
Glu	Arg	Ser	Thr	Thr	Pro	Asp	Ile	Thr	Gly	Tyr	Arg	Ile	Thr	Thr	Thr
	1170					1175					1180				
Pro	Thr	Asn	Gly	Gln	Gln	Gly	Asn	Ser	Leu	Glu	Glu	Val	Val	His	Ala
1185					1190					1195					1200
Asp	Gln	Ser	Ser	Cys	Thr	Phe	Asp	Asn	Leu	Ser	Pro	Gly	Leu	Glu	Tyr
				1205					1210					1215	
Asn	Val	Ser	Val	Tyr	Thr	Val	Lys	Asp	Asp	Lys	Glu	Ser	Val	Pro	Ile
			1220					1225					1230		
Ser	Asp	Thr	Ile	Ile	Pro	Ala	Val	Pro	Pro	Pro	Thr	Asp	Leu	Arg	Phe
		1235					1240					1245			
Thr	Asn	Ile	Gly	Pro	Asp	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro
	1250					1255					1260				
Ser	Ile	Asp	Leu	Thr	Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn
1265					1270					1275					1280
Glu	Glu	Asp	Val	Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val
			1285					1290						1295	
Val	Leu	Thr	Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser
			1300					1305					1310		

Ser Val Tyr Glu Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys
 1315 1320 1325
 Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala
 1330 1335 1340
 Asn Ser Phe Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly
 1345 1350 1355 1360
 Tyr Arg Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu
 1365 1370 1375
 Asp Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr
 1380 1385 1390
 Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg Glu
 1395 1400 1405
 Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro
 1410 1415 1420
 Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser
 1425 1430 1435 1440
 Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly
 1445 1450 1455
 Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser
 1460 1465 1470
 Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr
 1475 1480 1485
 Ile Thr Val Tyr Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser
 1490 1495 1500
 Lys Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln
 1505 1510 1515 1520
 Met Gln Val Thr Asp Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu
 1525 1530 1535
 Pro Ser Ser Ser Pro Val Thr Gly Tyr Arg Val Thr Thr Thr Pro Lys
 1540 1545 1550
 Asn Gly Pro Gly Pro Thr Lys Thr Lys Thr Ala Gly Pro Asp Gln Thr
 1555 1560 1565
 Glu Met Thr Ile Glu Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser
 1570 1575 1580
 Val Tyr Ala Gln Asn Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr
 1585 1590 1595 1600
 Ala Val Thr Asn Ile Asp Arg Pro Lys Gly Leu Ala Phe Thr Asp Val
 1605 1610 1615
 Asp Val Asp Ser Ile Lys Ile Ala Trp Glu Ser Pro Gln Gly Gln Val
 1620 1625 1630
 Ser Arg Tyr Arg Val Thr Tyr Ser Ser Pro Glu Asp Gly Ile His Glu
 1635 1640 1645
 Leu Phe Pro Ala Pro Asp Gly Glu Glu Asp Thr Ala Glu Leu Gln Gly
 1650 1655 1660
 Leu Arg Pro Gly Ser Glu Tyr Thr Val Ser Val Val Ala Leu His Asp
 1665 1670 1675 1680
 Asp Met Glu Ser Gln Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro
 1685 1690 1695
 Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser
 1700 1705 1710
 Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg
 1715 1720 1725
 Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala
 1730 1735 1740
 Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys
 1745 1750 1755 1760
 Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro
 1765 1770 1775
 Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg

1780	1785	1790
Ala Arg Val Thr Asp	Ala Thr Glu Thr Thr Ile Thr	Ile Ser Trp Arg
1795	1800	1805
Thr Lys Thr Glu Thr	Ile Thr Gly Phe Gln Val Asp	Ala Val Pro Ala
1810	1815	1820
Asn Gly Gln Thr Pro	Ile Gln Arg Thr Ile Lys Pro	Asp Val Arg Ser
1825	1830	1835
Tyr Thr Ile Thr Gly	Leu Gln Pro Gly Thr Asp Tyr	Lys Ile Tyr Leu
1845	1850	1855
Tyr Thr Leu Asn Asp	Asn Ala Arg Ser Ser Pro	Val Val Ile Asp Ala
1860	1865	1870
Ser Thr Ala Ile Asp	Ala Pro Ser Asn Leu Arg	Phe Leu Ala Thr Thr
1875	1880	1885
Pro Asn Ser Leu Leu	Val Ser Trp Gln Pro Pro	Arg Ala Arg Ile Thr
1890	1895	1900
Gly Tyr Ile Ile Lys	Tyr Glu Lys Pro Gly Ser	Pro Pro Arg Glu Val
1905	1910	1915
Val Pro Arg Pro Arg	Pro Gly Val Thr Glu Ala Thr	Ile Thr Gly Leu
1925	1930	1935
Glu Pro Gly Thr Glu	Tyr Thr Ile Tyr Val Ile Ala	Leu Lys Asn Asn
1940	1945	1950
Gln Lys Ser Glu Pro	Leu Ile Gly Arg Lys Lys Thr	Asp Glu Leu Pro
1955	1960	1965
Gln Leu Val Thr Leu	Pro His Pro Asn Leu His	Gly Pro Glu Ile Leu
1970	1975	1980
Asp Val Pro Ser Thr	Val Gln Lys Thr Pro Phe	Val Thr His Pro Gly
1985	1990	1995
Tyr Asp Thr Gly Asn	Gly Ile Gln Leu Pro Gly	Thr Ser Gly Gln Gln
2005	2010	2015
Pro Ser Val Gly Gln	Gln Met Ile Phe Glu Glu His	Gly Phe Arg Arg
2020	2025	2030
Thr Thr Pro Pro Thr	Thr Thr Ala Thr Pro Ile Arg	His Arg Pro Arg Pro
2035	2040	2045
Tyr Pro Pro Asn Val	Gly Gln Glu Ala Leu Ser	Gln Thr Thr Ile Ser
2050	2055	2060
Trp Ala Pro Phe Gln	Asp Thr Ser Glu Tyr Ile Ile	Ser Cys His Pro
2065	2070	2075
Val Gly Thr Asp Glu	Pro Leu Gln Phe Arg Val Pro	Gly Thr Ser
2085	2090	2095
Thr Ser Ala Thr Leu	Thr Gly Leu Thr Arg Gly Ala Thr	Tyr Asn Ile
2100	2105	2110
Ile Val Glu Ala Leu	Lys Asp Gln Gln Arg His Lys	Val Arg Glu Glu
2115	2120	2125
Val Val Thr Val Gly	Asn Ser Val Asn Glu Gly Leu	Asn Gln Pro Thr
2130	2135	2140
Asp Asp Ser Cys Phe	Asp Pro Tyr Thr Val Ser	His Tyr Ala Val Gly
2145	2150	2155
Asp Glu Trp Glu Arg	Met Ser Glu Ser Gly Phe Lys	Leu Leu Cys Gln
2165	2170	2175
Cys Leu Gly Phe Gly	Ser Gly His Phe Arg Cys Asp	Ser Ser Arg Trp
2180	2185	2190
Cys His Asp Asn Gly	Val Asn Tyr Lys Ile Gly Glu	Lys Trp Asp Arg
2195	2200	2205
Gln Gly Glu Asn Gly	Gln Met Met Ser Cys Thr Cys	Leu Gly Asn Gly
2210	2215	2220
Lys Gly Glu Phe Lys	Cys Asp Pro His Glu Ala Thr	Cys Tyr Asp Asp
2225	2230	2235
Gly Lys Thr Tyr His	Val Gly Glu Gln Trp Gln	Lys Glu Tyr Leu Gly
2245	2250	2255

Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys
 2260 2265 2270
 Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr
 2275 2280 2285
 Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn
 2290 2295 2300
 Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln
 2305 2310 2315 2320
 Ala Asp Arg Glu Asp Ser Arg Glu
 2325

<210> 65
 <211> 1844
 <212> DNA
 <213> Homo sapiens

<400> 65
 cgcgcggggg cgaggagggcg cgcgcagggg agggaccgag agacgcgcgcg acttttttaga 60
 gggagggatc ggggtggacaa ctgggtccgc ggcgctcgca gagccggaaa gaagtgcgtg 120
 aagggaacgct cgggggacgc tgttcctgag gtgtcgccgc ctccctgtcc tcgccctccg 180
 cggtggggga gaaaccacag agcgaagccc agagcccgcg gcgcggccgg cggaacgaacg 240
 agcgcgcagc agccgggtgc cgcccgcggc gagggcgggg gaagaaaaaac accctgtttc 300
 ctctccggcc cccaccgcgg atcatgtacc aggattatcc cggaacttt gacacctcgt 360
 cccggggcag cagcggctct cctgcgcacg ccgagtccta ctccagcggc ggcggcgggc 420
 agcagaaatt ccgggtagat atgcctggct caggcagtg c attcatcccc accatcaacg 480
 ccatcacgac cagccaggac ctgcagtga tggtgcagcc cacagtgate acctccatgt 540
 ccaaccata cctcgcctcg caccctaca gcccctgccc gggcctggcc tctgtccctg 600
 gacacatggc cctcccaaga cctggcgtga tcaagaccat tggcaccacc gtgggcgcga 660
 ggaggagaga tgagcagctg tctcctgaag aggaggagaa gcgtcgcatc cggcgggaga 720
 ggaacaagct ggctgcagcc aagtgcggga accgacgcgc ggagctgaca gagaagctgc 780
 aggcgagac agaggagctg gaggaggaga agtcaggcct gcagaaggag attgctgagc 840
 tgcagaagga gaaggagaag ctggagttca tgttggtggc tcacggccca gtgtgcaaga 900
 ttagccccga ggagcgccga tcgccccag cccctgggct gcagcccatg cgcagtgggg 960
 gtggctcggg gggcgctgta gtggtgaaac aggagcccct ggaagaggac agcccctcgt 1020
 cctcgtcggc ggggctggac aaggcccagc gctctgtcat caagcccatc agcattgctg 1080
 ggggcttcta cggtgaggag cccctgcaca ccccatcgt ggtgacctcc acacctgctg 1140
 tcaactccgg cacctcgaac ctctgttcca cctatcctag cgtcctggag caggagtcac 1200
 cgcacatctc ctccgaatcc tgctccaagg ctccaccgag aagcagtagc agcggggacc 1260
 aatcatcaga ctcttgaac tccccactc tgctggctct gtaaccagc gcacctccct 1320
 cccagctcc ggaggggggtc ctctcgtc ctcttcca gggaccagca cttcaagcg 1380
 ctccagggcc gtgagggcaa gagggggacc tgccaccagg gagcttcctg gctctggggg 1440
 acccaggtgg gacttagcag tgagtattgg aagacttggg ttgatctctt agaagccatg 1500
 ggacctctc cctcattcat cttgcaagca aatcccattt cttgaaaagc cttggagaac 1560
 tcggtttggg agacttggac atctctctgg cttctgaaga gcctgaagct ggcctggacc 1620
 attcctgtcc ctttgttacc atactgtctc tggagtgatg gtgtccttcc ctgccccacc 1680
 acgcatgctc agtgccctttt ggtttccact tccctcgact tgacccttcc ctccccagc 1740
 gtcagtttca ctccctcttg gtttttatca aatttgccat gacatttcat ctgggtgggtc 1800
 tgaatattaa agctcttcat ttctggaaaa aaaaaaaaaa aaaa 1844

<210> 66
 <211> 326
 <212> PRT
 <213> Homo sapiens

<400> 66
 Met Tyr Gln Asp Tyr Pro Gly Asn Phe Asp Thr Ser Ser Arg Gly Ser
 1 5 10 15
 Ser Gly Ser Pro Ala His Ala Glu Ser Tyr Ser Ser Gly Gly Gly Gly

```
<220>  
<221> misc_feature  
<222> 2087, 2093, 2098  
<223> n = A,T,C or G
```

<400> 67						
cgcgcggggg	cgggagggcg	cgcgcagggg	agggaccgag	agacgcgccg	acttttttaga	60
gggagggatc	gggtggaaca	ctgggtccgc	ggcgctcgca	gagccggaaa	gaagtgctgt	120
aagggacgct	cgggggacgc	tgttcctgag	gtgtcgccgc	ctccctgtcc	tcgcctccg	180
cgggtggggga	gaaacccagg	agcgaagccc	agagcccgcg	gcgcggccgg	cggacgaacg	240
agcgcgcgac	agccggtgcg	cggccgcggc	gagggcgggg	gaagaaaaac	accctgtttc	300
ctctccggcc	cccaccgcgt	atcatgtacc	aggattatcc	cgggaacttt	gacacctcgt	360
cccggggcgag	cagcggctct	cctgcgcacg	ccgagtccta	ctccagcggc	ggcggcggcc	420

```

agcagaaatt cccggtagat atgcctggct caggcagtgcc attcatcccc accatcaacg 480
ccatcacgac cagccaggac ctgcagtgga tgggtgcagcc cacagtgatc acctccatgt 540
ccaaccata ccctcgctcg cacccttaca gccccctgcc gggcctggcc tctgtccctg 600
gacacatggc cctcccaaga cctggcgtga tcaagaccat tggcaccacc gtgggcccga 660
ggaggagaga tgagcagctg tctcctgaag aggaggagaa gcgtcgcata cggcgggaga 720
ggaacaagct ggctgcagcc aagtgcggga accgacgccg ggagctgaca gagaagctgc 780
aggcggagac agaggagctg gaggaggaga agtcaggcct gcagaaggag attgctgagc 840
tgcagaagga gaaggagaag ctggagttca tgttggtggc tcacggccca gtgtgcaaga 900
ttagccccga ggagcgccga tcgccccag cccctgggct gcagcccatg cgcagtgggg 960
gtggctcggt gggcgtgta gtggtgaaac aggagccctt ggaagaggac agccctcgt 1020
cctcgtcgge ggggctggac aaggcccagc gctctgtcat caagccatc agcattgctg 1080
ggggcttcta cggtaggag cccctgcaca ccccatcgt ggtgacctcc acacctgctg 1140
tactccggg cacctgaac ctctcttca cctatcctag cgtcctggag caggagtcac 1200
ccgcatctcc ctccgaatcc tgctccaagg ctacccgag aagcagtagc agcggggacc 1260
aatcatcaga ctccctgaac tccccactc tgctggctct gtaaccagt gcacctccct 1320
ccccagctcc ggaggggggc ctctcgtct ctccttccca gggaccagca ccttcaagcg 1380
ctccagggcc gtgagggcaa gagggggacc tgccaccagg gagcttctct gctctggggg 1440
accaggtgg gacttagcag tgagtattgg aagacttggg ttgatctctt agaagccatg 1500
ggacctctcc cctcattcat cttgcaagca aatcccattt cttgaaaagc cttggagaac 1560
tcggtttggt agacttggac atctctctgg cttctgaaga gcctgaagct ggccctggac 1620
attcctgtcc ctttgttacc atactgtctc tggagtgatg gtgtcctcc ctgccccacc 1680
acgcatgctc agtgccctttt ggtttcacct tcctcgaact tgacctttc ctcccccagc 1740
gtcagtttca ctccctcttg gtttttatca aatttgccat gacatttcat ctgggtgggtc 1800
tgaatattaa agctcttcat ttctggagat ggggcagcag gtggctcttc tgctggggct 1860
gacttgtcca gaaggggaca aagtgcata cagagccttc cctacctga cgctcccag 1920
tcatcatctc cagaactccc agcggggctc cctgagctct caaggagatg ctgcatcac 1980
tgaggagctc agaggacct tcctgcccac ctctggagac ggcttctgga ggaacggctt 2040
ggccagaaga cagggtgtga gtgagacagt ggggcacagg ttgggtnttg ccnaaacngc 2100
ctaattacca gggcaggaag catgccaaca aagccacacg ggtgtcctag ccagcttccc 2160
ttcacctggt gtcttgagta gggcgtctcc tgtaattact gccttgccat tctgccccctg 2220
gacctttctc tccggaccag ggagggctcc ctccctatga gccacacatt atactccaag 2280
tcctgcccgg gctccgcctt tccccaccc tggctctcag ggtgacgcca cccacagaga 2340
tttaatgagc gtgggccttg accttcccca gatgctgcca ggcagccctt cccaagcct 2400
caaagaagca tttgctgagg atggagaggc aggggaggga ggcgggaggc cgtcactgga 2460
gtggcgtctg cagcagctgc tgccccagca cccgctcagc ctgtcctggc tgetcacctc 2520
ccgcagggc accgggcctt tcctgcccctc tgtggtcatc tgccacctgc tggatcaagt 2580
gctttctctt ttacactccc ctgtccccac cccagtgcac tcttctggcc caggcagcaa 2640
gcaagctgtg aacagctggc ctgagctgtc gctgtggctt gtggctcatg cgccattcct 2700
ggttgtctgt tgaatctttc tggctgctgg aattggagat aggatgtttt gcttcccact 2760
gcaggagagc tgcccccttt cacggggttg ggaagggtc cccctggcct ccagcaggag 2820
cacagctcag cagggtccct gctgccacc cctctgagcc ttttctcccc agggtatggc 2880
tcctgctgag tttcttgtcc agcagggcct tgacaggaat ccagggagta gctcctggcc 2940
agaaccagcc tctgcccggg ttgtgctctg caaagactct gctgctgggg attcagctct 3000
agaggtcaca gtatcctcgt ttgaaaagata attaatatcc cccgtggaga aagcagtgc 3060
acattcacac agctgttccc tcgcatgta tttcatgaac atgacctgtt ttcgtgcact 3120
agacacacag agtggacacg ccgtatgctt aaagtacatg ggccagtggg actggaagt 3180
acctgtacaa gtgatgcaga aaggagggtt tcaaagaaaa aggattttgt ttaaaatact 3240
ttaaaaaatg tatttctctg atcccttggc tgtgatgcc ctctcccgat tccccaggg 3300
ctctgggagg gaccttctc agaagattgg gcagttgggt ttctggcttg agatgaatcc 3360
aagcagcaga atgagccagg agtagcagga gatgggcaa gaaaactggg gtgcactcag 3420
ctctcacagg ggtaatcata tcaagtggta tttgtagcca agtgggagct attttctttt 3480
ttgtgcata agatattttt taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3600
aa

```

```

<210> 68
<211> 3252
<212> DNA
<213> Homo sapiens

```

<220>

<221> misc_feature

<222> 779

<223> n = A,T,C or G

<400> 68

```

acaaagtctt gctctgtcac ccaggctgga gtgcagtggc gcaatcacgg ctctctgcag 60
cctcgacctc cgrggctcaa gctattctcc tgcctcacc ccttgagtag atgggactac 120
aggtacgtgc ggctatctag ctaatttttt aaatcttaag tagagacatt ggtctcactg 180
tggtgccag actggtcttg aactcctagg ttgaagggat ctccagcct ctgcctcccg 240
aagtgtgta ttacagaaca tatgcagtaa tgtcacctca aaagagagtt aagaacgtcc 300
aggcacaaaa caggacttca caaggtagta gtagttttca gaccacgctt tcagcctgga 360
aagtaaaaca ggatccaagc aactcgaaga acatctcaaa acatggacaa aacaatccag 420
tgggagatta tgaacatgct gatgatcaag ctgaagaaga tgctttgcaa atggcagtgg 480
gatattttga gaaaggctcc attaaagctt cacagaataa agataaaaacc ttggaaaaac 540
acttgaaaaa tgtggaaaat gtggcttgga agaattgggt agcttcagaa gaaattgata 600
ttctattaaa tattgcactc agtggcaaat ttggaaatgc tgtaaacaca cggatattga 660
agtgcattgat cccagcaaca gtaatatcag aagattctgt gggttaaggca gtctcctggc 720
tttggtttgg caagtgttct ggtagcacca aggtactttt ttatcgtttg ctgggtgcna 780
tggttgactt cattgatcgy aaggagcaaa ttaacttgct ctatggcttc ttttttgctt 840
cattgcaaga tgatgcactg tgcccttatg tttgccatth gttatattht cttacgaaaa 900
aagagaatgt caaaccattt cgtgtgagaa aactgcttga tcttcaggcc aaaatgggaa 960
tgcagcctca tctccaggct ttggtgtcac tgtataagtt ctttgctcct gctctgattt 1020
cagtatcttt gcctgtaagg aagaagatat atcttcagaa ttcagagaa ctatggaaga 1080
cggctctgct tgccgtgaag caaagaaaacc ggggaccttc tccagaacct ctgaagttga 1140
tgtaggtcc agctaattgt cgtcctctaa aaagaaagt gaattctctc tcagttatac 1200
cagtgtccaa ttccagtagc tacactaaag aatgtggaaa aaaagagatg agtctttctg 1260
attgtctgaa tagaagtgg tcaattccac tagaacaact tcaaagcttc ccccaacttt 1320
tacagaacat ccattgctta gagctgcctt ctcatagagg ctcatgtcta aacaactctc 1380
tgctgcttca ctacattaac tgtgtcagag atgagccagt cttgctgagg ttctattact 1440
ggttgagtca aacattacaa gaagaatgta tttggtacaa ggtgaataat tatgaacatg 1500
gaaaagaatt taccaacttc ctggatacca tcatcagggc agagtgcctc ttacaagagg 1560
ggtattatth ctgtgaagca ttctgtata agagccttcc tctctgggat ggcttagtt 1620
gtcggtcaca gttccttcag cttgtgagct ggattccttt tagtagcttc tctgaggtga 1680
aaccattct ttttgaccat ctagcgcagc tctctttac atcaaccatt tatttcaagt 1740
gtagtgtgct tcagagctg aaagagctat tgcagaattg gctgttggtg ctttctatgg 1800
acattcacat gaaacctgtt acraacagtc ctctagagac aactttgggt ggatccatga 1860
actgtgtgtc taaaactgat cactatgtag ggtggctatc cactactgca atgogcttgg 1920
agagcaacaa tactttcttg ctgcacttta ttttggtatt ctatgagaag gtgtgtgaca 1980
tatatataaa ttatgacctt ccattagttg tattgtttcc tcttgggatc ttctattctg 2040
cactcctcag cctggatacc agcatcctga accagctgtg ttttattatg cacagataac 2100
gtaaaaattt gactgccgca aagaaaaatg agttggtaca aaagacaaaa tcagagttca 2160
atttcagcag caagacttat caagaattta attactattt gacatcaatg gttggttgcc 2220
tgtggacgtc caaacctttt gcgaaaggaa tatatatga cctgaaatc ctagaaaaaa 2280
ctggagtggc tgaatataaa aacagtttaa atgtagtcca tcatccttct ttcttgagtt 2340
acgctgttth ctttttgcta caggaaaagg cagaagaaag gacagtaaac gtgagctcta 2400
tycggggaaa gaaatggagc tggatthtgg actatthatt ttcacagggg ttacaaggct 2460
tgaaacttht tataagaagt agtgttcac atctctccat tccagagca gagggcataa 2520
actgcaacaa tcaatattaa atgaatgttg acataaactg aacacactgg actaaactca 2580
ctcctcattg ctagagcaaa gtggctcatc ttgagttccc attttcattt cactgacaga 2640
ctgccatcct caaggagtac tcagactggc cttctgttca tggcttagga gagccttgg 2700
gtgcctaact gatthtttcaa aatttagatt tttttagcct accagtga aaatgacctt 2760
tcatcatcag gctctgcgtt ctaccaaatt gtatgtaaaa agacacatct gttttgtgg 2820
aggatthttt cacatthttt ggtactatga tctgcattga tggagacag caggcaatat 2880
gtggtgacag ttaactcaca gacataaaca tgcaaaaatac tttgctgtct ctggggatat 2940
tgccatthtt cttactgtga gcaacagcac caacaccaag ttaacaggat gcaacatgtg 3000
tatgactcta aaagccctaa gtagttggta acttctggg ccttcaatca tagcaattt 3060
atgaggggag gaaggggaga ggatttggtt ggtaatcaag acattcccgt atatgtctga 3120

```



```

tttcatggaa ctgctctatt ttgtttgtgt gtattgtata tgtatatgtg tatgtgtgcg 3180
tgtatgtgtg tgtctgtagc ttcagttttt aagtgtgaagg actaaataaa ctaactgaaa 3240
ttttactttc ag 3252

```

<210> 69
 <211> 756
 <212> PRT
 <213> Homo sapiens

<400> 69
 Met Ser Pro Gln Lys Arg Val Lys Asn Val Gln Ala Gln Asn Arg Thr
 1 5 10 15
 Ser Gln Gly Ser Ser Ser Phe Gln Thr Thr Leu Ser Ala Trp Lys Val
 20 25 30
 Lys Gln Asp Pro Ser Asn Ser Lys Asn Ile Ser Lys His Gly Gln Asn
 35 40 45
 Asn Pro Val Gly Asp Tyr Glu His Ala Asp Asp Gln Ala Glu Glu Asp
 50 55 60
 Ala Leu Gln Met Ala Val Gly Tyr Phe Glu Lys Gly Pro Ile Lys Ala
 65 70 75 80
 Ser Gln Asn Lys Asp Lys Thr Leu Glu Lys His Leu Lys Thr Val Glu
 85 90 95
 Asn Val Ala Trp Lys Asn Gly Leu Ala Ser Glu Glu Ile Asp Ile Leu
 100 105 110
 Leu Asn Ile Ala Leu Ser Gly Lys Phe Gly Asn Ala Val Asn Thr Arg
 115 120 125
 Ile Leu Lys Cys Met Ile Pro Ala Thr Val Ile Ser Glu Asp Ser Val
 130 135 140
 Val Lys Ala Val Ser Trp Leu Cys Val Gly Lys Cys Ser Gly Ser Thr
 145 150 155 160
 Lys Val Leu Phe Tyr Arg Trp Leu Val Ala Met Phe Asp Phe Ile Asp
 165 170 175
 Arg Lys Glu Gln Ile Asn Leu Leu Tyr Gly Phe Phe Phe Ala Ser Leu
 180 185 190
 Gln Asp Asp Ala Leu Cys Pro Tyr Val Cys His Leu Leu Tyr Leu Leu
 195 200 205
 Thr Lys Lys Glu Asn Val Lys Pro Phe Arg Val Arg Lys Leu Leu Asp
 210 215 220
 Leu Gln Ala Lys Met Gly Met Gln Pro His Leu Gln Ala Leu Leu Ser
 225 230 235 240
 Leu Tyr Lys Phe Phe Ala Pro Ala Leu Ile Ser Val Ser Leu Pro Val
 245 250 255
 Arg Lys Lys Ile Tyr Leu Gln Asn Ser Glu Asn Leu Trp Lys Thr Ala
 260 265 270
 Leu Leu Ala Val Lys Gln Arg Asn Arg Gly Pro Ser Pro Glu Pro Leu
 275 280 285
 Lys Leu Met Leu Gly Pro Ala Asn Val Arg Pro Leu Lys Arg Lys Trp
 290 295 300
 Asn Ser Leu Ser Val Ile Pro Val Leu Asn Ser Ser Ser Tyr Thr Lys
 305 310 315 320
 Glu Cys Gly Lys Lys Glu Met Ser Leu Ser Asp Cys Leu Asn Arg Ser
 325 330 335
 Gly Ser Phe Pro Leu Glu Gln Leu Gln Ser Phe Pro Gln Leu Leu Gln
 340 345 350
 Asn Ile His Cys Leu Glu Leu Pro Ser Gln Met Gly Ser Val Leu Asn
 355 360 365
 Asn Ser Leu Leu Leu His Tyr Ile Asn Cys Val Arg Asp Glu Pro Val
 370 375 380
 Leu Leu Arg Phe His Tyr Trp Leu Ser Gln Thr Leu Gln Glu Glu Cys

```

385          390          395          400
Ile Trp Tyr Lys Val Asn Asn Tyr Glu His Gly Lys Glu Phe Thr Asn
      405          410          415
Phe Leu Asp Thr Ile Ile Arg Ala Glu Cys Phe Leu Gln Glu Gly Tyr
      420          425          430
Tyr Ser Cys Glu Ala Phe Leu Tyr Lys Ser Leu Pro Leu Trp Asp Gly
      435          440          445
Leu Ser Cys Arg Ser Gln Phe Leu Gln Leu Val Ser Trp Ile Pro Phe
      450          455          460
Ser Ser Phe Ser Glu Val Lys Pro Leu Leu Phe Asp His Leu Ala Gln
465          470          475          480
Leu Phe Phe Thr Ser Thr Ile Tyr Phe Lys Cys Ser Val Leu Gln Ser
      485          490          495
Leu Lys Glu Leu Leu Gln Asn Trp Leu Leu Trp Leu Ser Met Asp Ile
      500          505          510
His Met Lys Pro Val Thr Asn Ser Pro Leu Glu Thr Thr Leu Gly Gly
      515          520          525
Ser Met Asn Cys Val Ser Lys Leu Ile His Tyr Val Gly Trp Leu Ser
      530          535          540
Thr Thr Ala Met Arg Leu Glu Ser Asn Asn Thr Phe Leu Leu His Phe
545          550          555          560
Ile Leu Asp Phe Tyr Glu Lys Val Cys Asp Ile Tyr Ile Asn Tyr Asp
      565          570          575
Leu Pro Leu Val Val Leu Phe Pro Pro Gly Ile Phe Tyr Ser Ala Leu
      580          585          590
Leu Ser Leu Asp Thr Ser Ile Leu Asn Gln Leu Cys Phe Ile Met His
      595          600          605
Arg Tyr Arg Lys Asn Leu Thr Ala Ala Lys Lys Asn Glu Leu Val Gln
      610          615          620
Lys Thr Lys Ser Glu Phe Asn Phe Ser Ser Lys Thr Tyr Gln Glu Phe
625          630          635          640
Asn Tyr Tyr Leu Thr Ser Met Val Gly Cys Leu Trp Thr Ser Lys Pro
      645          650          655
Phe Ala Lys Gly Ile Tyr Ile Asp Pro Glu Ile Leu Glu Lys Thr Gly
      660          665          670
Val Ala Glu Tyr Lys Asn Ser Leu Asn Val Val His His Pro Ser Phe
      675          680          685
Leu Ser Tyr Ala Val Ser Phe Leu Leu Gln Glu Ser Pro Glu Glu Arg
      690          695          700
Thr Val Asn Val Ser Ser Ile Arg Gly Lys Lys Trp Ser Trp Tyr Leu
705          710          715          720
Asp Tyr Leu Phe Ser Gln Gly Leu Gln Gly Leu Lys Leu Phe Ile Arg
      725          730          735
Ser Ser Val His Ser Ser Ile Pro Arg Ala Glu Gly Ile Asn Cys
      740          745          750
Asn Asn Gln Tyr
      755

```

```

<210> 70
<211> 1559
<212> DNA
<213> Homo sapiens

```

```

<400> 70
gggcctgaac caaacggtgc catggggaac tgtctgcaca gggtagtat ggggccaggc 60
cccagagtcc cttatcccta tgccctcat tccccctgct gtttgcctt cagtctttat 120
atctcttcct tttctcctc atcttttctc ccttcccgt tttttcctct tccttcaaag 180
tctttttcct tctctcctc ctatgctagc ctctagctc cctcttgtgt cctcccttt 240

```

```

gcctttgagt cagttccatc ctggtctctt ggtgcctttc cttctgacct tgcactgctc 300
ctccagcccc agctgccttg gcttccccag gactgttccct gctccggctc ttcaggctcc 360
ctgctttgtc cttttccact gtccgcactg catctgactc ctgcagagac cttgttctcc 420
cacccgacct tcctctctgt cctccccctc cacctgcccc tcaattccca ggagactcct 480
ccggtgtaac tctgatggcc tcctctgggt atgtcctcca ggcgagctc tccccctcaa 540
ctgagaactc aagtcagctg gacttcgaag atgtatggaa ttcttctat ggtgtgaatg 600
attccttccc agatggagac tatgatgcca acctggaagc agctgcccc tgccactcct 660
gtaacctgct ggatgactct gcaactgccct tcttcatacct caccagtgtc ctgggtatcc 720
tagctagcag cactgtcctc ttcatgcttt tcagacctct cttccgctgg cagctctgcc 780
ctggctggcc tgtcctggca cagctggctg tgggcagtgc cctcttcagc attgtggtgc 840
cogtcttggc cccagggcta ggtagcactc gcagctctgc cctgtgtagc ctgggctact 900
gtgtctggta tggctcagcc tttgccagg ctttgctgct agggtgccat gcctccctgg 960
gccacagact ggggtgcaggc caggtccag gcctcaccct ggggctcact gtgggaattt 1020
ggggagtggc tgcctactg acactgcctg tcaccctggc cagtgggtgct tctgggtggac 1080
tctgcaccct gatatacagc acggagctga aggttttgc gccacacac actgtagcct 1140
gtcttgccat ctttgtcttg ttgccattgg gtttgtttgg agccaagggg ctgaagaagg 1200
cattgggtat ggggccaggc ccctggatga atatcctgtg ggcttggtt attttctggt 1260
ggcctcatgg ggtggttcta ggactggatt tcctgggtgag gtccaagctg ttgctgttgt 1320
caacatgtct ggcccagcag gctctggacc tgcctgtgaa cctggcagaa gccctggcaa 1380
ttttgcactg tgtggctacg cccctgctcc tcgccctatt ctgccaccag gccaccgca 1440
ccctcttgcc ctctctgccc ctccctgaag gatggtcttc tcactctggac acccttgaa 1500
gcaaataccta gttctcttcc cacctgtcaa cctgaattaa agtctacact gcctttgtg 1559

```

<210> 71
 <211> 338
 <212> PRT
 <213> Homo sapiens

<400> 71

Met	Ala	Ser	Ser	Gly	Tyr	Val	Leu	Gln	Ala	Glu	Leu	Ser	Pro	Ser	Thr
1				5					10					15	
Glu	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Glu	Asp	Val	Trp	Asn	Ser	Ser	Tyr
			20					25					30		
Gly	Val	Asn	Asp	Ser	Phe	Pro	Asp	Gly	Asp	Tyr	Asp	Ala	Asn	Leu	Glu
		35					40					45			
Ala	Ala	Ala	Pro	Cys	His	Ser	Cys	Asn	Leu	Leu	Asp	Asp	Ser	Ala	Leu
	50					55					60				
Pro	Phe	Phe	Ile	Leu	Thr	Ser	Val	Leu	Gly	Ile	Leu	Ala	Ser	Ser	Thr
65					70					75					80
Val	Leu	Phe	Met	Leu	Phe	Arg	Pro	Leu	Phe	Arg	Trp	Gln	Leu	Cys	Pro
			85						90					95	
Gly	Trp	Pro	Val	Leu	Ala	Gln	Leu	Ala	Val	Gly	Ser	Ala	Leu	Phe	Ser
			100					105					110		
Ile	Val	Val	Pro	Val	Leu	Ala	Pro	Gly	Leu	Gly	Ser	Thr	Arg	Ser	Ser
		115					120					125			
Ala	Leu	Cys	Ser	Leu	Gly	Tyr	Cys	Val	Trp	Tyr	Gly	Ser	Ala	Phe	Ala
	130					135					140				
Gln	Ala	Leu	Leu	Leu	Gly	Cys	His	Ala	Ser	Leu	Gly	His	Arg	Leu	Gly
145					150					155					160
Ala	Gly	Gln	Val	Pro	Gly	Leu	Thr	Leu	Gly	Leu	Thr	Val	Gly	Ile	Trp
			165						170					175	
Gly	Val	Ala	Ala	Leu	Leu	Thr	Leu	Pro	Val	Thr	Leu	Ala	Ser	Gly	Ala
		180						185					190		
Ser	Gly	Gly	Leu	Cys	Thr	Leu	Ile	Tyr	Ser	Thr	Glu	Leu	Lys	Ala	Leu
		195					200					205			
Gln	Ala	Thr	His	Thr	Val	Ala	Cys	Leu	Ala	Ile	Phe	Val	Leu	Leu	Pro
	210					215					220				
Leu	Gly	Leu	Phe	Gly	Ala	Lys	Gly	Leu	Lys	Lys	Ala	Leu	Gly	Met	Gly
225					230					235					240

<400>	72						
gaaccggttta	ctcgctgctg	tgcccatcta	tcagcaggct	cggggctgaa	gattgcttct	60	
cttctctcct	ccaaggtcta	gtgacggagc	ccgcgcgcgg	cgccaccatg	cggcagaagg	120	
cggtatcgct	tttcttgtgc	tacctgctgc	tcttcacttg	cagtgggggtg	gaggcaggta	180	
agaaaaagtg	ctcggagagc	tcggaacagc	gctccggggt	ctggaaggcc	ctgaccttca	240	
tggccgctcg	aggaggactc	gcagtcgccg	ggctgcgccg	gctgggcttc	accgcgcgcg	300	
gcatcgcggc	caactcggtg	gctgcctcgc	tgatgagctg	gtctgcgata	ctgaatgggg	360	
gcggcgtgcc	cgcggggggg	ctagtggcca	cgctgcagag	cctcggggct	ggtggcagca	420	
gcgtcgtcat	aggtaatat	ggtgccctga	tgggctacgc	caccacaag	tatctcgata	480	
gtgaggagga	tgaggagtag	ccagcagctc	ccagaacctc	tttttccttc	ttggcctaac	540	
tcttccagtt	aggatctaga	actttgcctt	tttttttttt	tttttttttt	tttgagatgg	600	
gttctcacta	tattgtccag	gctagagtgc	agtggctatt	cacagatgcg	aacatagtac	660	
actgcagcct	ccaactocta	gctcaagtg	atcctctctg	ctcaacctcc	caagtaggat	720	
tacaagcatg	cgcgacgat	gccagaaatc	cagaactttg	totatcactc	tccccaacaa	780	
cctagatgtg	aaaacagaat	aaacttcacc	cagaaaa			817	

<400> 73															
Met	Arg	Gln	Lys	Ala	Val	Ser	Leu	Phe	Leu	Cys	Tyr	Leu	Leu	Leu	Phe
1				5					10					15	
Thr	Cys	Ser	Gly	Val	Glu	Ala	Gly	Lys	Lys	Lys	Cys	Ser	Glu	Ser	Ser
			20					25					30		
Asp	Ser	Gly	Ser	Gly	Phe	Trp	Lys	Ala	Leu	Thr	Phe	Met	Ala	Val	Gly
		35					40					45			
Gly	Gly	Leu	Ala	Val	Ala	Gly	Leu	Pro	Ala	Leu	Gly	Phe	Thr	Gly	Ala
	50					55					60				
Gly	Ile	Ala	Ala	Asn	Ser	Val	Ala	Ala	Ser	Leu	Met	Ser	Trp	Ser	Ala
65				70						75				80	
Ile	Leu	Asn	Gly	Gly	Gly	Val	Pro	Ala	Gly	Gly	Leu	Val	Ala	Thr	Leu
			85						90					95	
Gln	Ser	Leu	Gly	Ala	Gly	Gly	Ser	Ser	Val	Val	Ile	Gly	Asn	Ile	Gly
			100					105					110		
Ala	Leu	Met	Gly	Tyr	Ala	Thr	His	Lys	Tyr	Leu	Asp	Ser	Glu	Glu	Asp
		115					120					125			

Glu Glu
130

<210> 74
<211> 2861
<212> DNA
<213> Homo sapiens

<400> 74

tcgagcggcc	gcccggggcag	gtcggcctct	cattttctcct	agcccttctg	ttcttctctg	60
gccaagctgc	aggggatttg	ggggatgtgg	gacctccaat	tcccagcccc	ggcttcagct	120
ctttccagg	tggtgactcc	agctccagct	tcagctccag	ctccaggctg	ggctccagct	180
ccagccgcag	cttaggcagc	ggaggttctg	tgtcccagtt	gttttccaat	ttcaccggct	240
ccgtggatga	ccgtgggacc	tgccagtgtc	ctgtttccct	gccagacacc	acctttcccg	300
tggacagagt	ggaacgcttg	gaattcacag	ctcatgttct	ttctcagaag	tttgagaaag	360
aactttccaa	agtgagggaa	tatgtccaat	taattagttt	gtatgaaaag	aaactgttaa	420
acctaactgt	ccgaattgac	atcatgggag	aaggatacat	ttcttacact	gaactggact	480
tcgagctgat	aaggtagaag	tgaaggagat	ggaaaaactg	gtcatacagc	tgaaggagag	540
ttttggtgga	agctcagaaa	ttggtgacca	gctggagggtg	gagataagaa	atatgactct	600
cttggtagag	aagcttgaga	cactagacaa	aaacaatgtc	cttgccattc	gccgagaaat	660
cgtggctctg	aagaccaagc	tgaagagagt	tgaggcctct	aaagatcaaa	acacccctgt	720
cgtccaccct	cctcccactc	cagggagctg	tggtcatggg	ggtgtgggtga	acatcagcaa	780
accgtctgtg	gttcagctca	actggagagg	gttttcttat	ctatatgggtg	cttggggtag	840
ggattactct	ccccagcatc	caaacaaagg	actgtattgg	gtggcgccat	tgaatacaga	900
tgggagactg	ttggagattt	atatactgta	caacacactg	gatgatttgc	tattgtatat	960
aatgctcga	gagttgcgga	tcacctatgg	ccaaggtagt	ggtacagcag	tttacaacaa	1020
caacatgtac	gtcaacatgt	acacaccggg	aatatgtcca	gagttaacct	gaccaccaac	1080
acgattgctg	tgactcaaac	tctccctaata	gctgcctata	ataaccgctt	ttcatatgct	1140
aatgttgctt	ggcaagcata	ttgactttgc	tgtggatgag	aatggattgt	gggttattta	1200
ttcaactgaa	gccagcactg	gttaacatgg	tgattagtaa	actcaatgac	accacacttc	1260
aggtgctaaa	cacttggtat	accaagcagt	ataaaccatc	tgcttctaac	gccttcatgg	1320
tatgtggggg	tctgtatgcc	accogtacta	tgaacaccag	aacagaagag	attttttact	1380
attatgacac	aaacacaggg	aaagagggca	aactagacat	tgtaatgcat	aagatgcagg	1440
aaaaagtgca	gagcattaac	tataaccctt	ttgaccagaa	actttatgtc	tataacgatg	1500
gttaccttct	gaattatgat	ctttctgtct	tgcagaagcc	ccagtaagct	gttttaggagt	1560
tagggtgaaa	gagaaaatgt	ttggtgaaaa	aatagtcttc	tccacttact	tagatatctg	1620
cagatatcta	agtaagtggg	gaagactatt	ttttcaacaa	acattttctc	tttcacccta	1680
actcctaaac	agcttactgg	ggcttctgca	agacagaaaag	atcataattc	agaaggtaac	1740
catcgttata	gacataaagt	ttctgggtcaa	aagggttata	gttaatgctc	tgcacttttt	1800
cctgcactct	atgcattaca	atgtctagtt	tgccctcttt	ccctgtgttt	gtgtcataat	1860
agtaaaaaat	ctcttctgtt	tggcgtatag	ggattccttg	tacaggaaat	attgoccaat	1920
gactagtcct	catccatgta	gcaccactaa	ttcttccatg	cctggaagaa	acctggggac	1980
ttagttaggt	agattaatat	ctggagctcc	tcgagggacc	aaatctccaa	cttttttttc	2040
ccctcactag	cacctggaat	gatgctttgt	atgtggcaga	taagtaaatt	tggcatgctt	2100
atatattcta	catctgtaaa	gtgctgagtt	ttatggagag	aggccttttt	atgcattaaa	2160
ttgtacatgg	caaataaatc	ccagaaggat	ctgtagatga	ggcacctgct	ttttcttttc	2220
tctcattgtc	caccttacta	aaagtcagta	gaatcttcta	cctcataact	tccttccaaa	2280
ggcagctcag	aagattagaa	ccagaacttac	taaccaattc	cacccccac	caacccccct	2340
ctactgccta	ctttaaaaaa	attaatagtt	ttctatggaa	ctgatctaag	attagaaaaa	2400
ttaattttct	ttaatttcat	tatgaacttt	tattttacatg	actctaagac	tataagaaaa	2460
tctgatggca	gtgacaaaagt	gctagcattt	attgttatct	aataaagacc	ttggagcata	2520
tgtgcaactt	atgagtgtat	cagttgttgc	atgtaatttt	tgcccttgtt	taagcctgga	2580
acttgtaaga	aaatgaaaat	ttaatttttt	tttctaggac	gagctataga	aaagctattg	2640
agagtatcta	gttaatcagt	gcagtagttg	gaaaccttgc	tgggtgatgt	gatgtgcttc	2700
tgtgcttttg	aatgacttta	tcacttagtc	tttgtctatt	tttcctttga	tgttcaagtc	2760
ctagtctata	ggattggcag	tttaaatgct	ttactcccc	ttttaaaata	aatgattaaa	2820
atgtgcttcg	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	a		2861

<210> 75
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 75
 Met Glu Lys Leu Val Ile Gln Leu Lys Glu Ser Phe Gly Gly Ser Ser
 1 5 10 15
 Glu Ile Val Asp Gln Leu Glu Val Glu Ile Arg Asn Met Thr Leu Leu
 20 25 30
 Val Glu Lys Leu Glu Thr Leu Asp Lys Asn Asn Val Leu Ala Ile Arg
 35 40 45
 Arg Glu Ile Val Ala Leu Lys Thr Lys Leu Lys Glu Cys Glu Ala Ser
 50 55 60
 Lys Asp Gln Asn Thr Pro Val Val His Pro Pro Pro Thr Pro Gly Ser
 65 70 75 80
 Cys Gly His Gly Gly Val Val Asn Ile Ser Lys Pro Ser Val Val Gln
 85 90 95
 Leu Asn Trp Arg Gly Phe Ser Tyr Leu Tyr Gly Ala Trp Gly Arg Asp
 100 105 110
 Tyr Ser Pro Gln His Pro Asn Lys Gly Leu Tyr Trp Val Ala Pro Leu
 115 120 125
 Asn Thr Asp Gly Arg Leu Leu Glu Tyr Tyr Ile Leu Tyr Asn Thr Leu
 130 135 140
 Asp Asp Leu Leu Leu Tyr Ile Asn Ala Arg Glu Leu Arg Ile Thr Tyr
 145 150 155 160
 Gly Gln Gly Ser Gly Thr Ala Val Tyr Asn Asn Asn Met Tyr Val Asn
 165 170 175
 Met Tyr Thr Pro Gly Ile Leu Pro Glu Leu Thr
 180 185

<210> 76
 <211> 956
 <212> DNA
 <213> Homo sapiens

<400> 76
 gatgagttcc gcaccaagtt tgagacagac caggccctgc gcctgagtgt ggaggccgac 60
 atcaatggcc tgcgcagggt gctggatgag ctgaccctgg ccagagccga cctggagatg 120
 cagattgaga acctcaagga ggagctggcc tacctgaaga agaaccacga ggaggagatg 180
 aacgccctgc gaggccaggt ggggtggtgag atcaatgtgg agatggacgc tgcccaggc 240
 gtggacctga gccgcaccc ctacacgagatg cgtgaccagt atgagaagat ggcagagaag 300
 aaccgcaagg atgccgagga ttggttcttc agcaagacag aggaactgaa ccgcgagggtg 360
 gccaccaaca gtgagctggt gcagagtggc aagagtgaga tctcggagct ccggcgacc 420
 atgcaggcct tggagataga gctgcagtc cagctcagca tgaaagcatc cctggagggc 480
 aacctggcgg agacagagaa ccgctactgc gtgcagctgt ccagatcca ggggctgatt 540
 ggcagcgtgg aggagcagct ggcccagctt cgctgcgaga tggagcagca gaaccaggaa 600
 tacaaaatcc tgctggatgt gaagacgcgg ctggagcagg agattgccac ctaccgccgc 660
 ctgctggagg gagaggatgc ccacctgact cagtacaaga aagaaccggt gaccaccgct 720
 cagggtgcgta ccattgtgga agaggtccag gatggcaagg tcatctcctc ccgcgagcag 780
 gtccaccaga ccaccgctg aggactcagc taccgccggc ggccaccag gaggcaggga 840
 cgcagccgcc ccattctgcc cacagtctcc ggcctctcca gcctcagccc cctgcttcag 900
 tcccttcccc atgcttcctt gcctgatgac aataaaagct tgttgactca gctatg 956

<210> 77
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 77

```

Asp Glu Phe Arg Thr Lys Phe Glu Thr Asp Gln Ala Leu Arg Leu Ser
 1           5           10           15
Val Glu Ala Asp Ile Asn Gly Leu Arg Arg Val Leu Asp Glu Leu Thr
          20           25           30
Leu Ala Arg Ala Asp Leu Glu Met Gln Ile Glu Asn Leu Lys Glu Glu
          35           40           45
Leu Ala Tyr Leu Lys Lys Asn His Glu Glu Glu Met Asn Ala Leu Arg
          50           55           60
Gly Gln Val Gly Gly Glu Ile Asn Val Glu Met Asp Ala Ala Pro Gly
65           70           75           80
Val Asp Leu Ser Arg Ile Leu Asn Glu Met Arg Asp Gln Tyr Glu Lys
          85           90           95
Met Ala Glu Lys Asn Arg Lys Asp Ala Glu Asp Trp Phe Phe Ser Lys
          100          105          110
Thr Glu Glu Leu Asn Arg Glu Val Ala Thr Asn Ser Glu Leu Val Gln
          115          120          125
Ser Gly Lys Ser Glu Ile Ser Glu Leu Arg Arg Thr Met Gln Ala Leu
130          135          140
Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ser Leu Glu Gly
145          150          155          160
Asn Leu Ala Glu Thr Glu Asn Arg Tyr Cys Val Gln Leu Ser Gln Ile
          165          170          175
Gln Gly Leu Ile Gly Ser Val Glu Glu Gln Leu Ala Gln Leu Arg Cys
          180          185          190
Glu Met Glu Gln Gln Asn Gln Glu Tyr Lys Ile Leu Leu Asp Val Lys
          195          200          205
Thr Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Gly
          210          215          220
Glu Asp Ala His Leu Thr Gln Tyr Lys Lys Glu Pro Val Thr Thr Arg
225          230          235          240
Gln Val Arg Thr Ile Val Glu Glu Val Gln Asp Gly Lys Val Ile Ser
          245          250          255
Ser Arg Glu Gln Val His Gln Thr Thr Arg
          260          265

```

<210> 78

<211> 1689

<212> DNA

<213> Homo sapiens

<400> 78

```

cgggagcgtg gggatatctog aggtgcccggg ttgcaggcgc tcagggggcgc tagggtttga 60
ggcctgcttt ctgctcgcg cagcagagca ctacctgagg cagcgaggcg cagcgagcct 120
agcctccccg cgccctgggc agtgtggcca tggagaatca ggtgttgacg ccgcatgtct 180
actgggctca gcgacaccgc gagctatatc tgcgcgtgga gctgagtga cgtacagaacc 240
ctgccatcag catcactgaa aacgtgctgc atttcaaagc tcaaggacat ggtgccaaag 300
gagacaatgt ctatgaattt cacctggagt tcttagacct tgtgaaacca gagcctgttt 360
acaaactgac ccagaggcag gtaaacatta cagtacagaa gaaagtgagt cagtgggtggg 420
agagactcac aaagcaggaa aagcgaccac tgtttttggc tcttgacttt gatcgttggc 480
tggatgaatc tgatgcggaa atggagctca gagctaagga agaagagcgc ctaaataaac 540
tccgactgga aagcgaaggc tctcctgaaa ctcttacaaa cttaaggaaa ggatacctgt 600
ttatgtataa tcttgtgcaa ttcttgggat tctcctggat ctttgtcaac ctgactgtgc 660
gattctgtat cttgggaaaa gagtcctttt atgacacatt ccatactgtg gctgacatga 720
tgtatttctg ccagatgctg gcagttgtgg aaactatcaa tgcagcaatt ggagtcacta 780
cgtcaccggt gctgccttct ctgatccagc ttcttgggaag aaattttatt ttgtttatca 840
tctttggcac catggaagaa atgcagaaca aagctgtggt tttctttgtg ttttatttgt 900

```

```

ggagtgcaat tgaatttttc aggtactctt tctacatgct gacgtgcatt gacatggatt 960
ggaaggtgct cacatggctt cgttacactc tgtggattcc cttatatcca ctgggatggt 1020
tggtggaagc tgtctcagtg attcagtcga ttccaatatt caatgagacc ggacgattca 1080
gtttcacatt gccatatcca gtgaaaatca aagttagatt ttcttttttt cttcagattt 1140
atcttataat gatatttttta ggtttatata taaatttttcg tcacctttat aaacagcgca 1200
gacggcgcta tggaaaaaaa agaaaaagat ccactaaaaa gaaagattta gatggcttct 1260
tgccagtttg agcctaattct gattcttaca gttttacctt cttgaaccaa tgtaaaagtt 1320
tttttaaatgt taaatgatta aattctcagt gaggctatct tcctttttccc cagtaacatt 1380
cctgaattta ctgttatctt attgtagtac ttgcatgaca tggattcctg atatctgatg 1440
agaggttcat tcttgtgtat tcagttaatg acacaaaaag gctcagccca cccaaccct 1500
atctcatggt cagtcgtgtc aatacatgcc agagattttt ttttcaaaaa gtgctttatc 1560
cctacaatgt actgacagtt cttacagttg aggatttggt tcttttcagc taattgcttg 1620
gtggattaaa aaaagcaaga ctaatgtcaa ctctaattgga aggctgggta aaagtggact 1680
caggcaagg                                     1689

```

<210> 79

<211> 373

<212> PRT

<213> Homo sapiens

<400> 79

```

Met Glu Asn Gln Val Leu Thr Pro His Val Tyr Trp Ala Gln Arg His
 1          5          10          15
Arg Glu Leu Tyr Leu Arg Val Glu Leu Ser Asp Val Gln Asn Pro Ala
          20          25          30
Ile Ser Ile Thr Glu Asn Val Leu His Phe Lys Ala Gln Gly His Gly
          35          40          45
Ala Lys Gly Asp Asn Val Tyr Glu Phe His Leu Glu Phe Leu Asp Leu
          50          55          60
Val Lys Pro Glu Pro Val Tyr Lys Leu Thr Gln Arg Gln Val Asn Ile
          65          70          75          80
Thr Val Gln Lys Lys Val Ser Gln Trp Trp Glu Arg Leu Thr Lys Gln
          85          90          95
Glu Lys Arg Pro Leu Phe Leu Ala Pro Asp Phe Asp Arg Trp Leu Asp
          100          105          110
Glu Ser Asp Ala Glu Met Glu Leu Arg Ala Lys Glu Glu Arg Leu
          115          120          125
Asn Lys Leu Arg Leu Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn
          130          135          140
Leu Arg Lys Gly Tyr Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly
          145          150          155          160
Phe Ser Trp Ile Phe Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly
          165          170          175
Lys Glu Ser Phe Tyr Asp Thr Phe His Thr Val Ala Asp Met Met Tyr
          180          185          190
Phe Cys Gln Met Leu Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly
          195          200          205
Val Thr Thr Ser Pro Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg
          210          215          220
Asn Phe Ile Leu Phe Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn
          225          230          235          240
Lys Ala Val Val Phe Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile
          245          250          255
Phe Arg Tyr Ser Phe Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys
          260          265          270
Val Leu Thr Trp Leu Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu
          275          280          285
Gly Cys Leu Val Glu Ala Val Ser Val Ile Gln Ser Ile Pro Ile Phe
          290          295          300

```


Asn Glu Thr Gly Arg Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile
 305 310 315 320
 Lys Val Arg Phe Ser Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe
 325 330 335
 Leu Gly Leu Tyr Ile Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Arg
 340 345 350
 Arg Tyr Gly Lys Lys Arg Lys Arg Ser Thr Lys Lys Lys Asp Leu Asp
 355 360 365
 Gly Phe Leu Pro Val
 370

<210> 80
 <211> 1824
 <212> DNA
 <213> Homo sapiens

<400> 80
 agcggcctgc agctcgcagg cgccgcgtag ccgtcgccac cgccgccagc ccgtgcgccc 60
 tcggcgggtac ccgcgcgcgt cccatccccg ccgcgcggcca ggggcgcgct cgccgcgccc 120
 ggacagtgtc ccgctgcggc tccgcggcga tggccaccaa gatcgacaaa gaggcttgcc 180
 gggcgggcgta caacctgggtg cgcgacgacg gctcggccgt catctgggtg actttttaa 240
 atgacggctc caccatcgct cccggcgagc agggagcgga gtaccagcac ttcatccagc 300
 agtgacacaga tgacgtccgg ttgtttgcct tcgtgcgctt caccaccggg gatgccatga 360
 gcaagagggtc caagtttgcc ctcatcacgt ggatcgggtga gaacgtcagc gggctgcagc 420
 gcgcacaaaac cgggacggac aagaccctgg tgaaggaggt cgtacagaat ttcgctaagg 480
 agttttgtgat cagtgatcgg aaggagctgg aggaagattt catcaagagc gagctgaaga 540
 aggcggggggg agccaattac gacgcccaga cggagtaacc ccagcccccg ccacaccacc 600
 ccttgccaaa gtcactctgcc tgctccccgg gggagaggac cgccggcctc agctactagc 660
 ccaccagccc accagggaga agagaagcca tgagaggcag cgcccgccac cctgtgtcca 720
 cagccccac cttcccgctt cccttagaac cctgccgtgt cctatctcat gacgctcatg 780
 gaacctcttt ctttgatctt ctttttcttt tctccccctc ttttttgttc taaagaaaag 840
 tcattttgat gcaaggctct gcctgccatc agatccgagg tgctctctgc agtgaccctc 900
 tttcctggca tttctcttcc acgcgacgag gtctgcctag tgagatctgc atgacctcac 960
 gttgctttcc agagcccggg cctattttgc catctcagtt ttcttgggcc ctgcttctctg 1020
 tgtaccactg aggggcagct gggccaggag ctgtgcccgg tgcttcagc cttcataagc 1080
 acacacgtcc attccctact aaggcccaga cctcctggtg tctgccccgg gctccctcat 1140
 cccacctcca tccggagttg cccaagatgc atgtccagca taggcaggat tgctcggttg 1200
 tgagaagggtt aggtccggct cagactgaat aagaagagat aaaatttgcc ttaaaactta 1260
 cctggcagtg gctttgctgc acggtctgaa accacctgtt cccaccctct tgaccgaaat 1320
 ttccttggtg cacagagaag ggcaaaggct ttgagcccag agttgacgga gggagtattt 1380
 cagggttcac ttcaggggct cccaaagcga caagatcgtt agggagagag gccagggtg 1440
 gggactggga atttaaggag agctgggaac ggatccctta ggttcaggaa gcttctgtgc 1500
 aagctgcgag gatggcttgg gccgaagggt tgctctgccc gccgcgctag ctgtgagctg 1560
 agcaaagccc tgggctcaca gcaccccaaa agcctgtggc ttcagtcctg cgtctgcacc 1620
 acacaatcaa aaggatcgtt ttgttttgtt tttaaagaaa ggtgagattg gcttggttct 1680
 tcatgagcac atttgatata gctcttttct tgcttttctt tgctcatttc gttttgggga 1740
 agaaatctgt actgtattgg gattgtaaag aacatctctg cactcagaca gtttacagaa 1800
 ataaatgttt tttttgtttt tcag 1824

<210> 81
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 81
 Met Ala Thr Lys Ile Asp Lys Glu Ala Cys Arg Ala Ala Tyr Asn Leu
 1 5 10 15
 Val Arg Asp Asp Gly Ser Ala Val Ile Trp Val Thr Phe Lys Tyr Asp

```
<210> 82
<211> 10174
<212> DNA
<213> Homo sapiens
```

<400>	82						
gactgggggtt	ttaaggggtg	tggcaggagg	ttttggactc	gatgagtttc	caccgaaatg	60	
tcggagaagt	caggccagag	cacaaaagca	aaggatggga	aaaagtatgc	aacactcagt	120	
ttattttaata	cttacaaggg	gaaatcatta	gaaacacaga	aaaccacagc	tcgacatgga	180	
ttacagagctc	ttgaaaaagt	cggtatttca	cggcgtatgc	ctccacctgc	taacctccca	240	
agtcttaaag	cagaaaaaca	aggaactgat	cctaattgta	acattgtacc	taagatggc	300	
acaggggtgg	catcaaaaaca	agagcaacat	gaagaagaaa	aaacaccaga	agtgccaca	360	
gcacagccaa	aacctggggt	tgcagctccc	ccagaagtag	cacctgctcc	caaatcatgg	420	
gccagtaaca	agcaagggtg	gcaaggagat	ggaatccaag	tgaatagtca	gtttcagcaa	480	
gaatttccca	gcctgcaggc	agctggggat	caggaaaaaa	aagaaaagga	aacaaatgat	540	
gacaactatg	gacctggacc	cagttttacgt	ccaccaaagt	ttgcttggtg	gagagatggt	600	
ggtaaggctg	ctggctcacc	ttcgtcatct	gatcaagatg	aaaagctccc	tggccaggat	660	
gaaagcacag	ctggcaacatc	agagcaaaat	gatatcctca	aagtgttgga	aaagaggata	720	
gcttgttggtc	ctccacaggc	taaactgaat	ggacagcagg	ctgctctcgc	ttcccagtat	780	
agagctatga	tgcctcctta	tatgttccaa	cagtatccga	ggatgacata	tcctcctcta	840	
catggtccca	tgagattccc	accttcttta	tctgaaacaa	acaaaggcct	tcgaggaaga	900	
ggcccacctc	cttcatgggc	ctctgagcct	gaacgcccat	ccattcttag	tgcatacaga	960	
ctgaaggagc	ttgatâaatt	tgataaccta	gatgctgaag	ctgatgaagg	ttgggcaggt	1020	
gctcagatgg	aagtagatta	tacagagcaa	ctgaatttca	gtgatgatga	tgaacaagga	1080	
agtaacagtc	ctaaagagaa	taacagttag	gatcaagatt	caaaaagctc	tgaaaaacaac	1140	
gaaaacaaaa	agaaacacaga	tgaaagtttc	aacactaaat	catcttccca	aataactgcc	1200	
caaccatcag	tagcaaaagt	tccttatggg	aaaggacctt	cattttaatca	ggaacgtgga	1260	
acatcttcac	atctgccacc	acctccaaag	ttgcttgcac	agcagcatcc	acctccagat	1320	
cgacaggcag	tacctggaag	accaggcccc	tttccttcca	agcagcaagt	agctgatgaa	1380	
gatgaaatat	ggaagcaaag	acgaagacaa	caatcagaaa	tttctgcagc	agtagaacgt	1440	
gctcgtaaac	ggcgtgaaga	ggaagagcga	agaatggaag	aacaaaggaa	ggcagcttgt	1500	
gcggagaaac	tgaaacgatt	ggatgagaag	cttggcattc	tggaaaaaca	accatctcca	1560	
gaggaaatta	gggaagggga	gcgagaaaaa	gaacgggagc	gtgagaaaga	acttgaaaaa	1620	
gaacaagaac	aggagcgaga	gaaggagagg	gaaaaagaca	gagagagaca	gcaggaaaag	1680	
gagaaagagc	tggagaagga	gcaggaaaaa	caaagagaaa	tggagaaaga	aagaaagcaa	1740	
gaaaaagaaa	aagaactaga	acggcagaaa	gaaaaggaaa	aagaactaca	aaagatgaaa	1800	
gaacaagaaa	aggaatgtga	gctggagaag	gaaagggaaa	aattagagga	gaaaattgaa	1860	
cccagagaa	ctaattttaga	gcccatggta	gaaaaacaag	aaagtgaaaa	cagctgtaat	1920	
aaagaggagg	aacccgtttt	cactagacaa	gacagcaatc	gcagtgaaaa	ggaagccaca	1980	
ccagtgggtc	atgaaacaga	accagaatca	gggtctcaac	ctcggccggc	tgtattatct	2040	
ggctattttca	aacagtttca	gaagtcttta	ctccacagat	tccagcggca	gcaggaacag	2100	
atgaaacagc	agcagttggc	gcagcagcaa	cagcaaggtg	tacttccaca	gactgttcct	2160	

tcacaaccgt	ccagtagtac	tgtccctcct	ccaccacaca	gacctcttta	tcagcctatg	2220
cagcctcatc	ctcagcattt	ggcttctatg	ggttttgatc	caaggtggct	catgatgcag	2280
tcctacatgg	atcctcgaat	gatgtcagga	agacctgcta	tggatattcc	acccattcat	2340
cctggaatga	ttcctcctaa	accattaatg	agaagagacc	agatggaagg	gtcaccgaac	2400
agttctgagt	catttgagca	tatagctcga	tctgcaagag	atcacgcaat	ttccctttct	2460
gagcctcgta	tgctgtgggg	gtcagatccc	tatcctcatg	ctgagcctca	acaagcaact	2520
actcccaaag	caacagaaga	gcctgaggat	gtaaggtctg	aagctgcgtt	ggaccaggaa	2580
cagattactg	ctgcttattc	tgtagaacat	aatcaattag	aggctcacc	aaaggcagac	2640
tttatcagag	aatcaagtga	ggcacaagta	caaaagtttt	taagcagatc	tgtggaagat	2700
gtagaacctc	accatactga	tgcaataatg	cagtcgtctt	gttttgaagc	acctgatcaa	2760
aagaccttat	ccgctcctca	agaggagcgg	atttcagctg	tagaaagtca	gccttcccgg	2820
aaaagaagtg	tttcccatgg	atctaaccat	acgcaaaaac	cagacgagca	gagaagtga	2880
ccatctgcag	gcattcctaa	agtaaccagc	agatgcattg	attcaaaaga	accaatgaa	2940
aggccagagg	agaaaccaa	aaaggaaggc	tttatacgat	cttctgaagg	acaaaaacct	3000
gaaaaagtat	ataaatctaa	atcagaaact	cgttggggcc	cacgaccaag	ctctaacaga	3060
agggaagaag	ttaatgatag	acctgtgaga	agatcaggtc	ccattaaaaa	acctgtactt	3120
agagatatga	aagaggaacg	ggaacagagg	aaggagaaa	aaggagaaaa	ggccgaaaag	3180
gtcactgaaa	aagtagttgt	aaagcctgaa	aagacggaaa	agaaggatct	tcctcctccc	3240
ccaccaccac	ctcagccacc	agcaccaatt	cagccacagt	cagttccacc	accaattcaa	3300
ccagaagcag	agaaatttcc	ttcaacagaa	actgcaactt	tggctcaaaa	accatctcag	3360
gatactgaga	agcctctgga	acctgtgagt	actgttcagg	tagagcctgc	agttaagact	3420
gtaaaccaac	agactatggc	agcaccagta	gtcaaagaag	aaaaacaacc	tgagaaagtc	3480
atcagraaag	accttgttat	agagaggcct	cgaccagatt	caagaccagc	agttaaaaaa	3540
gaatcaactt	tgctctccag	gacctattgg	aaagaagcta	gagagagaga	ttggtttcca	3600
gatcaaggat	acagaggtcg	aggccgaggt	gaatattact	ccagaggtcg	aagctataga	3660
ggttcttatg	gagggcggtg	caggggtggt	aggggacaca	ctcgagatta	tcctcagtat	3720
agagacaata	agccaagagc	agagcatata	ccctcagggc	ctctcagaca	gcgagaagaa	3780
agtgaacac	ggagtgcag	ctctgatttt	gaagttgtcc	ccaaaagaag	acgacagcgg	3840
ggttcagaga	ctgacacaga	cagtgaattt	catgaaagtg	caagtgacaa	ggacagttta	3900
agtaaaggca	aacttcccaa	aagagaggaa	cggcctgaaa	acaaaaaacc	tgtaaagcct	3960
cattcttctt	tcaagcctga	taatcatggt	cgaatagata	atagactgct	agaaaagcct	4020
tatgtaaggg	atgacgataa	agctaaacca	ggctttcttc	ctaaaggaga	gcctacaagg	4080
agaggcagag	ggggaacatt	caggcggtgt	ggaagggatc	ctggaggccg	tcctacacgc	4140
ccttccactt	tacgaagacc	agcttatcgg	gacaatcagt	ggaacccaag	gcagtcagaa	4200
gttccctaac	cagaagatgg	agagccgcca	agaagacatg	agcagtttat	tcctatagca	4260
gcagataaaa	gacctccaaa	atlttgagcga	aaatlttgacc	cagctagaga	aaggcctcga	4320
aggcagcgtc	ctactcgacc	accaaggcaa	gacaagccac	ctcgatttag	acggctaaga	4380
gagagggagg	ctgcttcaaa	atcaaattgag	gtggtagcag	tgccacaaa	tggcacagtt	4440
aataatgtgg	ctcaagaacc	agttaatact	cttgggggata	tttccgggaa	taagacacca	4500
gatttatcta	atcagaactc	ttcagatcag	gcaaatgaag	aatgggaaac	agcttctgaa	4560
agcagtgatt	tcaatgagag	gagagagagg	gatgaaaaaa	aaaatgctga	cttgaatgca	4620
caaacagttg	taaaggttgg	agagaatggt	ctacctccaa	agagggaaat	tgcaaagaga	4680
agtttttcta	gtcagagacc	agtagatcgt	cagaatcgac	gtggcaacaa	tgggtccacc	4740
aaatcaggaa	ggaatttctc	aggtcctaga	aatgaaagga	gaagtggccc	accatcaaaa	4800
agtgggaaga	gagggccatt	tgatgaccag	cctgcaggca	caactggggt	tgacctcatc	4860
aatggcagct	ctgcacacca	tcaggaagga	gtacctaatg	gtacaggaca	aaagaactcc	4920
aaagattcta	ctgggaaaaa	aagagaagac	cccaaaccag	gccctaataa	acaaaagag	4980
aaagtggatg	ctctatcaca	gtttgatctc	aacaattatg	caagtgttgt	tataattgat	5040
gatcatcctg	aagtaacagt	aattgaagat	ccccagtcac	atlttgatga	tgatggtttt	5100
actgaagtgg	tatccaaaaa	acaacaaaaa	cgtttacagg	atgaagaacg	ccgaaagaag	5160
gaagaacaag	tcatacaggt	ctggaacaaa	aagaatgcaa	atgaaaaaag	aagaagccag	5220
acttctaagc	ttcctccaag	atlttgccaa	aaacaggcta	cagggatcca	gcaagcacag	5280
tcttcagcct	cagttccacc	tctagcttcg	gtctcacttc	caacttcaac	ctcagcttca	5340
gttccagcct	caacctcagc	tccacttccg	gcaaccttaa	ctccagttcc	agcctcaacc	5400
tcagctccgg	ttccagctc	aacttttagc	ccagttctgg	cctcaacctc	agctccagtt	5460
ccagcctcac	ccttagctcc	agtttcagcc	tcagcctcag	tctcagcttc	agttccagcc	5520
tctacttcag	ctgcagctat	aacctcttct	tcagctccag	cctcagcccc	agctccaacc	5580
cccattcctg	cctcagtttc	aaccccagct	tctgtcacca	ttcttgccct	agcctcaatt	5640
cccatttctg	cttcagccct	agcatcaact	tcagctccaa	cgccagcccc	agcagcctct	5700

tccccagctg	ccccagtcac	cacagcacca	actatcccag	cctcagcccc	aactgcctca	5760
gtcccacttg	cccctgcctc	agcttcagcc	ccagccccag	cccctacccc	agtctcagcc	5820
ccaaatcctg	ccccacctgc	cccagcccag	actcaggcac	agacccacaa	accagtccag	5880
aatccactac	agactacatc	tcagtccttc	aaacaaccac	caccatcaat	taggctgcct	5940
tcagctcaaa	cacctaattg	cacagattat	gtagcctcag	gaaaatccat	ccagacccca	6000
cagtcacatg	gcactctgac	agctgaatta	tgggataaca	aggtggcccc	accagctgtg	6060
ctgaatgata	tctctaagaa	attaggtccc	attagtcac	cacagccacc	ttcagtcagt	6120
gcatggaata	agcccttaac	atcgtttgga	tcagctcctt	catcagaggg	agcgaagaat	6180
ggtcaagaaa	gtggactcga	aattggaact	gacacaatto	agtttggtgc	tccagcctca	6240
aatggaaatg	aaaatgaagt	tgttcctgtg	ctttcggaag	aatctgctga	caaaaatacct	6300
gaacctaaag	aacagcggca	gaagcagcca	cgagcaggac	ctatcaaagc	ccagaagctt	6360
ccagatttga	gtccagtaga	aaacaaagaa	cacaaacctg	gtcccattgg	aaaggaacgt	6420
tcattaaaaa	atagaaaagt	aaaagatgcc	caacaggtgg	agccagaagg	acaagagaaa	6480
ccaagcccag	ctacagtcag	aagcacagat	cctgtcacga	caaaggagac	taaagcagtc	6540
tcagaaatgt	ctactgaaat	aggaacaatg	atctcggtat	catctgcaga	atatggtact	6600
aatgcaaagg	agtctgtaac	agactatact	acaccctctt	cttctttgcc	taacaccgtg	6660
gctactaata	atacaaagat	ggaggatact	ttggtttaata	atgtgcccct	gcccacaccc	6720
cttccccctc	ctaagaggga	gactatacaa	cagagctcca	gocctaacctt	agttcctccc	6780
actactttca	gcctcacctt	caagatggag	tctgcacgca	aagcatggga	gaattctcca	6840
aatgttaagg	aaaaggggtc	tccagtaact	tccacagcac	ctccaattgc	aactggagtc	6900
agcagtagtg	ccagtgggacc	aagcactgct	aattacaatt	cgttctcaag	tgcattccatg	6960
ccccagattc	ctgttgcttc	agtcaactct	acagcatcac	tatcaggagc	tggtacatac	7020
actacctctt	ctttgagcac	aaaatctaca	accacatcgg	accctccaaa	tatttgtaaa	7080
gtgaaacctc	agcagttaca	gacaagcagc	ctgccttctg	caagtcattt	ttcacagtta	7140
agctgtatgc	cttccccttat	tgcccagcag	caacagaatc	cgcaagttta	tgtgtctcag	7200
tctgcagcag	ctcaaatccc	agccttctat	atggacacaa	gtcattttatt	caataacccaa	7260
catgcacgat	tggtctccgcc	atccttggtc	caacaacagg	gtttccaacc	aggtctctct	7320
cagccaaact	cagttcagca	gattccaact	cctattttatg	caccactgca	agggcagcat	7380
caagcccaac	tgagtttggg	ggctggccct	gctgtttccc	aggctcagga	attggtcagc	7440
tcctcacttc	aaccatatag	atctcagcca	gctttttatgc	aaagcagttt	atcccagcca	7500
tctgtggtcc	tttctggtac	tgtatttcac	aacttttcaa	ctgtccaaca	ccaagaactt	7560
gccaaggcac	aatccggtct	tgcttttcag	caaacatcaa	atactcagcc	cattcctata	7620
ttgtatgaac	atcaactggg	gcaggcatca	ggactaggag	gttcccagct	gattgacaca	7680
catcttctcc	aggccagagc	aaatcttacc	caggcctcaa	atctttattc	tggacaagta	7740
caacagcctg	gtcagacaaa	tttttataac	actgcccagt	caccaagtgc	totccagcag	7800
ggtacagtac	ctttaccagc	atcgcagctt	tccttgctta	attttggatc	tacagggcaa	7860
cctctaattg	ctttgcctoa	gactcttcag	ccccattac	agcataccac	tccccaaagca	7920
caggctcaga	gtctgagtcg	tcctgcacaa	gtaagccagc	ctttcagagg	attaattcct	7980
gctggaacac	agcatagcat	gattgcaacc	acaggaaaaa	tgtctgaaat	ggaactaaaa	8040
gcctttggaa	gtggcattga	tataaaacca	ggcacacctc	caatcgctgg	tagaagcacc	8100
acaccaacat	ctagtccctc	cgggctactt	ctacaagtcc	gaacagccag	tccagcaaaa	8160
tgaacagcat	tgtctaccag	aagcagttcc	agtcagcccc	tgccactgtg	agaatgacac	8220
aaccatttcc	tacacagttt	gcaccccagg	caaagcagag	agcagagggt	cttcagttcca	8280
cgcaacgggt	cttctctgaa	cagcaacaga	gcaaacagat	aggaggaggc	aaagcccaga	8340
aagtggacag	tgattcaagt	aaacctcctg	aaacactgac	cgacctcctc	ggggtctgtc	8400
aggaaaaagt	agaagaaaag	ccaccccctg	cacctccat	agccaccaaa	cctgttagaa	8460
ctggaccaat	caaacctcag	gcgatcaaaa	ccgaagaaac	aaaatcttaa	aggctatggg	8520
ttattgcagg	ggattgggag	gggggcggga	aaacatggag	aattaagtca	gataatgctg	8580
gcagccaaag	gggcaaaatg	gcctgtgaca	ttatcctgtt	cagagcttgg	agatgtacaa	8640
gggacatagg	agcaattttac	actgacacac	agctgctgta	ccagtgaata	cgaggctttg	8700
caagcttgta	cctactatat	aacatgtgct	tggttgatgg	ccatgcatct	tcagtcagaa	8760
tttatatata	aatgtatgca	cccatTTTTT	tgagtgcata	taatttagac	ctaaaaatcc	8820
ttatgattag	atgaaacacc	aaaaatataa	ggaaaataac	acagcagagg	aatagotcag	8880
cctgaacagt	gtgatggctc	cagctactac	atcagatgcg	gtttttttgc	tcccttatgt	8940
tcttcggata	ttgttatggc	atttgtaggc	ttggaggtaa	agaactgaag	ataactggtg	9000
ctggatagag	gagccttatt	ttttattatg	gcagcttgct	atTTTTtataa	catggtgatt	9060
gagttgaaca	caatcaaagt	acagtagtaa	ctgatgtccc	cttcttcctg	gatgaatgag	9120
cagataaata	ttgatgtcag	catccttgaa	ccatatcaaa	gtgagcagtg	tttggctact	9180
gcttctatTT	gaaatgggtgc	tgtgttttgg	ttgtggtctg	aagctttgaa	gcgctactta	9240

```

gcatctcctt tcttccatgg agctctcacg attcaaacat gacagatttg gtaaaatgct 9300
ggttagggtt agtcttcctt gcccctactc agtcatcttt gtatgaatcc catgatttgg 9360
gggttttttt cttttttttt ttataccagt ttttagctgg tgtttatgaa gaacagttag 9420
tacctagaac tgtgccacta attaaaggaa atcctaagaa ggtgcatttc ttacagagc 9480
tgtgtcatgc catccttttg gccctctgct ggaaaagtag aatcaagtct caaataatgc 9540
ctttttaatt gtatcctcta gtattataga tataggacag tactgtatca tacctctgtg 9600
aatgtaaaat atottgtacc tgctttatga tacgtagtag tgaccgtgct ttatcagagc 9660
tgtttttaat gatgttattc tagaatgttt tctttccaga tgatgattca gaagctaatt 9720
ttaaaaaacg gtgccaggta ccacaacagt aacagaactt tgcaattttc tgggggtttt 9780
ttttttacct ttttcccccc ttttttttaa atggagtgtg ctggatgtct ctataatttt 9840
attcagatga ctgcagaacc tggaaaagct gttgctgcta ttgatgcata acatactgct 9900
attggtcttt ttatataaat atatatatat atatacatat atatatataa tttgaatttt 9960
tggaaaacttt agctgtgctg tcaacttttg aaaaagtatc ccgggtttact gtgttgagtt 10020
ggcattgtac agaaattaac agccatattg gtctagaaac gttaaaactta atttttttcc 10080
atttgtacag gggtaacgca ctgtattaaa tatgtaaggt cttatctaca tgggtttgat 10140
tacagaaact aataaagtat tctctaaata atga 10174

```

<210> 83

<211> 2701

<212> PRT

<213> Homo sapiens

<400> 83

```

Met Ser Glu Lys Ser Gly Gln Ser Thr Lys Ala Lys Asp Gly Lys Lys
1          5          10          15
Tyr Ala Thr Leu Ser Leu Phe Asn Thr Tyr Lys Gly Lys Ser Leu Glu
20          25          30
Thr Gln Lys Thr Thr Ala Arg His Gly Leu Gln Ser Leu Gly Lys Val
35          40          45
Gly Ile Ser Arg Arg Met Pro Pro Pro Ala Asn Leu Pro Ser Leu Lys
50          55          60
Ala Glu Asn Lys Gly Asn Asp Pro Asn Val Asn Ile Val Pro Lys Asp
65          70          75          80
Gly Thr Gly Trp Ala Ser Lys Gln Glu Gln His Glu Glu Glu Lys Thr
85          90          95
Pro Glu Val Pro Pro Ala Gln Pro Lys Pro Gly Val Ala Ala Pro Pro
100          105          110
Glu Val Ala Pro Ala Pro Lys Ser Trp Ala Ser Asn Lys Gln Gly Gly
115          120          125
Gln Gly Asp Gly Ile Gln Val Asn Ser Gln Phe Gln Gln Glu Phe Pro
130          135          140
Ser Leu Gln Ala Ala Gly Asp Gln Glu Lys Lys Glu Lys Glu Thr Asn
145          150          155          160
Asp Asp Asn Tyr Gly Pro Gly Pro Ser Leu Arg Pro Pro Asn Val Ala
165          170          175
Cys Trp Arg Asp Gly Gly Lys Ala Ala Gly Ser Pro Ser Ser Asp
180          185          190
Gln Asp Glu Lys Leu Pro Gly Gln Asp Glu Ser Thr Ala Gly Thr Ser
195          200          205
Glu Gln Asn Asp Ile Leu Lys Val Val Glu Lys Arg Ile Ala Cys Gly
210          215          220
Pro Pro Gln Ala Lys Leu Asn Gly Gln Gln Ala Ala Leu Ala Ser Gln
225          230          235          240
Tyr Arg Ala Met Met Pro Pro Tyr Met Phe Gln Gln Tyr Pro Arg Met
245          250          255
Thr Tyr Pro Pro Leu His Gly Pro Met Arg Phe Pro Pro Ser Leu Ser
260          265          270
Glu Thr Asn Lys Gly Leu Arg Gly Arg Gly Pro Pro Pro Ser Trp Ala
275          280          285

```

Ser	Glu	Pro	Glu	Arg	Pro	Ser	Ile	Leu	Ser	Ala	Ser	Glu	Leu	Lys	Glu	290	295	300
Leu	Asp	Lys	Phe	Asp	Asn	Leu	Asp	Ala	Glu	Ala	Asp	Glu	Gly	Trp	Ala	305	310	315
Gly	Ala	Gln	Met	Glu	Val	Asp	Tyr	Thr	Glu	Gln	Leu	Asn	Phe	Ser	Asp	325	330	335
Asp	Asp	Glu	Gln	Gly	Ser	Asn	Ser	Pro	Lys	Glu	Asn	Asn	Ser	Glu	Asp	340	345	350
Gln	Gly	Ser	Lys	Ala	Ser	Glu	Asn	Asn	Glu	Asn	Lys	Lys	Glu	Thr	Asp	355	360	365
Glu	Val	Ser	Asn	Thr	Lys	Ser	Ser	Ser	Gln	Ile	Pro	Ala	Gln	Pro	Ser	370	375	380
Val	Ala	Lys	Val	Pro	Tyr	Gly	Lys	Gly	Pro	Ser	Phe	Asn	Gln	Glu	Arg	385	390	395
Gly	Thr	Ser	Ser	His	Leu	Pro	Pro	Pro	Pro	Lys	Leu	Leu	Ala	Gln	Gln	405	410	415
His	Pro	Pro	Pro	Asp	Arg	Gln	Ala	Val	Pro	Gly	Arg	Pro	Gly	Pro	Phe	420	425	430
Pro	Ser	Lys	Gln	Gln	Val	Ala	Asp	Glu	Asp	Glu	Ile	Trp	Lys	Gln	Arg	435	440	445
Arg	Arg	Gln	Gln	Ser	Glu	Ile	Ser	Ala	Ala	Val	Glu	Arg	Ala	Arg	Lys	450	455	460
Arg	Arg	Glu	Glu	Glu	Glu	Arg	Arg	Met	Glu	Glu	Gln	Arg	Lys	Ala	Ala	465	470	475
Cys	Ala	Glu	Lys	Leu	Lys	Arg	Leu	Asp	Glu	Lys	Leu	Gly	Ile	Leu	Glu	485	490	495
Lys	Gln	Pro	Ser	Pro	Glu	Glu	Ile	Arg	Glu	Arg	Glu	Arg	Glu	Lys	Glu	500	505	510
Arg	Glu	Arg	Glu	Lys	Glu	Leu	Glu	Lys	Glu	Gln	Glu	Gln	Glu	Arg	Glu	515	520	525
Lys	Glu	Arg	Glu	Lys	Asp	Arg	Glu	Arg	Gln	Gln	Glu	Lys	Glu	Lys	Glu	530	535	540
Leu	Glu	Lys	Glu	Gln	Glu	Lys	Gln	Arg	Glu	Met	Glu	Lys	Glu	Arg	Lys	545	550	555
Gln	Glu	Lys	Glu	Lys	Glu	Leu	Glu	Arg	Gln	Lys	Glu	Lys	Glu	Lys	Glu	565	570	575
Leu	Gln	Lys	Met	Lys	Glu	Gln	Glu	Lys	Glu	Cys	Glu	Leu	Glu	Lys	Glu	580	585	590
Arg	Glu	Lys	Leu	Glu	Glu	Lys	Ile	Glu	Pro	Arg	Glu	Pro	Asn	Leu	Glu	595	600	605
Pro	Met	Val	Glu	Lys	Gln	Glu	Ser	Glu	Asn	Ser	Cys	Asn	Lys	Glu	Glu	610	615	620
Glu	Pro	Val	Phe	Thr	Arg	Gln	Asp	Ser	Asn	Arg	Ser	Glu	Lys	Glu	Ala	625	630	635
Thr	Pro	Val	Val	His	Glu	Thr	Glu	Pro	Glu	Ser	Gly	Ser	Gln	Pro	Arg	645	650	655
Pro	Ala	Val	Leu	Ser	Gly	Tyr	Phe	Lys	Gln	Phe	Gln	Lys	Ser	Leu	Pro	660	665	670
Pro	Arg	Phe	Gln	Arg	Gln	Gln	Glu	Gln	Met	Lys	Gln	Gln	Gln	Trp	Gln	675	680	685
Gln	Gln	Gln	Gln	Gln	Gly	Val	Leu	Pro	Gln	Thr	Val	Pro	Ser	Gln	Pro	690	695	700
Ser	Ser	Ser	Thr	Val	Pro	Pro	Pro	Pro	His	Arg	Pro	Leu	Tyr	Gln	Pro	705	710	715
Met	Gln	Pro	His	Pro	Gln	His	Leu	Ala	Ser	Met	Gly	Phe	Asp	Pro	Arg	725	730	735
Trp	Leu	Met	Met	Gln	Ser	Tyr	Met	Asp	Pro	Arg	Met	Met	Ser	Gly	Arg	740	745	750
Pro	Ala	Met	Asp	Ile	Pro	Pro	Ile	His	Pro	Gly	Met	Ile	Pro	Pro	Lys			

755	760	765
Pro Leu Met Arg Arg Asp Gln Met Glu Gly Ser Pro Asn Ser Ser Glu		
770	775	780
Ser Phe Glu His Ile Ala Arg Ser Ala Arg Asp His Ala Ile Ser Leu		
785	790	795
Ser Glu Pro Arg Met Leu Trp Gly Ser Asp Pro Tyr Pro His Ala Glu		800
	805	810
		815
Pro Gln Gln Ala Thr Thr Pro Lys Ala Thr Glu Glu Pro Glu Asp Val		
	820	825
		830
Arg Ser Glu Ala Ala Leu Asp Gln Glu Gln Ile Thr Ala Ala Tyr Ser		
	835	840
		845
Val Glu His Asn Gln Leu Glu Ala His Pro Lys Ala Asp Phe Ile Arg		
	850	855
		860
Glu Ser Ser Glu Ala Gln Val Gln Lys Phe Leu Ser Arg Ser Val Glu		
865	870	875
		880
Asp Val Arg Pro His His Thr Asp Ala Asn Asn Gln Ser Ala Cys Phe		
	885	890
		895
Glu Ala Pro Asp Gln Lys Thr Leu Ser Ala Pro Gln Glu Glu Arg Ile		
	900	905
		910
Ser Ala Val Glu Ser Gln Pro Ser Arg Lys Arg Ser Val Ser His Gly		
	915	920
		925
Ser Asn His Thr Gln Lys Pro Asp Glu Gln Arg Ser Glu Pro Ser Ala		
	930	935
		940
Gly Ile Pro Lys Val Thr Ser Arg Cys Ile Asp Ser Lys Glu Pro Ile		
945	950	955
		960
Glu Arg Pro Glu Glu Lys Pro Lys Lys Glu Gly Phe Ile Arg Ser Ser		
	965	970
		975
Glu Gly Pro Lys Pro Glu Lys Val Tyr Lys Ser Lys Ser Glu Thr Arg		
	980	985
		990
Trp Gly Pro Arg Pro Ser Ser Asn Arg Arg Glu Glu Val Asn Asp Arg		
	995	1000
		1005
Pro Val Arg Arg Ser Gly Pro Ile Lys Lys Pro Val Leu Arg Asp Met		
	1010	1015
		1020
Lys Glu Glu Arg Glu Gln Arg Lys Glu Lys Glu Gly Glu Lys Ala Glu		
1025	1030	1035
		1040
Lys Val Thr Glu Lys Val Val Val Lys Pro Glu Lys Thr Glu Lys Lys		
	1045	1050
		1055
Asp Leu Pro Pro Pro Pro Pro Pro Pro Pro Ala Pro Ile Gln		
	1060	1065
		1070
Pro Gln Ser Val Pro Pro Pro Ile Gln Pro Glu Ala Glu Lys Phe Pro		
	1075	1080
		1085
Ser Thr Glu Thr Ala Thr Leu Ala Gln Lys Pro Ser Gln Asp Thr Glu		
	1090	1095
		1100
Lys Pro Leu Glu Pro Val Ser Thr Val Gln Val Glu Pro Ala Val Lys		
1105	1110	1115
		1120
Thr Val Asn Gln Gln Thr Met Ala Ala Pro Val Val Lys Glu Glu Lys		
	1125	1130
		1135
Gln Pro Glu Lys Val Ile Ser Lys Asp Leu Val Ile Glu Arg Pro Arg		
	1140	1145
		1150
Pro Asp Ser Arg Pro Ala Val Lys Lys Glu Ser Thr Leu Pro Pro Arg		
	1155	1160
		1165
Thr Tyr Trp Lys Glu Ala Arg Glu Arg Asp Trp Phe Pro Asp Gln Gly		
	1170	1175
		1180
Tyr Arg Gly Arg Gly Arg Gly Glu Tyr Tyr Ser Arg Gly Arg Ser Tyr		
1185	1190	1195
		1200
Arg Gly Ser Tyr Gly Gly Arg Gly Arg Gly Gly Arg Gly His Thr Arg		
	1205	1210
		1215
Asp Tyr Pro Gln Tyr Arg Asp Asn Lys Pro Arg Ala Glu His Ile Pro		
	1220	1225
		1230

Ser Gly Pro Leu Arg Gln Arg Glu Glu Ser Glu Thr Arg Ser Glu Ser
 1235 1240 1245
 Ser Asp Phe Glu Val Val Pro Lys Arg Arg Arg Gln Arg Gly Ser Glu
 1250 1255 1260
 Thr Asp Thr Asp Ser Glu Ile His Glu Ser Ala Ser Asp Lys Asp Ser
 1265 1270 1275 1280
 Leu Ser Lys Gly Lys Leu Pro Lys Arg Glu Glu Arg Pro Glu Asn Lys
 1285 1290 1295
 Lys Pro Val Lys Pro His Ser Ser Phe Lys Pro Asp Asn His Val Arg
 1300 1305 1310
 Ile Asp Asn Arg Leu Leu Glu Lys Pro Tyr Val Arg Asp Asp Lys
 1315 1320 1325
 Ala Lys Pro Gly Phe Leu Pro Lys Gly Glu Pro Thr Arg Arg Gly Arg
 1330 1335 1340
 Gly Gly Thr Phe Arg Arg Gly Gly Arg Asp Pro Gly Gly Arg Pro Ser
 1345 1350 1355 1360
 Arg Pro Ser Thr Leu Arg Arg Pro Ala Tyr Arg Asp Asn Gln Trp Asn
 1365 1370 1375
 Pro Arg Gln Ser Glu Val Pro Lys Pro Glu Asp Gly Glu Pro Pro Arg
 1380 1385 1390
 Arg His Glu Gln Phe Ile Pro Ile Ala Ala Asp Lys Arg Pro Pro Lys
 1395 1400 1405
 Phe Glu Arg Lys Phe Asp Pro Ala Arg Glu Arg Pro Arg Arg Gln Arg
 1410 1415 1420
 Pro Thr Arg Pro Pro Arg Gln Asp Lys Pro Pro Arg Phe Arg Arg Leu
 1425 1430 1435 1440
 Arg Glu Arg Glu Ala Ala Ser Lys Ser Asn Glu Val Val Ala Val Pro
 1445 1450 1455
 Thr Asn Gly Thr Val Asn Asn Val Ala Gln Glu Pro Val Asn Thr Leu
 1460 1465 1470
 Gly Asp Ile Ser Gly Asn Lys Thr Pro Asp Leu Ser Asn Gln Asn Ser
 1475 1480 1485
 Ser Asp Gln Ala Asn Glu Glu Trp Glu Thr Ala Ser Glu Ser Ser Asp
 1490 1495 1500
 Phe Asn Glu Arg Arg Glu Arg Asp Glu Lys Lys Asn Ala Asp Leu Asn
 1505 1510 1515 1520
 Ala Gln Thr Val Val Lys Val Gly Glu Asn Val Leu Pro Pro Lys Arg
 1525 1530 1535
 Glu Ile Ala Lys Arg Ser Phe Ser Ser Gln Arg Pro Val Asp Arg Gln
 1540 1545 1550
 Asn Arg Arg Gly Asn Asn Gly Pro Pro Lys Ser Gly Arg Asn Phe Ser
 1555 1560 1565
 Gly Pro Arg Asn Glu Arg Arg Ser Gly Pro Pro Ser Lys Ser Gly Lys
 1570 1575 1580
 Arg Gly Pro Phe Asp Asp Gln Pro Ala Gly Thr Thr Gly Val Asp Leu
 1585 1590 1595 1600
 Ile Asn Gly Ser Ser Ala His His Gln Glu Gly Val Pro Asn Gly Thr
 1605 1610 1615
 Gly Gln Lys Asn Ser Lys Asp Ser Thr Gly Lys Lys Arg Glu Asp Pro
 1620 1625 1630
 Lys Pro Gly Pro Lys Lys Pro Lys Glu Lys Val Asp Ala Leu Ser Gln
 1635 1640 1645
 Phe Asp Leu Asn Asn Tyr Ala Ser Val Val Ile Ile Asp Asp His Pro
 1650 1655 1660
 Glu Val Thr Val Ile Glu Asp Pro Gln Ser Asn Leu Asn Asp Asp Gly
 1665 1670 1675 1680
 Phe Thr Glu Val Val Ser Lys Lys Gln Gln Lys Arg Leu Gln Asp Glu
 1685 1690 1695
 Glu Arg Arg Lys Lys Glu Glu Gln Val Ile Gln Val Trp Asn Lys Lys

1700	1705	1710
Asn Ala Asn Glu Lys Gly Arg Ser Gln Thr Ser Lys Leu Pro Pro Arg		
1715	1720	1725
Phe Ala Lys Lys Gln Ala Thr Gly Ile Gln Gln Ala Gln Ser Ser Ala		
1730	1735	1740
Ser Val Pro Pro Leu Ala Ser Ala Pro Leu Pro Pro Ser Thr Ser Ala		
1745	1750	1755
Ser Val Pro Ala Ser Thr Ser Ala Pro Leu Pro Ala Thr Leu Thr Pro		
1765	1770	1775
Val Pro Ala Ser Thr Ser Ala Pro Val Pro Ala Ser Thr Leu Ala Pro		
1780	1785	1790
Val Leu Ala Ser Thr Ser Ala Pro Val Pro Ala Ser Pro Leu Ala Pro		
1795	1800	1805
Val Ser Ala Ser Ala Ser Val Ser Ala Ser Val Pro Ala Ser Thr Ser		
1810	1815	1820
Ala Ala Ala Ile Thr Ser Ser Ser Ala Pro Ala Ser Ala Pro Ala Pro		
1825	1830	1835
Thr Pro Ile Leu Ala Ser Val Ser Thr Pro Ala Ser Val Thr Ile Leu		
1845	1850	1855
Ala Ser Ala Ser Ile Pro Ile Leu Ala Ser Ala Leu Ala Ser Thr Ser		
1860	1865	1870
Ala Pro Thr Pro Ala Pro Ala Ala Ser Ser Pro Ala Ala Pro Val Ile		
1875	1880	1885
Thr Ala Pro Thr Ile Pro Ala Ser Ala Pro Thr Ala Ser Val Pro Leu		
1890	1895	1900
Ala Pro Ala Ser Ala Ser Ala Pro Ala Pro Ala Pro Thr Pro Val Ser		
1905	1910	1915
Ala Pro Asn Pro Ala Pro Pro Ala Pro Ala Gln Thr Gln Ala Gln Thr		
1925	1930	1935
His Lys Pro Val Gln Asn Pro Leu Gln Thr Thr Ser Gln Ser Ser Lys		
1940	1945	1950
Gln Pro Pro Pro Ser Ile Arg Leu Pro Ser Ala Gln Thr Pro Asn Gly		
1955	1960	1965
Thr Asp Tyr Val Ala Ser Gly Lys Ser Ile Gln Thr Pro Gln Ser His		
1970	1975	1980
Gly Thr Leu Thr Ala Glu Leu Trp Asp Asn Lys Val Ala Pro Pro Ala		
1985	1990	1995
Val Leu Asn Asp Ile Ser Lys Lys Leu Gly Pro Ile Ser Pro Pro Gln		
2005	2010	2015
Pro Pro Ser Val Ser Ala Trp Asn Lys Pro Leu Thr Ser Phe Gly Ser		
2020	2025	2030
Ala Pro Ser Ser Glu Gly Ala Lys Asn Gly Gln Glu Ser Gly Leu Glu		
2035	2040	2045
Ile Gly Thr Asp Thr Ile Gln Phe Gly Ala Pro Ala Ser Asn Gly Asn		
2050	2055	2060
Glu Asn Glu Val Val Pro Val Leu Ser Glu Lys Ser Ala Asp Lys Ile		
2065	2070	2075
Pro Glu Pro Lys Glu Gln Arg Gln Lys Gln Pro Arg Ala Gly Pro Ile		
2085	2090	2095
Lys Ala Gln Lys Leu Pro Asp Leu Ser Pro Val Glu Asn Lys Glu His		
2100	2105	2110
Lys Pro Gly Pro Ile Gly Lys Glu Arg Ser Leu Lys Asn Arg Lys Val		
2115	2120	2125
Lys Asp Ala Gln Gln Val Glu Pro Glu Gly Gln Glu Lys Pro Ser Pro		
2130	2135	2140
Ala Thr Val Arg Ser Thr Asp Pro Val Thr Thr Lys Glu Thr Lys Ala		
2145	2150	2155
Val Ser Glu Met Ser Thr Glu Ile Gly Thr Met Ile Ser Val Ser Ser		
2165	2170	2175

Ala Glu Tyr Gly Thr Asn Ala Lys Glu Ser Val Thr Asp Tyr Thr Thr
 2180 2185 2190
 Pro Ser Ser Ser Leu Pro Asn Thr Val Ala Thr Asn Asn Thr Lys Met
 2195 2200 2205
 Glu Asp Thr Leu Val Asn Asn Val Pro Leu Pro Asn Thr Leu Pro Leu
 2210 2215 2220
 Pro Lys Arg Glu Thr Ile Gln Gln Ser Ser Ser Leu Thr Ser Val Pro
 2225 2230 2235 2240
 Pro Thr Thr Phe Ser Leu Thr Phe Lys Met Glu Ser Ala Arg Lys Ala
 2245 2250 2255
 Trp Glu Asn Ser Pro Asn Val Arg Glu Lys Gly Ser Pro Val Thr Ser
 2260 2265 2270
 Thr Ala Pro Pro Ile Ala Thr Gly Val Ser Ser Ser Ala Ser Gly Pro
 2275 2280 2285
 Ser Thr Ala Asn Tyr Asn Ser Phe Ser Ser Ala Ser Met Pro Gln Ile
 2290 2295 2300
 Pro Val Ala Ser Val Thr Pro Thr Ala Ser Leu Ser Gly Ala Gly Thr
 2305 2310 2315 2320
 Tyr Thr Thr Ser Ser Leu Ser Thr Lys Ser Thr Thr Thr Ser Asp Pro
 2325 2330 2335
 Pro Asn Ile Cys Lys Val Lys Pro Gln Gln Leu Gln Thr Ser Ser Leu
 2340 2345 2350
 Pro Ser Ala Ser His Phe Ser Gln Leu Ser Cys Met Pro Ser Leu Ile
 2355 2360 2365
 Ala Gln Gln Gln Gln Asn Pro Gln Val Tyr Val Ser Gln Ser Ala Ala
 2370 2375 2380
 Ala Gln Ile Pro Ala Phe Tyr Met Asp Thr Ser His Leu Phe Asn Thr
 2385 2390 2395 2400
 Gln His Ala Arg Leu Ala Pro Pro Ser Leu Ala Gln Gln Gln Gly Phe
 2405 2410 2415
 Gln Pro Gly Leu Ser Gln Pro Thr Ser Val Gln Gln Ile Pro Ile Pro
 2420 2425 2430
 Ile Tyr Ala Pro Leu Gln Gly Gln His Gln Ala Gln Leu Ser Leu Gly
 2435 2440 2445
 Ala Gly Pro Ala Val Ser Gln Ala Gln Glu Leu Phe Ser Ser Ser Leu
 2450 2455 2460
 Gln Pro Tyr Arg Ser Gln Pro Ala Phe Met Gln Ser Ser Leu Ser Gln
 2465 2470 2475 2480
 Pro Ser Val Val Leu Ser Gly Thr Ala Ile His Asn Phe Pro Thr Val
 2485 2490 2495
 Gln His Gln Glu Leu Ala Lys Ala Gln Ser Gly Leu Ala Phe Gln Gln
 2500 2505 2510
 Thr Ser Asn Thr Gln Pro Ile Pro Ile Leu Tyr Glu His Gln Leu Gly
 2515 2520 2525
 Gln Ala Ser Gly Leu Gly Gly Ser Gln Leu Ile Asp Thr His Leu Leu
 2530 2535 2540
 Gln Ala Arg Ala Asn Leu Thr Gln Ala Ser Asn Leu Tyr Ser Gly Gln
 2545 2550 2555 2560
 Val Gln Gln Pro Gly Gln Thr Asn Phe Tyr Asn Thr Ala Gln Ser Pro
 2565 2570 2575
 Ser Ala Leu Gln Gln Val Thr Val Pro Leu Pro Ala Ser Gln Leu Ser
 2580 2585 2590
 Leu Pro Asn Phe Gly Ser Thr Gly Gln Pro Leu Ile Ala Leu Pro Gln
 2595 2600 2605
 Thr Leu Gln Pro Pro Leu Gln His Thr Thr Pro Gln Ala Gln Ala Gln
 2610 2615 2620
 Ser Leu Ser Arg Pro Ala Gln Val Ser Gln Pro Phe Arg Gly Leu Ile
 2625 2630 2635 2640
 Pro Ala Gly Thr Gln His Ser Met Ile Ala Thr Thr Gly Lys Met Ser

	2645		2650		2655
Glu Met Glu Leu Lys Ala Phe Gly Ser Gly Ile Asp Ile Lys Pro Gly					
	2660		2665		2670
Thr Pro Pro Ile Ala Gly Arg Ser Thr Thr Pro Thr Ser Ser Pro Ser					
	2675		2680		2685
Gly Leu Leu Leu Gln Val Arg Thr Ala Ser Pro Ala Lys					
	2690		2695		2700

<210> 84
 <211> 597
 <212> DNA
 <213> Homo sapiens

<400> 84
 agctgaagtt gaggatctct tactctcttaa gccacggaat taacccgagc aggcattggag 60
 gcctctgctc tcacctcatc agcagtgaac agtgtggcca aagtggtcag ggtggcctct 120
 ggctctgccc tagttttgcc cctggccagg attgctacag ttgtgattgg aggagttgtg 180
 gccatggcgg ctgtgcccac ggtgctcagt gccatgggct tcaactgcggc gggaatcgcc 240
 tcgtcctcca tagcagccaa gatgatgtcc gcggcggcca ttgccaatgg ggggtggagt 300
 gcctcgggca gccttgtggg tactctgcag tcactgggag caactggact ctccggattg 360
 accaagttca tcctgggctc cattgggtct gccattgcgg ctgtcattgc gaggttctac 420
 tagctccctg cccctcgccc tgcagagaag agaaccatgc caggggagaa ggcacccagc 480
 catcctgacc cagcgaggag ccaactatcc caaatatacc tgggtgaaat ataccaaatt 540
 ctgcatctcc agaggaaaat aagaaataaa gatgaattgt tgcaactctt aaaaaaa 597

<210> 85
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 85
 Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
 1 5 10 15
 Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
 20 25 30
 Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Met Ala Ala Val Pro
 35 40 45
 Met Val Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser
 50 55 60
 Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly
 65 70 75 80
 Gly Val Ala Ser Gly Ser Leu Val Gly Thr Leu Gln Ser Leu Gly Ala
 85 90 95
 Thr Gly Leu Ser Gly Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser
 100 105 110
 Ala Ile Ala Ala Val Ile Ala Arg Phe Tyr
 115 120

<210> 86
 <211> 1032
 <212> DNA
 <213> Homo sapiens

<400> 86
 ggagggtggg cagcactcgc tttattgtcc agcattccac atggatagtc gccacacctt 60
 tgcccctgct gcgatgacc tgtgccact tctgtgttct ctgccaccgc tgctgctgct 120
 gctggacgct cccacggcgg cgggtgcaggc gtcccctctg caagcgtag acttctttgg 180

```

gaatggggcca ccagttaact acaagacagg caatctatac ctgcggggggc ccctgaagaa 240
gtccaatgca ccgcttgta atgtgaccct ctactatgaa gcactgtgcg gtggctgccg 300
agccttcctg atccgggagc tcttcccaac atggctgttg gtcattggaga tcctcaatgt 360
cacgtcggtg ccctacggaa acgcacagga acaaaatgtc agtggcaggt gggagttcaa 420
gtgccagctt ggagaagagg agtgcaaatt caacaagggt gaggcctgcg tgttgatga 480
acttgacatg gagctagcct tcctgaccat gtctggcatg gcatggaaga gtttgaggac 540
atggagagaa gtctgccact atgcctgcag ctctacgccc cagggtctgtc gccagaacta 600
tcatggagtg tgcaatgggg gaccgcgga tgcagctcat gcacgccaac gccagcgga 660
cagatgctct ccagccaccg cagcagtatg tgccctgggt caccgtcaat gggaaaccct 720
tggaagatca gaccagctc cttacccttg tctgccagtt gtaccagggc aagaagccgg 780
atgtctgccc ttctcaacc agctccctcc ggagtgtttg cttcgagtgt tggccggtgg 840
gtgcggaga gctcatggaa ggcgagtggg aactcggctg cctgcctttt tttctgatcc 900
agaccctcgg cacctgctac ttaccaactg gaaaatttta tgcattccat gaagcccaga 960
tacacaaaat tccacccta gatcaagaat cctgctccac taagaatggt gctaaagtaa 1020
aactagttta at 1032

```

<210> 87

<211> 303

<212> PRT

<213> Homo sapiens

<400> 87

```

Met Asp Ser Arg His Thr Phe Ala Pro Ala Ala Met Thr Leu Ser Pro
 1          5          10          15
Leu Leu Leu Phe Leu Pro Pro Leu Leu Leu Leu Leu Asp Val Pro Thr
 20          25          30
Ala Ala Val Gln Ala Ser Pro Leu Gln Ala Leu Asp Phe Phe Gly Asn
 35          40          45
Gly Pro Pro Val Asn Tyr Lys Thr Gly Asn Leu Tyr Leu Arg Gly Pro
 50          55          60
Leu Lys Lys Ser Asn Ala Pro Leu Val Asn Val Thr Leu Tyr Tyr Glu
 65          70          75          80
Ala Leu Cys Gly Gly Cys Arg Ala Phe Leu Ile Arg Glu Leu Phe Pro
 85          90          95
Thr Trp Leu Leu Val Met Glu Ile Leu Asn Val Thr Ser Val Pro Tyr
100          105          110
Gly Asn Ala Gln Glu Gln Asn Val Ser Gly Arg Trp Glu Phe Lys Cys
115          120          125
Gln Leu Gly Glu Glu Glu Cys Lys Phe Asn Lys Val Glu Ala Cys Val
130          135          140
Leu Asp Glu Leu Asp Met Glu Leu Ala Phe Leu Thr Met Ser Gly Met
145          150          155          160
Ala Trp Lys Ser Leu Arg Thr Trp Arg Glu Val Cys His Tyr Ala Cys
165          170          175
Ser Ser Thr Pro Gln Gly Cys Arg Gln Asn Tyr His Gly Val Cys Asn
180          185          190
Gly Gly Pro Arg His Ala Ala His Ala Arg Gln Arg Pro Ala Asp Arg
195          200          205
Cys Ser Pro Ala Thr Ala Arg Val Cys Ala Leu Gly His Arg Gln Trp
210          215          220
Glu Thr Leu Gly Arg Ser Asp Pro Ala Pro Tyr Pro Cys Leu Pro Val
225          230          235          240
Val Pro Gly Gln Glu Ala Gly Cys Leu Pro Phe Leu Asn Gln Leu Pro
245          250          255
Pro Glu Cys Leu Leu Arg Val Leu Ala Gly Gly Leu Arg Arg Ala His
260          265          270
Gly Arg Arg Val Gly Thr Arg Leu Pro Ala Phe Phe Ser Asp Pro Asp
275          280          285
Pro Arg His Leu Leu Leu Thr Asn Trp Lys Ile Leu Cys Ile Pro

```

290

295

300

<210> 88
 <211> 905
 <212> DNA
 <213> Homo sapiens

<400> 88
 caacacaggg gcagtctcca ggacctccac accattaaca agatgagcct tgtgctccct 60
 tgggctctag agaggaagcc cctctgagcc ctccagcccct ctttcctccc tctcctaaag 120
 taatttgatc ctccaggaatt tgttctgccc tcatctggcc ctggccagct ctgcatttga 180
 caaatgccag gaagaggaaa ctggtgagaa aacggaaacta ctggggaaaag ggagggctca 240
 ctgagaacca tcccggtaac ccgaccgccg ctggtcacca tgaaccacat tgtgcaaacc 300
 ttctctcctg tcaacagcgg ccagcctccc aactacgaga tgctcaagga ggagcaggaa 360
 gtggctatgc tggggggggcc ccacaaccct gctccccga cgtccaccgt gatccacatc 420
 cgcagcgaga cctccgtgcc tgaccatgtc gtctggtccc tgttcaacac cctcttcatg 480
 aacacctgct gcctgggctt catagcattc gcctactccg tgaagtctag ggacaggaag 540
 atggttggcg acgtgaccgg ggcccaggcc tatgcctcca ccgccaagtg cctgaacatc 600
 tgggcccctga ttttgggcat cttcatgacc attctgctcg tcatcatccc agtggttggtc 660
 gtccaggccc agcgatagat caggaggcat cattgaggcc aggagctctg cccgtgacct 720
 gtatcccacg tactctatct tccattcctc gccctgcccc cagaggccag gagctctgcc 780
 cttgacctgt attccactta ctccaccttc cattcctcgc cctgtcccca cagccgagtc 840
 ctgcatcagc cctttatcct cacacgcttt tctacaatgg cattcaataa agtgatatatg 900
 tttct 905

<210> 89
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 89
 Met Asn His Ile Val Gln Thr Phe Ser Pro Val Asn Ser Gly Gln Pro
 1 5 10 15
 Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met Leu Gly
 20 25 30
 Gly Pro His Asn Pro Ala Pro Pro Thr Ser Thr Val Ile His Ile Arg
 35 40 45
 Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe Asn Thr
 50 55 60
 Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr Ser
 65 70 75 80
 Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly Ala Gln
 85 90 95
 Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu Ile Leu
 100 105 110
 Gly Ile Phe Met Thr Ile Leu Leu Val Ile Ile Pro Val Leu Val Val
 115 120 125
 Gln Ala Gln Arg
 130

<210> 90
 <211> 2499
 <212> DNA
 <213> Homo sapiens

<400> 90
 agatgcgagc actgoggctg ggcgctgagg atcagccgct tcctgcctgg attccacagc 60

```

ttcgcgcgcgt gtactgtgcg cccatccctg cgcgcgccagc ctgccaagca gcgtgccccg 120
gttgccaggcg tcatgcagcg ggcgcgaccc acgctctggg ccgctgcgct gactctgctg 180
gtgctgctcc gcgggcccgc ggtggcgcg gctggcgcg gctcgggggg cttgggtccc 240
gtggtgcgct gcgagccgtg cgacgcgcgt gcactggccc agtgcgcgcc tccgcccgcc 300
gtgtgcgcgg agctggtgcg cgagccgggc tgcggctgct gcctgaagtgc cgactgagc 360
gagggccagc cgtgcggcat ctacaccgag cgctgtggct ccggccttcg ctgccagccg 420
tcgcccgcagc aggcgcgacc gctgcaggcg ctgctggacg gccgcgggct ctgcgtcaac 480
gctagtgcgc tcagccgcct gcgcgcctac ctgctgccag cgccgccagc tccaggaaat 540
gctagtgcgt cggaggaaga ccgcagcgcc ggcagtgtgg agagcccgtc cgtctccagc 600
acgcaccggg tgtctgatcc caagtccatt cccctccatt caaagataat catcatcaag 660
aaagggcatg ctaaagacag ccagcgctac aaagttgact acgagtctca gagcacagat 720
accagaact tctcctccga gtccaagcgg gagacagaat atggtccctg ccgtagagaa 780
atggaagaca cactgaatca cctgaagtgc ctcaatgtgc tgagtccagc ggggtgtacac 840
attcccaact gtgacaagaa gggattttat aagaaaaagc agtgctcgccc ttccaaaggc 900
aggaagcggg gcttctgctg gtgtgtggat aagtatgggc agcctctccc aggtacacc 960
accaagggga aggaggacgt gcactgctac agcatgcaga gcaagtagac gcctgccgca 1020
aggttaatgt ggagctcaaa tatgccttat tttctacaaa agactgcca ggacatgacc 1080
agcagctggc tacagcctcg atttatattt ctgtttgtgg tgaactgatt ttttttaaac 1140
caaagtttag aaagaggttt ttgaaatgcc tatggtttct ttgaatggta aacttgagca 1200
tcttttctac ttccagtagt cagcaaagag cagtttgaat tttcttgcg ctctcatca 1260
aaatatctag agactcgagc acagcaccca gacttcatgc gcccgaggaa tgctcaccac 1320
atgttggtcg aagcgccga ccaactgactt tgtgacttag gcggtgtgt tgctatgta 1380
gagaacacgc ttcaccccca ctccctgtac agtgcgcaca ggctttatcg agaataggaa 1440
aacctttaaa ccccggtcat ccgacatcc caacgcagtc tctggagct cacagccttc 1500
tgtggtgtca tttctgaaac aaggcggtg atccctcaac ccagaagagt gtttatgtct 1560
tcaagtgacc tgtactgctt ggggactatt tgagaaaata aggtggagtc ctacttgttt 1620
cacaaatatg tatctaagaa tgttctaggg cactctggga acctataaag gcaggatatt 1680
cgggcccctcc tcttcaggaa tcttctgaa gacatggccc agtcgaaggc ccaggatggc 1740
ttttgctgcg gcccggtggg gtaggagggg cagagagaca gggagagtoa gcctccacat 1800
tcagaggcat cacaagtaat ggcacaattc ttcggatgac tgcagaaaat agtgttttgt 1860
agttcaacaa ctcaagacga agcttatttc tgaggataag ctcttttaaag acaaagcttt 1920
attttcatct ctcatctttt gtcctcctta gcacaatgca aaaaagaata gtaatatcag 1980
aacaggaagg aggaatggct tgctggggag cccatccagg acactgggag cacatagaga 2040
ttcacccatg tttgttgaac ttagagtcac tctcatgctt ttctttataa ttcacacata 2100
tatgcagaga agatatgttc ttgttaacat tgtatacaac atagcccca atatagtaag 2160
atctatacta gataatccta gatgaaatgt tagagatgct atatgatata actgtggcca 2220
tgactgagga aaggagctca cgcccagaga ctgggctgct ctcccggagg ccaaaccaca 2280
gaaggtctgg caaagtcagg ctccaggaga ctctgccctg ctgcagacct cgggtgtggc 2340
acacgctgca tagagctctc cttgaaaaca gaggggtctc aagacattct gcctacctat 2400
tagcttttct ttattttttt aacttttttg ggggaaaagt atttttgaga agtttgtctt 2460
gcaatgtatt tataaatagt aaataaagtt tttaccatt 2499

```

<210> 91

<211> 291

<212> PRT

<213> Homo sapiens

<400> 91

```

Met Gln Arg Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu Thr Leu Leu
 1             5             10             15
Val Leu Leu Arg Gly Pro Pro Val Ala Arg Ala Gly Ala Ser Ser Gly
      20             25             30
Gly Leu Gly Pro Val Val Arg Cys Glu Pro Cys Asp Ala Arg Ala Leu
      35             40             45
Ala Gln Cys Ala Pro Pro Pro Ala Val Cys Ala Glu Leu Val Arg Glu
      50             55             60
Pro Gly Cys Gly Cys Cys Leu Thr Cys Ala Leu Ser Glu Gly Gln Pro
      65             70             75             80
Cys Gly Ile Tyr Thr Glu Arg Cys Gly Ser Gly Leu Arg Cys Gln Pro

```

```
<210> 92
<211> 1639
<212> DNA
<213> Homo sapiens
```

<400> 92						
agcagagcac	acaagcttct	aggacaagag	ccaggaagaa	accaccggaa	ggaaccatct	60
cactgtgtgt	aaacatgact	tccaagctgg	cogtggctct	cttggcagcc	ttcctgattt	120
ctgcagctct	gtgtgaagg	gcagttttgc	caaggagtgc	taaagaactt	agatgtcagt	180
gcataaagac	atactccaaa	cctttccacc	ccaaatttat	caaagaactg	agagtgattg	240
agctgtggcc	acactgcgcc	aacacagaaa	tatttgtaaa	gctttctgat	ggaagagagc	300
tctgtctgga	ccccaaaggaa	aactgggtgc	agagggttgt	ggagaagttt	ttgaagaggg	360
ctgagaattc	ataaaaaaat	tcattctctg	tggtatocaa	gaatcagtga	agatgccagt	420
gaaacttcaa	gcaaatctac	ttcaacactt	catgtattgt	gtgggtctgt	tgtagggttg	480
ccagatgcaa	tacaagattc	ctggttaaat	ttgaatttca	gtaaacaatg	aatagttttt	540
cattgtacca	tgaaatatcc	agaacatact	tatatgtaaa	gtattattta	tttgaatcta	600
caaaaaacaa	caaataattt	ttaaatataa	ggattttcct	agatattgca	cgggagaata	660
tacaaaatgc	aaaattgagc	caaggggccaa	gagaatatcc	gaactttaat	ttcaggaatt	720
gaatggggtt	gctagaatgt	gatatttgaa	gcatcacata	aaaatgatgg	gacaataaat	780
tttgccataa	agtcaaaattt	agctggaaat	cctggatttt	tttctgttaa	atctggcaac	840
cctagtctgc	tagccaggat	ccacaaggctc	ttgttcocact	gtgccttggt	ttctccttta	900
tttctaagtg	gaaaaagtat	tagccaccat	cttacctcac	agtgatgttg	tgaggacatg	960
tggaagcact	ttaagttttt	tcatcataac	ataaattatt	ttcaagtgtg	acttattaac	1020
ctattttatta	tttatgtatt	tattttaagca	tcaaataattt	gtgcaagaat	ttggaaaaat	1080
agaagatgaa	tcattgattg	aatagttata	aagatgttat	agtaaattta	ttttatttta	1140
gatattaaat	gatgttttat	tagataaatt	tcaatcaggg	tttttagatt	aaacaaagaa	1200
acaattgggt	accagtttaa	attttcattt	cagataaaca	acaaataaatt	ttttagtata	1260
agtcattat	tgtttatctg	aaagtttttaa	ttgaactaac	aatcctagtt	tgatactccc	1320
agtcttgca	ttgccacgtg	tgttggtagt	gctgtgttga	attacggaat	gaatagtttag	1380
aactattaaa	acagccaaaa	ctccacagtc	aatattagta	attttcttgc	ggttgaaact	1440

```

tggtttattat gtacaaatag attcattataa tattatttaa atgactgcat ttttaaatac 1500
aaggcttttat atttttaact ttaagatggt tttatgtgct ctccaaattt tttttactgt 1560
ttctgattgt atggaaatat aaaagtaa atgaaacatt taaaatataa tttgttgtca 1620
aagtaaaaaa aaaaaaaaaa 1639

```

<210> 93
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 93

Met	Thr	Ser	Lys	Leu	Ala	Val	Ala	Leu	Leu	Ala	Ala	Phe	Leu	Ile	Ser
1				5				10						15	
Ala	Ala	Leu	Cys	Glu	Gly	Ala	Val	Leu	Pro	Arg	Ser	Ala	Lys	Glu	Leu
		20						25					30		
Arg	Cys	Gln	Cys	Ile	Lys	Thr	Tyr	Ser	Lys	Pro	Phe	His	Pro	Lys	Phe
		35				40						45			
Ile	Lys	Glu	Leu	Arg	Val	Ile	Glu	Ser	Gly	Pro	His	Cys	Ala	Asn	Thr
	50					55					60				
Glu	Ile	Ile	Val	Lys	Leu	Ser	Asp	Gly	Arg	Glu	Leu	Cys	Leu	Asp	Pro
65					70				75					80	
Lys	Glu	Asn	Trp	Val	Gln	Arg	Val	Val	Glu	Lys	Phe	Leu	Lys	Arg	Ala
				85					90					95	
Glu	Asn	Ser													

<210> 94
 <211> 1840
 <212> DNA
 <213> Homo sapiens

<400> 94

tccacacaca	caaaaaaacct	gcgcggtgagg	ggggaggaaa	agcagggcct	ttaaaaaggc	60
aatcacaaca	acttttgctg	ccaggatgcc	cttgcttttg	ctgagaggat	ttctgttggc	120
aagttgctgg	attatagtga	ggagttcccc	caccccagga	tccgaggggc	acagcgcggc	180
ccccgactgt	ccgtcctgtg	cgctggccgc	cctcccaaag	gatgtacca	actctcagcc	240
agagatggtg	gaggccgtca	agaagcacat	tttaaacaatg	ctgcacttga	agaagagacc	300
cgatgtcacc	cagccggtac	ccaaggcggc	gcttctgaac	gcgatcagaa	agcttcatgt	360
gggcaaagtc	ggggagaacg	ggtatgtgga	gatagaggat	gacattggaa	ggagggcaga	420
aatgaatgaa	cttatggagc	agacctcgga	gatcatcacg	tttgccgagt	caggaacagc	480
caggaagacg	ctgcacttcg	agattttocaa	ggaaggcagt	gacctgtcag	tggtggagcg	540
tgcagaagtc	tggtctcttc	taaaagtccc	caaggccaac	aggaccagga	ccaaagtcac	600
catccgcctc	ttccagcagc	agaagcaccc	gcagggcagc	ttggacacag	gggaagaggc	660
cgaggaagtg	ggcttaaagg	gggagaggag	tgaactgttg	ctctctgaaa	aagtagtaga	720
cgctcggaag	agcacctggc	atgtcttccc	tgtctccagc	agcatccagc	ggttgctgga	780
ccagggcaag	agctccctgg	acgttcggat	tgcctgtgag	cagtgccagg	agagtggcgc	840
cagcttggtt	ctcctgggca	agaagaagaa	gaaagaagag	gagggggaag	ggaaaaagaa	900
gggcggaggt	gaaggtgggg	caggagcaga	tgaggaaaag	gagcagtcgc	acagaccttt	960
cctcatgctg	caggcccggc	agtctgaaga	ccaccctcat	cgccggcgctc	ggcggggcctt	1020
ggagtgtgat	ggcaaggtca	acatctgctg	taagaaacag	ttctttgtca	gtttcaagga	1080
catcggctgg	aatgactgga	tcattgctcc	ctctggctat	catgccaaact	actgcgaggg	1140
tgagtgcctg	agccatatag	caggcacgtc	cgggtcctca	ctgtccttcc	actcaacagt	1200
catcaaccac	taccgcatgc	ggggccatag	cccctttgcc	aacctcaaat	cgtgctgtgt	1260
gcccaccaag	ctgagaccca	tgtccatggt	gtactatgat	gatggtcaaa	acatcatcaa	1320
aaaggacatt	cagaacatga	tcgtggagga	gtgtgggtgc	tcataagagt	gcccagccca	1380
gggggaaagg	gagcaagagt	tgtccagaga	agacagtggc	aaaatgaaga	aatttttaag	1440
gtttctgagt	taaccagaaa	aatagaaatt	aaaaacaaaa	caaaacaaaa	aaaaaaacaa	1500
aaaaaaacaa	aagtaaatta	aaaacaaacc	tgatgaaaca	gatgaaacag	atgaaggaag	1560


```

atgtggaaat cttagcctgc cttagccagg gctcagagat gaagcagtga agagacagat 1620
tgggaggggaa aggggagaatg gtgtaccctt tatttcttct gaaatcacac tgatgacatc 1680
agttgttttaa acgggggtatt gtcctttccc cccttgaggt tcccttgtga gcttgaatca 1740
accaatctga tctgcagtag tgtggactag aacaacccaa atagcatcta gaaagccatg 1800
agtttgaaag ggcccatcac aggcactttc ctagcctaata 1840

```

<210> 95
 <211> 426
 <212> PRT
 <213> Homo sapiens

<400> 95

Met	Pro	Leu	Leu	Trp	Leu	Arg	Gly	Phe	Leu	Leu	Ala	Ser	Cys	Trp	Ile	1	5	10	15
Ile	Val	Arg	Ser	Ser	Pro	Thr	Pro	Gly	Ser	Glu	Gly	His	Ser	Ala	Ala	20	25	30	
Pro	Asp	Cys	Pro	Ser	Cys	Ala	Leu	Ala	Ala	Leu	Pro	Lys	Asp	Val	Pro	35	40	45	
Asn	Ser	Gln	Pro	Glu	Met	Val	Glu	Ala	Val	Lys	Lys	His	Ile	Leu	Asn	50	55	60	
Met	Leu	His	Leu	Lys	Lys	Arg	Pro	Asp	Val	Thr	Gln	Pro	Val	Pro	Lys	65	70	75	80
Ala	Ala	Leu	Leu	Asn	Ala	Ile	Arg	Lys	Leu	His	Val	Gly	Lys	Val	Gly	85	90	95	
Glu	Asn	Gly	Tyr	Val	Glu	Ile	Glu	Asp	Asp	Ile	Gly	Arg	Arg	Ala	Glu	100	105	110	
Met	Asn	Glu	Leu	Met	Glu	Gln	Thr	Ser	Glu	Ile	Ile	Thr	Phe	Ala	Glu	115	120	125	
Ser	Gly	Thr	Ala	Arg	Lys	Thr	Leu	His	Phe	Glu	Ile	Ser	Lys	Glu	Gly	130	135	140	
Ser	Asp	Leu	Ser	Val	Val	Glu	Arg	Ala	Glu	Val	Trp	Leu	Phe	Leu	Lys	145	150	155	160
Val	Pro	Lys	Ala	Asn	Arg	Thr	Arg	Thr	Lys	Val	Thr	Ile	Arg	Leu	Phe	165	170	175	
Gln	Gln	Gln	Lys	His	Pro	Gln	Gly	Ser	Leu	Asp	Thr	Gly	Glu	Glu	Ala	180	185	190	
Glu	Glu	Val	Gly	Leu	Lys	Gly	Glu	Arg	Ser	Glu	Leu	Leu	Leu	Ser	Glu	195	200	205	
Lys	Val	Val	Asp	Ala	Arg	Lys	Ser	Thr	Trp	His	Val	Phe	Pro	Val	Ser	210	215	220	
Ser	Ser	Ile	Gln	Arg	Leu	Leu	Asp	Gln	Gly	Lys	Ser	Ser	Leu	Asp	Val	225	230	235	240
Arg	Ile	Ala	Cys	Glu	Gln	Cys	Gln	Glu	Ser	Gly	Ala	Ser	Leu	Val	Leu	245	250	255	
Leu	Gly	Lys	Lys	Lys	Lys	Lys	Glu	Glu	Gly	Glu	Gly	Lys	Lys	Lys		260	265	270	
Gly	Gly	Gly	Glu	Gly	Gly	Ala	Gly	Ala	Asp	Glu	Glu	Lys	Glu	Gln	Ser	275	280	285	
His	Arg	Pro	Phe	Leu	Met	Leu	Gln	Ala	Arg	Gln	Ser	Glu	Asp	His	Pro	290	295	300	
His	Arg	Arg	Arg	Arg	Arg	Gly	Leu	Glu	Cys	Asp	Gly	Lys	Val	Asn	Ile	305	310	315	320
Cys	Cys	Lys	Lys	Gln	Phe	Phe	Val	Ser	Phe	Lys	Asp	Ile	Gly	Trp	Asn	325	330	335	
Asp	Trp	Ile	Ile	Ala	Pro	Ser	Gly	Tyr	His	Ala	Asn	Tyr	Cys	Glu	Gly	340	345	350	
Glu	Cys	Pro	Ser	His	Ile	Ala	Gly	Thr	Ser	Gly	Ser	Ser	Leu	Ser	Phe	355	360	365	
His	Ser	Thr	Val	Ile	Asn	His	Tyr	Arg	Met	Arg	Gly	His	Ser	Pro	Phe				

370	375	380
Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys	Leu Arg Pro Met Ser	
385	390	395
Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile	Lys Lys Asp Ile Gln	400
	405	410
Asn Met Ile Val Glu Glu Cys Gly Cys Ser		415
	420	425

<210> 96
 <211> 4637
 <212> DNA
 <213> Homo sapiens

<400> 96

```

agggtgaacag gtcctcacgc ccagctccgc cccctcacgc gctctgcgcg ggaccccgct 60
tccgctggca gccatggggc cgggccccag ccgcgcgcgc cgcgccccac gcctgatgct 120
ctgtgcgcgc gcccttgatgg tggcgggccgg cggtgcgcgc gtctccgcct tcaacctgga 180
tacccgattc ctggtagtga aggaggccgg gaaccggggc agcctcttcg gctactcggc 240
cgccctccat cggcagacag agcggcagca gcgtacctg ctctggctg gtgcccccg 300
ggagctcgct gtgcccgatg gctacaccaa ccggactggg gctgtgtacc tgtgcccact 360
cactgcccac aaggatgact gtgagcggat gaacatcaca gtgaaaaatg accctggcca 420
tcacattatt gaggacatgt ggcttggagt gactgtggcc agccagggcc ctgcaggcag 480
agttctggtc tgtgcccacc gctacacca ggtgctgtgg tcagggtcag aagaccagcg 540
gcgcctgggtg ggcaagtgtc acgtgcgagg caatgaccta gagctggact ccagtgatga 600
ctggcagacc taccacaacg agatgtgcaa tagcaacaca gactacctgg agacgggcat 660
gtgcccagctg ggcaccagcg gtggcttcac ccagaacact gtgtacttcg gcgcccccg 720
tgcctacaac tggaaaggaa acagctacat gattcagcgc aaggagtggg acttatctga 780
gtatagttaa aaggaccacg aggaccaagg aaacctctat attgggtaca cgatgcagg 840
aggcagcttc atcctgcacc ccaaaaacat caccattgtg acaggtgccc caccggcacc 900
acatatgggc gcggtgttct tgctgagcca ggaggcaggc ggagacotgc ggaggaggca 960
ggtgctggag ggctgcgagg tgggcgccta ttttggcagc gcaattgccc tggcagacct 1020
gaacaatgat ggggtggcagg acctcctggt gggcgcccco tactacttcg agaggaaaga 1080
ggaagtggg ggtgccatct atgtcttcat gaaccaggcg ggaacctcct tccctgctca 1140
cccctcactc ctctcttcatg gcccagtggt ctctgccttt ggtttatctg tggccagcat 1200
tggtgacatc aaccaggatg gatcttcagga tattgctgtg ggagctccgt ttgaaggctt 1260
gggcaaagtg tacatctatc acagtagctc taaggggctc cttagacagc ccagcagg 1320
aatccatgga gagaagctgg gactgcctgg gttggccacc ttcggctatt cctcagtg 1380
gcagatggat gtggatgaga acttctaccc agaccttcta gtgggaagcc tgtcagacca 1440
cattgtgctg ctgcggggcc ggccagtcac caacatcgtc cacaagacct tggtgcccag 1500
gccagctgtg ctggaccctg cactttgcac ggccacctct tgtgtgcaag tggagctgtg 1560
ctttgcttac aaccagagtg ccgggaaccc caactacagg cgaacatca ccctggccta 1620
cactctggag gctgacaggg accgccggcc gccccggctc cgctttgcgc gcagtgagtc 1680
cgctgtcttc cacggcttct tctccatgcc cgagatgcgc tgccagaagc tggagctgct 1740
cctgatggac aacctccgtg acaaactccg ccccatcatc atctccatga actactcttt 1800
acctttgcgg atgcccgate gccccggct ggggctgcgc tccctggacg cctaccgat 1860
cctcaaccag gcacaggctc tggagaacca cactgaggtc cagttccaga aggagtgcg 1920
gcctgacaac aagtgtgaga gcaacttgca gatgcgggca gccttcgtgt cagagcagca 1980
gcagaagctg agcaggctcc agtacagcag agacgtccgg aaattgctcc tgagcatcaa 2040
cgtgacgaac acccgacct cggagcgctc cggggaggac gccacgagg ogctgctcac 2100
cctgggtggtg cctcccgccc tgctgctgtc ctcaagtgcg cccccgggg cctgccaaag 2160
taatgagacc atcttttgcg agctggggaa ccccttcaaa cggaaccaga ggatggagct 2220
gctcatcgcc tttgaggtca tcggggtgac cctgcacaca agggaccttc aggtgcagct 2280
gcagctctcc acgtcgagtc accaggacaa cctgtggccc atgactctca ctctgctgtg 2340
ggactataca ctcagacct cgcttagcat ggtaaatcac cggctacaaa gcttctttgg 2400
ggggacagtg atgggtgagt ctggcatgaa aactgtggag gatgtaggaa gccccctcaa 2460
gtatgaattc cagggtgggc caatggggga ggggctggtg ggctgggga ccctggtcct 2520
aggtctggag tggccctacg aagtcagcaa tggcaagtgg ctgctgtatc ccacggagat 2580
caccgctccat ggcaatgggt cctggccctg ccgaccacct ggagacctta tcaacctct 2640

```

```

caacctcact ctttctgacc ctggggacag gccatcatcc ccacagcgca ggcgccgaca 2700
gctggatcca gggggaggcc agggccccc acctgtcact ctggctgctg ccaaaaaagc 2760
caagtctgag actgtgctga cctgtgccac agggcgtgcc cactgtgtgt ggctagagtg 2820
ccccatccct gatgcccccg ttgtcaccaa cgtgactgtg aaggcacgag tgtggaacag 2880
caccttcacg gaggattaca gagactttga ccgagtcagg gtaaatggct gggctaccct 2940
attcctccga accagcatcc ccaccatcaa catggagaac aagaccacgt ggttctctgt 3000
ggacattgac tcggagctgg tggaggagct gccggccgaa atcgagctgt ggctggtgct 3060
ggtggccgtg ggtgcagggc tgctgctgct ggggctgac atcctcctgc tgtggaagtg 3120
cggcttcttc aagcgagccc gcaactcgcg cctgtatgaa gctaagaggc agaaggcgga 3180
gatgaagagc cagccgtcag agacagagag gctgaccgac gactactgag ggggcagccc 3240
ccgcccccg gccacactgg tgtgacttct ttaagcggac ccgctattat cagatcatgc 3300
ccaagtacca cgcagtgcgg atccgggagg aggagcgcta ccacactcca gggagcacc 3360
tgccaccaa gaagcactgg gtgaccagct ggcagactcg ggaccaatac tactgacgtc 3420
ctccctgac ccacccccct ctccccaggt gtcccccttc ttctatttta tcataagtta 3480
tgcctctgac agtccacagg ggccaccacc tttggctggt agcagcaggc tcaggcacat 3540
acacctcgtc aagagcatgc acatgctgtc tggccctggg gatcttccca caggaggggc 3600
agcgtctgtg acctataaac gccgagtgc ctgcattcct gtgccctaga tgcaagtggg 3660
gccactgct cgtggactgt gctggtgcat cacggatggt gcatgggctc gccgtgtctc 3720
agcctctgcc agcgccagcg ccaaaacaag ccaaagagcc tcccaccaga gccgggagga 3780
aaaggcccc gcaatgtggt gacacctccc ctttcacacc tggatccatc ttgagagcca 3840
cagtcaactg attgactttg ctgtcaaaac tactgacagg gagcagcccc cgggcoctg 3900
gctggtgggc cccaattga caccatgcc agagaggtgg ggatcctgcc taaggttgtc 3960
tacgggggca cttggaggac ctggcgtgct cagacccaac agcaaaggaa ctagaaagaa 4020
ggaccagaa ggcttgcttt cctgcattct tgtgaagcct ctctccttgg ccacagactg 4080
aactcgcagg gagtgcagca ggaaggaaca aagacaggca aacggcaacg tagcctgggc 4140
tcaactgtgt ggggcatggc gggatcctcc acagagagga ggggaccaat tctggacaga 4200
cagatgttgg gaggatacag aggagatgcc acttctcact caccactacc agccagcctc 4260
cagaaggccc cagagagacc ctgcaagacc acggaggagg ccgacacttg aatgtagtaa 4320
taggcagggg gccctgccac cccatccagc cagaccccag ctgaaccatg cgtcaggggc 4380
ctagaggtgg agttcttagc tatccttggc tttctgtgcc agcctggctc tgccccctcc 4440
ccatgggctg tgtcctaagg cccatttgag aagctgaggc tagttccaaa aacctctcct 4500
gaccctgcc tgttggcagc ccactcccca gcccagccc cttccatggt actgtagcag 4560
gggaattccc tccccctcct tgtgccttct ttgtatatag gcttctcacc gcgaccaata 4620
aacagctccc agtttgt 4637

```

<210> 97

<211> 1051

<212> PRT

<213> Homo sapiens

<400> 97

```

Met Gly Pro Gly Pro Ser Arg Ala Pro Arg Ala Pro Arg Leu Met Leu
1          5          10          15
Cys Ala Leu Ala Leu Met Val Ala Ala Gly Gly Cys Val Val Ser Ala
20          25          30
Phe Asn Leu Asp Thr Arg Phe Leu Val Val Lys Glu Ala Gly Asn Pro
35          40          45
Gly Ser Leu Phe Gly Tyr Ser Val Ala Leu His Arg Gln Thr Glu Arg
50          55          60
Gln Gln Arg Tyr Leu Leu Leu Ala Gly Ala Pro Arg Glu Leu Ala Val
65          70          75          80
Pro Asp Gly Tyr Thr Asn Arg Thr Gly Ala Val Tyr Leu Cys Pro Leu
85          90          95
Thr Ala His Lys Asp Asp Cys Glu Arg Met Asn Ile Thr Val Lys Asn
100         105         110
Asp Pro Gly His His Ile Ile Glu Asp Met Trp Leu Gly Val Thr Val
115         120         125
Ala Ser Gln Gly Pro Ala Gly Arg Val Leu Val Cys Ala His Arg Tyr
130         135         140

```

Thr	Gln	Val	Leu	Trp	Ser	Gly	Ser	Glu	Asp	Gln	Arg	Arg	Met	Val	Gly	145	150	155	160
Lys	Cys	Tyr	Val	Arg	Gly	Asn	Asp	Leu	Glu	Leu	Asp	Ser	Ser	Asp	Asp	165	170	175	
Trp	Gln	Thr	Tyr	His	Asn	Glu	Met	Cys	Asn	Ser	Asn	Thr	Asp	Tyr	Leu	180	185	190	
Glu	Thr	Gly	Met	Cys	Gln	Leu	Gly	Thr	Ser	Gly	Gly	Phe	Thr	Gln	Asn	195	200	205	
Thr	Val	Tyr	Phe	Gly	Ala	Pro	Gly	Ala	Tyr	Asn	Trp	Lys	Gly	Asn	Ser	210	215	220	
Tyr	Met	Ile	Gln	Arg	Lys	Glu	Trp	Asp	Leu	Ser	Glu	Tyr	Ser	Tyr	Lys	225	230	235	240
Asp	Pro	Glu	Asp	Gln	Gly	Asn	Leu	Tyr	Ile	Gly	Tyr	Thr	Met	Gln	Val	245	250	255	
Gly	Ser	Phe	Ile	Leu	His	Pro	Lys	Asn	Ile	Thr	Ile	Val	Thr	Gly	Ala	260	265	270	
Pro	Arg	His	Arg	His	Met	Gly	Ala	Val	Phe	Leu	Leu	Ser	Gln	Glu	Ala	275	280	285	
Gly	Gly	Asp	Leu	Arg	Arg	Arg	Gln	Val	Leu	Glu	Gly	Ser	Gln	Val	Gly	290	295	300	
Ala	Tyr	Phe	Gly	Ser	Ala	Ile	Ala	Leu	Ala	Asp	Leu	Asn	Asn	Asp	Gly	305	310	315	320
Trp	Gln	Asp	Leu	Leu	Val	Gly	Ala	Pro	Tyr	Tyr	Phe	Glu	Arg	Lys	Glu	325	330	335	
Glu	Val	Gly	Gly	Ala	Ile	Tyr	Val	Phe	Met	Asn	Gln	Ala	Gly	Thr	Ser	340	345	350	
Phe	Pro	Ala	His	Pro	Ser	Leu	Leu	His	Gly	Pro	Ser	Gly	Ser	Ala		355	360	365	
Phe	Gly	Leu	Ser	Val	Ala	Ser	Ile	Gly	Asp	Ile	Asn	Gln	Asp	Gly	Phe	370	375	380	
Gln	Asp	Ile	Ala	Val	Gly	Ala	Pro	Phe	Glu	Gly	Leu	Gly	Lys	Val	Tyr	385	390	395	400
Ile	Tyr	His	Ser	Ser	Ser	Lys	Gly	Leu	Leu	Arg	Gln	Pro	Gln	Gln	Val	405	410	415	
Ile	His	Gly	Glu	Lys	Leu	Gly	Leu	Pro	Gly	Leu	Ala	Thr	Phe	Gly	Tyr	420	425	430	
Ser	Leu	Ser	Gly	Gln	Met	Asp	Val	Asp	Glu	Asn	Phe	Tyr	Pro	Asp	Leu	435	440	445	
Leu	Val	Gly	Ser	Leu	Ser	Asp	His	Ile	Val	Leu	Leu	Arg	Ala	Arg	Pro	450	455	460	
Val	Ile	Asn	Ile	Val	His	Lys	Thr	Leu	Val	Pro	Arg	Pro	Ala	Val	Leu	465	470	475	480
Asp	Pro	Ala	Leu	Cys	Thr	Ala	Thr	Ser	Cys	Val	Gln	Val	Glu	Leu	Cys	485	490	495	
Phe	Ala	Tyr	Asn	Gln	Ser	Ala	Gly	Asn	Pro	Asn	Tyr	Arg	Arg	Asn	Ile	500	505	510	
Thr	Leu	Ala	Tyr	Thr	Leu	Glu	Ala	Asp	Arg	Asp	Arg	Arg	Pro	Pro	Arg	515	520	525	
Leu	Arg	Phe	Ala	Gly	Ser	Glu	Ser	Ala	Val	Phe	His	Gly	Phe	Phe	Ser	530	535	540	
Met	Pro	Glu	Met	Arg	Cys	Gln	Lys	Leu	Glu	Leu	Leu	Leu	Met	Asp	Asn	545	550	555	560
Leu	Arg	Asp	Lys	Leu	Arg	Pro	Ile	Ile	Ile	Ser	Met	Asn	Tyr	Ser	Leu	565	570	575	
Pro	Leu	Arg	Met	Pro	Asp	Arg	Pro	Arg	Leu	Gly	Leu	Arg	Ser	Leu	Asp	580	585	590	
Ala	Tyr	Pro	Ile	Leu	Asn	Gln	Ala	Gln	Ala	Leu	Glu	Asn	His	Thr	Glu	595	600	605	
Val	Gln	Phe	Gln	Lys	Glu	Cys	Gly	Pro	Asp	Asn	Lys	Cys	Glu	Ser	Asn				

610	615	620
Leu Gln Met Arg Ala Ala Phe Val Ser Glu Gln Gln Lys Leu Ser		
625	630	635
Arg Leu Gln Tyr Ser Arg Asp Val Arg Lys Leu Leu Leu Ser Ile Asn		640
	645	650
Val Thr Asn Thr Arg Thr Ser Glu Arg Ser Gly Glu Asp Ala His Glu		655
	660	665
Ala Leu Leu Thr Leu Val Val Pro Pro Ala Leu Leu Ser Ser Val		670
	675	680
Arg Pro Pro Gly Ala Cys Gln Ala Asn Glu Thr Ile Phe Cys Glu Leu		685
	690	695
Gly Asn Pro Phe Lys Arg Asn Gln Arg Met Glu Leu Leu Ile Ala Phe		700
705	710	715
Glu Val Ile Gly Val Thr Leu His Thr Arg Asp Leu Gln Val Gln Leu		720
	725	730
Gln Leu Ser Thr Ser Ser His Gln Asp Asn Leu Trp Pro Met Ile Leu		735
	740	745
Thr Leu Leu Val Asp Tyr Thr Leu Gln Thr Ser Leu Ser Met Val Asn		750
	755	760
His Arg Leu Gln Ser Phe Phe Gly Gly Thr Val Met Gly Glu Ser Gly		765
	770	775
Met Lys Thr Val Glu Asp Val Gly Ser Pro Leu Lys Tyr Glu Phe Gln		780
785	790	795
Val Gly Pro Met Gly Glu Gly Leu Val Gly Leu Gly Thr Leu Val Leu		800
	805	810
Gly Leu Glu Trp Pro Tyr Glu Val Ser Asn Gly Lys Trp Leu Leu Tyr		815
	820	825
Pro Thr Glu Ile Thr Val His Gly Asn Gly Ser Trp Pro Cys Arg Pro		830
	835	840
Pro Gly Asp Leu Ile Asn Pro Leu Asn Leu Thr Leu Ser Asp Pro Gly		845
	850	855
Asp Arg Pro Ser Ser Pro Gln Arg Arg Arg Arg Gln Leu Asp Pro Gly		860
865	870	875
Gly Gly Gln Gly Pro Pro Pro Val Thr Leu Ala Ala Ala Lys Lys Ala		880
	885	890
Lys Ser Glu Thr Val Leu Thr Cys Ala Thr Gly Arg Ala His Cys Val		895
	900	905
Trp Leu Glu Cys Pro Ile Pro Asp Ala Pro Val Val Thr Asn Val Thr		910
	915	920
Val Lys Ala Arg Val Trp Asn Ser Thr Phe Ile Glu Asp Tyr Arg Asp		925
	930	935
Phe Asp Arg Val Arg Val Asn Gly Trp Ala Thr Leu Phe Leu Arg Thr		940
945	950	955
Ser Ile Pro Thr Ile Asn Met Glu Asn Lys Thr Thr Trp Phe Ser Val		960
	965	970
Asp Ile Asp Ser Glu Leu Val Glu Glu Leu Pro Ala Glu Ile Glu Leu		975
	980	985
Trp Leu Val Leu Val Ala Val Gly Ala Gly Leu Leu Leu Leu Gly Leu		990
	995	1000
Ile Ile Leu Leu Leu Trp Lys Cys Gly Phe Phe Lys Arg Ala Arg Thr		1005
	1010	1015
Arg Ala Leu Tyr Glu Ala Lys Arg Gln Lys Ala Glu Met Lys Ser Gln		1020
1025	1030	1035
Pro Ser Glu Thr Glu Arg Leu Thr Asp Asp Tyr		1040
	1045	1050

<210> 98

<211> 4495

<212> DNA

<213> Homo sapiens

<400> 98

```

aggtgaacag gtccctcacgc ccagctccgc cccctcacgc gctctcgccg ggaccccgcct 60
tccgctggca gccatgggcc ccggccccag ccgcgcgcgc cgcgccccac gcctgatgct 120
ctgtgcgcct gccttgatgg tggcggccgg cggctgcgtc gtctccgcct tcaacctgga 180
tacccgattc ctggtagtga aggaggccgg gaaccggggc agcctcttcg gctactcggc 240
cgccctccat cggcagacag agcggcagca gcgctacctg ctccctggctg gtgccccccg 300
ggagctcgct gtgcccgatg gctacaccaa ccggactggc gctgtgtacc tgtgcccact 360
cactgccccc aaggatgact gtgagcggat gaacatcaca gtgaaaaatg accctggcca 420
tcacattatt gaggacatgt ggcttgagat gactgtggcc agccaggggc ctgcaggcag 480
agttctggtc tgtgcccacc gctacaccca ggtgctgtgg tcagggtcag aagaccagcg 540
gcgcctgggt ggcaagtgtc acgtgcgagg caatgacctc gagctggact ccagtgatga 600
ctggcagacc taccacaacg agatgtgcaa tagcaacaca gactacctgg agacgggcat 660
gtgccagctg ggcaccagcg gtggcttcac ccagaacact gtgtacttcg gcgccccccg 720
tgcctacaac tggaaaggaa acagctacat gattcagcgc aaggagtggg acttatctga 780
gtatagttac aaggacccag aggaccaagg aaacctctat attgggtaca cgatgcaggc 840
aggcagcttc atcctgcacc ccaaaaacat caccattgtg acaggtgccc cacggcaccg 900
acatatgggc gcggtgttct tgcctgagca ggaggcaggc ggagacctgc ggaggaggca 960
ggtgctggag ggctcgcagg tggcgcccta ttttggcagc gcaattgccc tggcagacct 1020
gaacaatgat ggggtggcagg acctcctggt gggcgccccc tactacttcg agaggaaaaga 1080
ggaagtgggg ggtgccatct atgtcttcac gaaccaggcg ggaacctcct tccctgctca 1140
cccctcactc cttcttcacg gcccagtggt ctctgccttt ggtttatctg tggccagcat 1200
tggtgacatc aaccaggatg gatttcagga tattgctgtg ggagctccgt ttgaaggctt 1260
gggcaaagtg tacatctatc acagttagctc taaggggctc cttagacagc cccagcaggc 1320
aatccatgga gagaagctgg gactgcctgg gttggccacc ttcggtatc cctcagtggt 1380
gcagatggat gtggatgaga acttctaccc agaccttcta gtgggaagcc tgtcagacca 1440
cattgtgctg ctgcggggcc ggccagtcgc caacatcgtc cacaagacct tgggtgccag 1500
gccagctgtg ctggaccctg cactttgcac ggccacctct tgtgtgcaag tggagctgtg 1560
ctttgcttac aaccagagtg ccgggaaccc caactacagg cgaaacatca ccctggccta 1620
cactctggag gctgacaggg accgcgggcc gcccggctc cgctttgccc gcagtgagtc 1680
cgctgtcttc cacggcttct tctccatgcc cgagatgcgc tgccagaagc tggagctgct 1740
cctgatggac aacctccgtg acaaactccg ccccatcatc atctccatga actactcttt 1800
acctttgccc atgcccgatc gcccccggtc ggggctgcgg tccctggacg cctacccgat 1860
cctcaaccag gcacaggctc tggagaacca cactgaggtc cagttccaga aggagtgcgg 1920
gcctgacaac aagtgtgaga gcaacttgca gatgcgggca gccttcgtgt cagagcagca 1980
gcagaagctg agcaggctcc agtacagcag agacgtccgg aaattgctcc tgagcatcaa 2040
cgtgacgaac acccggacct cggagcgctc cggggaggac gccacgagg cgctgctcac 2100
cctgggtggt cctcccggcc tgcctgctgc ctgagtcgc cccccgggg cctgccaaagc 2160
taatgagacc atcttttgcc agctggggaa ccccttcaaa cggaaccaga ggatggagct 2220
gctcatcgcc tttgaggtca tcggggtgac cctgcacaca agggaccttc aggtgcagct 2280
gcagctctcc acgtcgagtc accaggacaa cctgtggccc atgacctca ctctgctggt 2340
ggactataca ctccagacct cgcttagcat ggtaaatcac cggtacaaa gcttcttttg 2400
ggggacagtg atgggtgagt ctggcatgaa aactgtggag gatgtaggaa gccccctcaa 2460
gtatgaattc caggtgggcc caatggggga gggctgggtg ggccctggga cctgggtcct 2520
aggtctggag tggccctacg aagtcagcaa tggcaagtgg ctgctgtatc ccacggagat 2580
cacgctccat ggcaatgggt cctggccctg ccgaccacct ggagacctta tcaacctct 2640
caacctcact ctttctgacc ctggggacag gccatcatcc ccacagcgca ggcgccgaca 2700
gctggatcca gggggaggcc agggcccccc acctgtcact ctggctgctg ccaaaaaagc 2760
caagtctgag actgtgctga cctgtgccac agggcgctgc cactgtgtgt ggctagagtg 2820
ccccatccct gatgcccccg ttgtcaccaa cgtgactgtg aaggcacgag tgtggaacag 2880
caccttcato gaggattaca gagactttga ccgagtcagg gtaaatggct gggctaccct 2940
attcctccga accagcatcc ccacctcaa catggagaac aagaccacgt ggttctctgt 3000
ggacattgac tcggagctgg tggaggagct gccggccgaa atcgagctgt ggctggtgct 3060
ggtgcccggt ggtgcagggc tgcctgctgt gggctgtgat atcctcctgc tgtggaagtg 3120
tgacttcttt aagcggaccc gctattatca gatcatgcc aagtaccacg cagtgcggat 3180
ccgggaggag gagcgctacc cacctccagg gagcacctg cccaccaaga agcactgggt 3240
gaccagctgg cagactcggg accaatacta ctgacgtcct ccctgatccc accccctcct 3300

```

```

ccccagtggt cccctttctt cctattttatc ataagttatg cctctgacag tccacagggg 3360
ccaccacctt tggctggtag cagcaggctc aggcacatac acctogtcaa gagcatgcac 3420
atgctgtctg gccctgggga tcttcccaca ggagggccag cgctgtggac cttacaacgc 3480
cgagtgcact gcattcctgt gccctagatg cacgtggggc ccaactgctcg tggactgtgc 3540
tggtgcatca cggatgggtgc atgggctcgc cgtgtctcag cctctgccag cgccagcgcc 3600
aaaacaagcc aaagagcctc ccaccagagc cgggaggaaa agggccctgc aatgtggtga 3660
cacctcccct ttcacacctg gatccatctt gagagccaca gtcactggat tgactttgct 3720
gtcaaaaacta ctgacaggga gcagcccccg ggccgctggc tgggtgggccc ccaattgaca 3780
cccattgccag agaggtgggg atcctgccta aggttgtcta cggggggcact tggaggacct 3840
ggcgtgctca gacccaacag caaaggaact agaaagaagg acccagaagg cttgctttcc 3900
tgcattctctg tgaagcctct ctcttggcc acagactgaa ctgcagggga gtgcagcagg 3960
aaggaacaaa gacaggcaaa cggcaacgta gcctgggctc actgtgctgg ggcattggcg 4020
gatcctccac agagaggagg ggaccaattc tggacagaca gatgttgga ggatacagag 4080
gagatgccac ttctcactca ccactaccag ccagcctcca gaaggcccca gagagacct 4140
gcaagaccac ggaggggagc gacacttgaa tgtagtaata ggcagggggc cctgccaccc 4200
catccagcca gacccagct gaacctatgc tcaggggcct agaggtggag ttcttagcta 4260
tccttggctt tctgtgccag cctggctctg cccctcccc atgggctgtg tcctaaggcc 4320
catttgagaa gctgaggcta gttccaaaaa cctctcctga cccctgcctg ttggcagccc 4380
actccccagc cccagccct tccatggtac tgtagcaggg gaattccctc cccctccttg 4440
tgccttcttt gtatataggc ttctcaccgc gaccaataaa cagctcccag tttgt 4495

```

<210> 99

<211> 1066

<212> PRT

<213> Homo sapiens

<400> 99

```

Met Gly Pro Gly Pro Ser Arg Ala Pro Arg Ala Pro Arg Leu Met Leu
 1          5          10          15
Cys Ala Leu Ala Leu Met Val Ala Ala Gly Gly Cys Val Val Ser Ala
 20          25          30
Phe Asn Leu Asp Thr Arg Phe Leu Val Val Lys Glu Ala Gly Asn Pro
 35          40          45
Gly Ser Leu Phe Gly Tyr Ser Val Ala Leu His Arg Gln Thr Glu Arg
 50          55          60
Gln Gln Arg Tyr Leu Leu Ala Gly Ala Pro Arg Glu Leu Ala Val
 65          70          75          80
Pro Asp Gly Tyr Thr Asn Arg Thr Gly Ala Val Tyr Leu Cys Pro Leu
 85          90          95
Thr Ala His Lys Asp Asp Cys Glu Arg Met Asn Ile Thr Val Lys Asn
100          105          110
Asp Pro Gly His His Ile Ile Glu Asp Met Trp Leu Gly Val Thr Val
115          120          125
Ala Ser Gln Gly Pro Ala Gly Arg Val Leu Val Cys Ala His Arg Tyr
130          135          140
Thr Gln Val Leu Trp Ser Gly Ser Glu Asp Gln Arg Arg Met Val Gly
145          150          155          160
Lys Cys Tyr Val Arg Gly Asn Asp Leu Glu Leu Asp Ser Ser Asp Asp
165          170          175
Trp Gln Thr Tyr His Asn Glu Met Cys Asn Ser Asn Thr Asp Tyr Leu
180          185          190
Glu Thr Gly Met Cys Gln Leu Gly Thr Ser Gly Gly Phe Thr Gln Asn
195          200          205
Thr Val Tyr Phe Gly Ala Pro Gly Ala Tyr Asn Trp Lys Gly Asn Ser
210          215          220
Tyr Met Ile Gln Arg Lys Glu Trp Asp Leu Ser Glu Tyr Ser Tyr Lys
225          230          235          240
Asp Pro Glu Asp Gln Gly Asn Leu Tyr Ile Gly Tyr Thr Met Gln Val
245          250          255

```

Gly	Ser	Phe	Ile	Leu	His	Pro	Lys	Asn	Ile	Thr	Ile	Val	Thr	Gly	Ala	
			260					265					270			
Pro	Arg	His	Arg	His	Met	Gly	Ala	Val	Phe	Leu	Leu	Ser	Gln	Glu	Ala	
		275					280					285				
Gly	Gly	Asp	Leu	Arg	Arg	Arg	Gln	Val	Leu	Glu	Gly	Ser	Gln	Val	Gly	
	290					295					300					
Ala	Tyr	Phe	Gly	Ser	Ala	Ile	Ala	Leu	Ala	Asp	Leu	Asn	Asn	Asp	Gly	
305					310					315					320	
Trp	Gln	Asp	Leu	Leu	Val	Gly	Ala	Pro	Tyr	Tyr	Phe	Glu	Arg	Lys	Glu	
			325						330					335		
Glu	Val	Gly	Gly	Ala	Ile	Tyr	Val	Phe	Met	Asn	Gln	Ala	Gly	Thr	Ser	
			340					345					350			
Phe	Pro	Ala	His	Pro	Ser	Leu	Leu	Leu	His	Gly	Pro	Ser	Gly	Ser	Ala	
		355					360					365				
Phe	Gly	Leu	Ser	Val	Ala	Ser	Ile	Gly	Asp	Ile	Asn	Gln	Asp	Gly	Phe	
	370					375				380						
Gln	Asp	Ile	Ala	Val	Gly	Ala	Pro	Phe	Glu	Gly	Leu	Gly	Lys	Val	Tyr	
385					390					395					400	
Ile	Tyr	His	Ser	Ser	Ser	Lys	Gly	Leu	Leu	Arg	Gln	Pro	Gln	Gln	Val	
			405						410					415		
Ile	His	Gly	Glu	Lys	Leu	Gly	Leu	Pro	Gly	Leu	Ala	Thr	Phe	Gly	Tyr	
		420						425					430			
Ser	Leu	Ser	Gly	Gln	Met	Asp	Val	Asp	Glu	Asn	Phe	Tyr	Pro	Asp	Leu	
	435						440					445				
Leu	Val	Gly	Ser	Leu	Ser	Asp	His	Ile	Val	Leu	Leu	Arg	Ala	Arg	Pro	
	450					455					460					
Val	Ile	Asn	Ile	Val	His	Lys	Thr	Leu	Val	Pro	Arg	Pro	Ala	Val	Leu	
465					470					475					480	
Asp	Pro	Ala	Leu	Cys	Thr	Ala	Thr	Ser	Cys	Val	Gln	Val	Glu	Leu	Cys	
			485						490					495		
Phe	Ala	Tyr	Asn	Gln	Ser	Ala	Gly	Asn	Pro	Asn	Tyr	Arg	Arg	Asn	Ile	
		500						505				510				
Thr	Leu	Ala	Tyr	Thr	Leu	Glu	Ala	Asp	Arg	Asp	Arg	Arg	Pro	Pro	Arg	
	515						520					525				
Leu	Arg	Phe	Ala	Gly	Ser	Glu	Ser	Ala	Val	Phe	His	Gly	Phe	Phe	Ser	
	530					535				540						
Met	Pro	Glu	Met	Arg	Cys	Gln	Lys	Leu	Glu	Leu	Leu	Leu	Met	Asp	Asn	
545					550					555					560	
Leu	Arg	Asp	Lys	Leu	Arg	Pro	Ile	Ile	Ile	Ser	Met	Asn	Tyr	Ser	Leu	
			565						570					575		
Pro	Leu	Arg	Met	Pro	Asp	Arg	Pro	Arg	Leu	Gly	Leu	Arg	Ser	Leu	Asp	
		580						585					590			
Ala	Tyr	Pro	Ile	Leu	Asn	Gln	Ala	Gln	Ala	Leu	Glu	Asn	His	Thr	Glu	
	595						600					605				
Val	Gln	Phe	Gln	Lys	Glu	Cys	Gly	Pro	Asp	Asn	Lys	Cys	Glu	Ser	Asn	
	610					615					620					
Leu	Gln	Met	Arg	Ala	Ala	Phe	Val	Ser	Glu	Gln	Gln	Gln	Lys	Leu	Ser	
625					630					635					640	
Arg	Leu	Gln	Tyr	Ser	Arg	Asp	Val	Arg	Lys	Leu	Leu	Leu	Ser	Ile	Asn	
			645						650					655		
Val	Thr	Asn	Thr	Arg	Thr	Ser	Glu	Arg	Ser	Gly	Glu	Asp	Ala	His	Glu	
		660						665					670			
Ala	Leu	Leu	Thr	Leu	Val	Val	Pro	Pro	Ala	Leu	Leu	Leu	Ser	Ser	Val	
	675						680					685				
Arg	Pro	Pro	Gly	Ala	Cys	Gln	Ala	Asn	Glu	Thr	Ile	Phe	Cys	Glu	Leu	
	690					695					700					
Gly	Asn	Pro	Phe	Lys	Arg	Asn	Gln	Arg	Met	Glu	Leu	Leu	Ile	Ala	Phe	
705					710					715					720	
Glu	Val	Ile	Gly	Val	Thr	Leu	His	Thr	Arg	Asp	Leu	Gln	Val	Gln	Leu	


```
<210> 100
<211> 4647
<212> DNA
<213> Homo sapiens
```

<400> 100						
gtagcctctg	ttttcatttc	agtcttaatg	aaaactttct	aacttatatc	tcaagtttct	60
tttcaaagca	gtgtaagtag	tatttaaaat	gttatacttc	aagaaagaaa	gactttaacg	120
atattcagcg	ttggtcttgt	aacgctgaag	gtaattcatt	ttttaatcgg	tctgcacagc	180
agaactgaa	acgaatgggg	attgaactgc	tttgccctgt	ctttctattt	ctaggaagga	240
atgatcacgt	acaaggtggc	tgtgccctgc	gagggtcaga	aacctgtgaa	gactgcctgc	300
ttattggacc	tcagtggtgc	tgggtgtgct	aggagaattt	tactcatcca	tctggagttg	360
gcgaaaggtg	tgatacccca	gcaaaccttt	tagctaaggg	atgtcaatta	aacttcatcg	420
aaaaccctgt	ctcccaagta	gaaatactta	aaaataagcc	tctcagtgtg	ggcagacaga	480

aaaatagttc	tgacattggt	cagattgcgc	ctcaaagctt	gataccttaag	ttgagaccag	540
gtgggtgcga	gactctgcag	gtgcatgtcc	gccagactga	ggactaccgc	gtggatttgt	600
attacctcat	ggacctctcc	gcctccatgg	atgacgacct	caacacaata	aaggagctgg	660
gctcccggt	ttccaaagag	atgtctaaat	taaccagcaa	ctttagactg	ggcttcggat	720
cttttgtgga	aaaacctgta	tcccccttgc	tgaaaacaac	accagaagaa	attgccaaac	780
cttgacgtag	tattccatac	ttctgtttac	ctacatttgg	attcaagcac	attttgccat	840
tgacaaatga	tgctgaaaga	ttcaatgaaa	ttgtgaagaa	tcagaaaatt	tctgctaata	900
ttgacacacc	cgaagggtga	tttgatgcaa	ttatgcaagc	tgctgtgtgt	aaggaaaaaa	960
ttggctggcg	gaatgactcc	ctccacctcc	tggtctttgt	gagtgtgtgt	gattctcatt	1020
ttggaatgga	cagcaaaacta	gcaggcatcg	tcattcctaa	tgacgggctc	tgtcacttgg	1080
acagcaagaa	tgaatactcc	atgtcaactg	tcttggaata	tccaacaatt	ggacaactca	1140
ttgataaaact	ggtacaaaac	aacgtgttat	tgatcttcgc	tgtaacccaa	gaacaagtgc	1200
atztatatga	gaattacgca	aaactttatc	ctggagctac	agtaggtcta	cttcagaagg	1260
actccggaag	cattctccag	ctgatcatct	cagcttatga	agaactgcgg	tctgaggtgg	1320
aactggaagt	attaggagac	actgaaggac	tcaactgtgc	atttacagcc	atctgtaaca	1380
acggtaccct	cttccaacac	caaaagaaat	gctctcacat	gaaagtggga	gacacagctt	1440
ccttcagcgt	gactgtgaat	atcccacact	gcgagagaag	aagcaggcac	attatcataa	1500
agcctgtggg	gctgggggat	gccctggaat	tacttgtcag	cccagaatgc	aactgogact	1560
gtcagaaaga	agtggaagtg	aacagctcca	aatgtcacca	cgggaacggc	tctttccagt	1620
gtgggggtgt	tgcttgccac	cctggccaca	tggggcctcg	ctgtgagtgt	ggcagggaca	1680
tgctgagcac	agattcctgc	aaggaggccc	cagatcatcc	ctcctgcagc	ggaagggtgt	1740
actgctactg	tgggcagtgt	atctgccact	tgtctcccta	tggaaacatt	tatgggcctt	1800
attgccagtgt	tgacaatttc	tcctgogtga	gacacaaagg	gctgctctgc	ggaggttaacg	1860
gcgactgtga	ctgtggtgaa	tgtgtgtgca	ggagcggctg	gactggcgag	tactgcaact	1920
gcaccaccag	cacggactcc	tgcgtctctg	aagatggagt	gctctgcagc	gggcgcgggg	1980
actgtgtttg	tggcaagtgt	gtttgcacaa	accctggagc	ctcaggacca	acctgtgaac	2040
gatgtcctac	ctgtggtgac	ccctgtaact	ctaaacggag	ctgcattgag	tgccacctgt	2100
cagcagctgg	ccaagccoga	gaagaatgtg	tggacaagtg	caaactagct	ggtgcgacca	2160
tcagtgaaga	agaagatttc	tcaaaggatg	gttctgtttc	ctgctctctg	caaggagaaa	2220
atgaatgtct	tattacattc	ctaataacta	cagataatga	ggggaaaacc	atcattcaca	2280
gcatcaatga	aaaagattgt	ccgaagcctc	caaacattcc	catgatcatg	ttaggggttt	2340
ccctggctat	tcttctcctc	ggggttgtcc	tactgtgcat	ctggaagcta	ctggtgtcat	2400
ttcatgatcg	taaagaagt	gccaaatttg	aagcagaacg	atcaaaagcc	aagtggcaaa	2460
cgggaaccaa	tccactctac	agaggatcca	caagtacttt	taaaaatgta	acttataaac	2520
acagggaana	acaaaaggta	gacctttcca	cagattgcta	gaactacttt	atgcatgaaa	2580
aaagtctgtt	tactgatata	gaaatgttaa	tgcactattt	aatttttttc	tctttgttgc	2640
ttcaaaatga	ggttggttta	agataataat	aggacatctg	cagataagtc	atcctctaca	2700
tgaagggtga	gactgtttgg	cagtttcaaa	ataatcaaga	agagaaatat	ccttagcaaa	2760
gagatgactt	tggggatcat	ttgaggaata	ctaactctgt	tgcattaatg	cttcaaaaaa	2820
tcatcaaatg	attcatgggg	gcctgatttg	catttgaaaa	atgtttgaaa	ttagagtctc	2880
atttgtttca	ggaatgcagc	tacctgagtt	ttttgtctcg	gcaaagtcac	aaagcccata	2940
tactcacatt	gtgtgtctat	acttgccaat	taattctaaa	ctttagaggaa	atatgccctc	3000
tcttaaagga	gaattttttt	taaatctctg	agaaatgaga	ttctgagttt	atttcagcta	3060
aaaggttgca	attcttctga	agatatctca	aatataaggt	tgaaagttaa	gtgttaataa	3120
tttttgtgaa	tttatacaca	cctaaacgtt	aagtaacaaa	atattttatt	tgtttttaca	3180
ataaggaata	agtaatttat	aaattaagaa	gttacctata	aaaataaaaa	gataacaacc	3240
ctatcatata	gcttattttt	aaattacctg	aaaaaacgata	ttctacactg	tttccttttt	3300
gactctgagt	tttcaaaactg	ttactttctc	catattttctc	aatccatttc	actcagttgc	3360
acagtctttt	aaacctgtga	attgtcatac	caaagtttct	ttttaaaaaa	aaattacttt	3420
aaatgcttag	tttattcaaa	gagcgatcca	ataatataaa	aggaacatgt	gttaaacaca	3480
ataaaatttt	aaatggctct	aatcaagca	catcaagagt	atacaagtct	taaaggcttt	3540
ttaatacata	ctctttttcc	atctatgtaa	cccaacttgc	acatttcagc	tgcatgtggg	3600
gaatatgcat	catatattta	ctttaagagg	taagatttta	cttgcaaaat	acatgtgcaa	3660
attagatcc	atcagttgat	ggaagagatg	gactctagaa	tattattttc	tgtggttatt	3720
actcctttac	aaagcacttt	cgtctcacta	gatcctcata	aggaaactaa	ggctcagaat	3780
gagtagagct	gggttcagaa	tctagctctt	ctaactccaa	gccatctcct	ctttccactg	3840
caggaaactg	cctcttttgt	cagtgaataa	atagaaagat	tgtgttagtt	aagtataaac	3900
tgtcatttgt	ttgaaaatgt	tcgagactga	acaaatagca	tttaaactgc	tggcatatag	3960
atgagatatt	gtacttttgt	gcaatgttta	ttacctttga	ttaaattgta	atgtgaagct	4020

```

tttactaggt gaatagttca ttatgtagtg gaggcttcgt ggttggtccat tgaattgtca 4080
cagcaaaaatc tataagtttc ttcaattcta caagatagat ccatatacct ttgatcactt 4140
ggagactctt tttttgctgg tttctagata actcaggtaa atcagacctt tacagagtac 4200
agggctaggt gaaagaatta ctgaaaaatc acctgaaaaa tccgaagggc tgatataccc 4260
tttatgttcc tgactgatgc gcagaacctg ggggaaatct acagcaatat acaggttgca 4320
atgctgataa cacaacagca atcctctcct ctacgtggac ttactgttgt ttttttaatt 4380
attattggaa tgggatttta gaaaatagaa gttacctttg tgtgtgtttt aggggaaggta 4440
gagaagaatc tgctctttct ctgaatactg ttttgacccc aggcaggacc ttggaaaaggc 4500
caaaacatta acagtagtac ttctgttcac tgaagagtta tgttacatga agataaaaatg 4560
gttttgctcg gtattattatt gtattttgtg ttgatataaa taaacatggt aatttaaaca 4620
atgaaaaaaaa aaaaaaaaaa aaaaaaa 4647

```

<210> 101
 <211> 788
 <212> PRT
 <213> Homo sapiens

<400> 101

Met	Gly	Ile	Glu	Leu	Leu	Cys	Leu	Phe	Phe	Leu	Phe	Leu	Gly	Arg	Asn
1				5					10					15	
Asp	His	Val	Gln	Gly	Gly	Cys	Ala	Leu	Gly	Gly	Ala	Glu	Thr	Cys	Glu
			20					25					30		
Asp	Cys	Leu	Leu	Ile	Gly	Pro	Gln	Cys	Ala	Trp	Cys	Ala	Gln	Glu	Asn
		35					40					45			
Phe	Thr	His	Pro	Ser	Gly	Val	Gly	Glu	Arg	Cys	Asp	Thr	Pro	Ala	Asn
	50					55					60				
Leu	Leu	Ala	Lys	Gly	Cys	Gln	Leu	Asn	Phe	Ile	Glu	Asn	Pro	Val	Ser
65					70				75						80
Gln	Val	Glu	Ile	Leu	Lys	Asn	Lys	Pro	Leu	Ser	Val	Gly	Arg	Gln	Lys
				85					90					95	
Asn	Ser	Ser	Asp	Ile	Val	Gln	Ile	Ala	Pro	Gln	Ser	Leu	Ile	Leu	Lys
			100					105					110		
Leu	Arg	Pro	Gly	Gly	Ala	Gln	Thr	Leu	Gln	Val	His	Val	Arg	Gln	Thr
		115				120						125			
Glu	Asp	Tyr	Pro	Val	Asp	Leu	Tyr	Tyr	Leu	Met	Asp	Leu	Ser	Ala	Ser
	130					135					140				
Met	Asp	Asp	Asp	Leu	Asn	Thr	Ile	Lys	Glu	Leu	Gly	Ser	Arg	Leu	Ser
145					150				155						160
Lys	Glu	Met	Ser	Lys	Leu	Thr	Ser	Asn	Phe	Arg	Leu	Gly	Phe	Gly	Ser
				165					170					175	
Phe	Val	Glu	Lys	Pro	Val	Ser	Pro	Phe	Val	Lys	Thr	Thr	Pro	Glu	Glu
			180					185					190		
Ile	Ala	Asn	Pro	Cys	Ser	Ser	Ile	Pro	Tyr	Phe	Cys	Leu	Pro	Thr	Phe
		195					200					205			
Gly	Phe	Lys	His	Ile	Leu	Pro	Leu	Thr	Asn	Asp	Ala	Glu	Arg	Phe	Asn
	210					215					220				
Glu	Ile	Val	Lys	Asn	Gln	Lys	Ile	Ser	Ala	Asn	Ile	Asp	Thr	Pro	Glu
225					230					235					240
Gly	Gly	Phe	Asp	Ala	Ile	Met	Gln	Ala	Ala	Val	Cys	Lys	Glu	Lys	Ile
				245					250					255	
Gly	Trp	Arg	Asn	Asp	Ser	Leu	His	Leu	Leu	Val	Phe	Val	Ser	Asp	Ala
			260					265					270		
Asp	Ser	His	Phe	Gly	Met	Asp	Ser	Lys	Leu	Ala	Gly	Ile	Val	Ile	Pro
		275					280					285			
Asn	Asp	Gly	Leu	Cys	His	Leu	Asp	Ser	Lys	Asn	Glu	Tyr	Ser	Met	Ser
	290					295					300				
Thr	Val	Leu	Glu	Tyr	Pro	Thr	Ile	Gly	Gln	Leu	Ile	Asp	Lys	Leu	Val
305					310					315					320
Gln	Asn	Asn	Val	Leu	Leu	Ile	Phe	Ala	Val	Thr	Gln	Glu	Gln	Val	His

					325					330					335
Leu	Tyr	Glu	Asn	Tyr	Ala	Lys	Leu	Ile	Pro	Gly	Ala	Thr	Val	Gly	Leu
			340					345					350		
Leu	Gln	Lys	Asp	Ser	Gly	Asn	Ile	Leu	Gln	Leu	Ile	Ile	Ser	Ala	Tyr
		355					360					365			
Glu	Glu	Leu	Arg	Ser	Glu	Val	Glu	Leu	Glu	Val	Leu	Gly	Asp	Thr	Glu
		370					375				380				
Gly	Leu	Asn	Leu	Ser	Phe	Thr	Ala	Ile	Cys	Asn	Asn	Gly	Thr	Leu	Phe
385					390					395					400
Gln	His	Gln	Lys	Lys	Cys	Ser	His	Met	Lys	Val	Gly	Asp	Thr	Ala	Ser
				405					410					415	
Phe	Ser	Val	Thr	Val	Asn	Ile	Pro	His	Cys	Glu	Arg	Arg	Ser	Arg	His
			420					425					430		
Ile	Ile	Ile	Lys	Pro	Val	Gly	Leu	Gly	Asp	Ala	Leu	Glu	Leu	Leu	Val
		435					440					445			
Ser	Pro	Glu	Cys	Asn	Cys	Asp	Cys	Gln	Lys	Glu	Val	Glu	Val	Asn	Ser
		450				455					460				
Ser	Lys	Cys	His	His	Gly	Asn	Gly	Ser	Phe	Gln	Cys	Gly	Val	Cys	Ala
465					470					475					480
Cys	His	Pro	Gly	His	Met	Gly	Pro	Arg	Cys	Glu	Cys	Gly	Glu	Asp	Met
				485					490					495	
Leu	Ser	Thr	Asp	Ser	Cys	Lys	Glu	Ala	Pro	Asp	His	Pro	Ser	Cys	Ser
			500					505					510		
Gly	Arg	Gly	Asp	Cys	Tyr	Cys	Gly	Gln	Cys	Ile	Cys	His	Leu	Ser	Pro
		515					520					525			
Tyr	Gly	Asn	Ile	Tyr	Gly	Pro	Tyr	Cys	Gln	Cys	Asp	Asn	Phe	Ser	Cys
		530				535					540				
Val	Arg	His	Lys	Gly	Leu	Leu	Cys	Gly	Gly	Asn	Gly	Asp	Cys	Asp	Cys
545					550					555					560
Gly	Glu	Cys	Val	Cys	Arg	Ser	Gly	Trp	Thr	Gly	Glu	Tyr	Cys	Asn	Cys
				565					570					575	
Thr	Thr	Ser	Thr	Asp	Ser	Cys	Val	Ser	Glu	Asp	Gly	Val	Leu	Cys	Ser
			580					585					590		
Gly	Arg	Gly	Asp	Cys	Val	Cys	Gly	Lys	Cys	Val	Cys	Thr	Asn	Pro	Gly
		595					600					605			
Ala	Ser	Gly	Pro	Thr	Cys	Glu	Arg	Cys	Pro	Thr	Cys	Gly	Asp	Pro	Cys
		610				615					620				
Asn	Ser	Lys	Arg	Ser	Cys	Ile	Glu	Cys	His	Leu	Ser	Ala	Ala	Gly	Gln
625					630				635						640
Ala	Arg	Glu	Glu	Cys	Val	Asp	Lys	Cys	Lys	Leu	Ala	Gly	Ala	Thr	Ile
				645					650					655	
Ser	Glu	Glu	Glu	Asp	Phe	Ser	Lys	Asp	Gly	Ser	Val	Ser	Cys	Ser	Leu
			660					665					670		
Gln	Gly	Glu	Asn	Glu	Cys	Leu	Ile	Thr	Phe	Leu	Ile	Thr	Thr	Asp	Asn
		675					680</								

<210> 102
 <211> 2231
 <212> DNA
 <213> Homo sapiens

<400> 102
 ctttcaaata ttttttattg aaatgacaat aaaataaaaa aagaacagtg atcacttta 60
 ccaaacttac tttacaaata taaaaaatat aaccaaact tgggaattcc aggccacggc 120
 gcggggcgagg agggggcgcg gcgaggcccg ccggcggggc aaaaccggcc tgggccctgg 180
 cggccgcagg agcgcgtagc gcgtggactt tgccgggctc gccacacagc cccagaccgc 240
 tttaggaccg ggagaccgaa cgcagcgctc agccggggag tttcgggcggc gttctccggg 300
 caccgcgcgc gggaagccag acgcagcggg gggacacatc tcgcggtggc gttgccagag 360
 tgaggagtta gcaggcagga cttgacgagg ctctttggtt tttctagtcc tcaaccactg 420
 aagaagaagc ttgatgcttg gctgtcagaa gacatgaatt acgcacgggt catcacggca 480
 gcgagcgcag ccagaaaccc ttctcccatc cggaccatga ctgacatatt gagcagagga 540
 ccaaaatcga tgatctcctt ggctggtggc ttaccaaact caaacatgtt tccttttaag 600
 actgccgtaa tcaactgtaga aaatggaaag accatccaat ttggagaaga gatgatgaag 660
 agagcacttc agtattctcc gagtgtctga attccagagc ttttgcctg gctaaaacag 720
 ttacaaataa aattgcataa tcctcctacc atccattacc caccagtc aaggacaaatg 780
 gatctatgtg tcacatctgg cagccaacaa ggtctttgta aggtgtttga aatgatcatt 840
 aatcctggag ataatgtcct cctagatgaa cctgcttatt caggaactct tcaaagtctg 900
 caccactgg gctgcaacat tattaatgtt gccagtgat aaagtgggat tgttccagat 960
 tccctaagag acatactttc cagatggaaa ccagaagatg caaagaatcc ccagaaaaac 1020
 acccccaaat ttctttatac tgttccaaat ggcaacaacc ctactggaaa ctcatataacc 1080
 agtgaacgca aaaaggaaat ctatgagctt gcaagaaaat atgatttctt cataatagaa 1140
 gatgatcctt actattttct ccagtttaac aagttcaggg taccaacatt tctttccatg 1200
 gatgttgatg gacgtgtcat cagagctgac tccttttcaa aaatcatttc ctctgggttg 1260
 agaataggat ttttaactgg tccaaaaccc ttaatagaga gagttatatt acacatacaa 1320
 gtttcaacat tgcaccccag cacttttaac cagctcatga tatcacagct tctacacgaa 1380
 tggggagaag aaggtttcat ggctcatgta gacagggtta ttgatttcta tagtaaccag 1440
 aaggatgcaa tactggcagc tgcagacaag tggttaactg gtttggcaga atggcatgtt 1500
 cctgctgctg gaatgttttt atggattaaa gttaaaggca ttaatgatgt aaaagaactg 1560
 attgaagaaa aggccgttaa gatgggggta ttaatgctcc ctggaaatgc tttctacgtc 1620
 gatagctcag ctctagccc ttacttgaga gcctccttct cttcagcttc tccagaacag 1680
 atggatgtgg ccttcagggt attagcacia ctataaaaag aatcctttat aagaaattaa 1740
 actaggttgg gcatggtgag tcacacctat aatcccagca ctttgggagg cagaggaggg 1800
 aggatcactt gaacccagga attcaggctg cagtaagcta cgatcacacc actgcactct 1860
 ggctgcatg cactctggcc tgcattggcag aacaagaccc tgtctctaaa aaaagagaaa 1920
 gaaatcaaac taatcatgct gctcatggat ttttccaata aatttcttgt tttggcagga 1980
 agaaatgaac actggtatta gacttaaaga ttaaatttcc tcaaacatgt cctatctgta 2040
 gtagttcaac tagacacctt ttaaagtgcc tctaaattca tcagatggcc aaactgtatt 2100
 tataatccac ttaggcattt tgaaaaactt tcaacctgta aaaagttact tttatcttgg 2160
 atttattatg aagaactttg tagttgcttt gtaatttccc ataaattgtc tttgaaacta 2220
 aaaaaaaaaa a 2231

<210> 103
 <211> 425
 <212> PRT
 <213> Homo sapiens

<400> 103
 Met Asn Tyr Ala Arg Phe Ile Thr Ala Ala Ser Ala Ala Arg Asn Pro
 1 5 10 15
 Ser Pro Ile Arg Thr Met Thr Asp Ile Leu Ser Arg Gly Pro Lys Ser
 20 25 30
 Met Ile Ser Leu Ala Gly Gly Leu Pro Asn Pro Asn Met Phe Pro Phe
 35 40 45

```

Lys Thr Ala Val Ile Thr Val Glu Asn Gly Lys Thr Ile Gln Phe Gly
 50          55          60
Glu Glu Met Met Lys Arg Ala Leu Gln Tyr Ser Pro Ser Ala Gly Ile
65          70          75          80
Pro Glu Leu Leu Ser Trp Leu Lys Gln Leu Gln Ile Lys Leu His Asn
      85          90          95
Pro Pro Thr Ile His Tyr Pro Pro Ser Gln Gly Gln Met Asp Leu Cys
      100          105          110
Val Thr Ser Gly Ser Gln Gln Gly Leu Cys Lys Val Phe Glu Met Ile
      115          120          125
Ile Asn Pro Gly Asp Asn Val Leu Leu Asp Glu Pro Ala Tyr Ser Gly
      130          135          140
Thr Leu Gln Ser Leu His Pro Leu Gly Cys Asn Ile Ile Asn Val Ala
145          150          155          160
Ser Asp Glu Ser Gly Ile Val Pro Asp Ser Leu Arg Asp Ile Leu Ser
      165          170          175
Arg Trp Lys Pro Glu Asp Ala Lys Asn Pro Gln Lys Asn Thr Pro Lys
      180          185          190
Phe Leu Tyr Thr Val Pro Asn Gly Asn Asn Pro Thr Gly Asn Ser Leu
      195          200          205
Thr Ser Glu Arg Lys Lys Glu Ile Tyr Glu Leu Ala Arg Lys Tyr Asp
      210          215          220
Phe Leu Ile Ile Glu Asp Asp Pro Tyr Tyr Phe Leu Gln Phe Asn Lys
225          230          235          240
Phe Arg Val Pro Thr Phe Leu Ser Met Asp Val Asp Gly Arg Val Ile
      245          250          255
Arg Ala Asp Ser Phe Ser Lys Ile Ile Ser Ser Gly Leu Arg Ile Gly
      260          265          270
Phe Leu Thr Gly Pro Lys Pro Leu Ile Glu Arg Val Ile Leu His Ile
      275          280          285
Gln Val Ser Thr Leu His Pro Ser Thr Phe Asn Gln Leu Met Ile Ser
      290          295          300
Gln Leu Leu His Glu Trp Gly Glu Glu Gly Phe Met Ala His Val Asp
305          310          315          320
Arg Val Ile Asp Phe Tyr Ser Asn Gln Lys Asp Ala Ile Leu Ala Ala
      325          330          335
Ala Asp Lys Trp Leu Thr Gly Leu Ala Glu Trp His Val Pro Ala Ala
      340          345          350
Gly Met Phe Leu Trp Ile Lys Val Lys Gly Ile Asn Asp Val Lys Glu
      355          360          365
Leu Ile Glu Glu Lys Ala Val Lys Met Gly Val Leu Met Leu Pro Gly
      370          375          380
Asn Ala Phe Tyr Val Asp Ser Ser Ala Pro Ser Pro Tyr Leu Arg Ala
385          390          395          400
Ser Phe Ser Ser Ala Ser Pro Glu Gln Met Asp Val Ala Phe Gln Val
      405          410          415
Leu Ala Gln Leu Ile Lys Glu Ser Leu
      420          425

```

<210> 104
 <211> 3176
 <212> DNA
 <213> Homo sapiens

<400> 104
 tgataaccca aggtattcac agcaagatac agtgagtctt aaagttaagc accgtgcaat 60
 tagcttttgct tccttgggtt ttgaaacat gcatctgtat aaacctgcct gtgcagacat 120
 cccgagcccc aagctgggtc tgccaaaatc cagtgaatcg gctctaaaat gtagatggca 180

```

cctagcagtg accaagactc agcctcaggc ggcctgcaaa cctgtgaggc ccagtggagc 240
agccgaacag aaatatgtgg aaaagtctct acgtgttcat ggaatttctg tgcaggaaac 300
caccagagca gagacgggca tggcatacag gaatcttgga aaatcaggac tcagagtttc 360
ttgcttgggt cttggaacat gggtgacatt tggaggtcaa atttcagatg aggttgctga 420
acggctgatg accatgcct atgaaagtgg tgtaaacctc tttgatactg ccgaagtcta 480
tgctgctgga aaggctgaag tgattctggg gagcatcatc aagaagaaag gctggaggag 540
gtccagtctg gtcataacaa ccaaaactcta ctgggggtgga aaagctgaaa cagaaagagg 600
gctgtcaaga aagcatatta ttgaaggatt gaagggctcc ctccagaggc tgcagctcga 660
gtatgtggat gtggtctttg caaatcgacc ggacagtaac actcccatgg aagaaattgt 720
ccgagccatg acacatgtga taaaccaagg catggcgatg tactggggca cctcgagatg 780
gagtgcctag gagatcatgg aagcctattc tgtagcaaga cagttcaata tgatcccacc 840
ggctgtgtaa caagctgagt accatctttt ccagagagag aaagtggagg tccagctgcc 900
agagctctac cacaaaatag gtgttggcgc aatgacatgg tctccacttg cctgtggaat 960
catctcagga aaatacggaa acggggtgcc tgaaagttcc agggcttcac tgaagtgcta 1020
ccagtgggtg aaagaaagaa ttgtaagtga agaagggaga aaacagcaaa acaagctaaa 1080
agacctttcc ccaattgcgg agcgtctggg atgcacacta cctcagctag ctgttgctg 1140
gtgcctgaga aatgaagggtg tgagttctgt gctcctggga tcatccactc ctgaacaact 1200
cattgaaaac cttggtgccca ttcaggttct cccaaagatg acatcacatg tggtaaataga 1260
gattgataac atactgcgca acaagcccta cagcaagaag gactatagat cataaggcaa 1320
tgcatagaac acagaagctg catggttaaa atagcggcct gtgccagta cagaagggtg 1380
ttactaacca gtcttttgaa tcacttagca gcttgctcgt caacctctag tgtccctccc 1440
tggattcttt gaggtgtctg ctgtcgctac cactgtgcac atctgaaaac tcacaacca 1500
gaaaatccat tctattttct tatcttgac tggagtcacc tattcttgca ttgctgtata 1560
cacctcatgc ttatgcaatg ggaagaatat gggggccagg ggggtgtggt ctaccttcag 1620
gcatttggtg actcaaagaa ggctgtacag atatatcttt tcaaaaagaa caaatccac 1680
agatgcaatg tgagttgcgt aagaaacaga gtagatagac taaattcagt gaaggaaagg 1740
aattgagaga tttttcttag taaatagatt attgttaagt aaatagttat taaaaatata 1800
tctcactgca aaaaaaaaaa aagcagtatc ttcactcaaa agtcttgctt ggaagaataa 1860
gcagaaagaa ttttttatat ttttttcta ttttcacatt catactaaca agttttgttc 1920
catttgttat tcaataaaac aaaaatttct aggtatttgc tttattacct ttcaaatatt 1980
tactgttgct tggccccaag aatggccttg tacaacttat ccagaatgtc tattaggatt 2040
ctaattgttat gtccacttac aagtagagac agtaaaagga tgaataccca atcttttagt 2100
acaatgcagc tgatttatga aagagagggc tacactgcta tggaaactta gcttcaaaga 2160
aaatgcaatg tatctgcaat taggtgttca ttttttacta cattttatta aaacctgctt 2220
tatactttca actgcttgta ggcacaactt ctgcaagttt aaatatttga gctttacaaa 2280
taaacatata catgctcagt ttttttaagt aaacctgtaa aatacccagg aaggcaaatg 2340
ttcattgttt aattagctt gggattttat aatataatgt ttggtatttt tgaggcattg 2400
ttaacatgaa agtcaaccac tggctttgtg aaaaatgcta tgtcactatt cagaatatgc 2460
tgggtaaatt aacttgcta gtgaaaagca aaatgttaaa gaaagaactt ctggttctat 2520
aatcatatta tatgactaa actatatgca tgaaagttct ttgcatggat taatggggct 2580
tacccttggt gcactcgaaa tctgaggtgt atctagccct gccactattg gctacttacc 2640
ctcatataa tcccacttga gaaaaattgt gagactatac tgtgtcaata tctgtaaaaa 2700
gagagaaaac atgttttttt ttttttgaag ggggtgggtg gggagtggcc ctttaactcc 2760
tatttggtca tctgaggatg tacaaaattc tcatttaatt ttctggctag caagttcccc 2820
acacagaaat cactctgagg ttacagaag aactgtaata ttattttaaa atgcatattt 2880
ctgtcattag ttctagatat gtacttcatg gttaaattct aaatctgaaa atgctagtgg 2940
gagatatcaa gaaattttct ttttgattac tagtacctgt attctaacag agagtttgaa 3000
ttttttgccc gtgttatcag aatgatggaa attgatcatt ttcagttgtt cattgtgtat 3060
tcaatccagc tgaactgctg tatgtataga ggagcttgag gtgctgtcta atgggaaatg 3120
tgatttgatt gatatttttg cttagagtaa taaaagcatt ttgtgcattc aatctt 3176

```

<210> 105

<211> 408

<212> PRT

<213> Homo sapiens

<400> 105

Met His Leu Tyr Lys Pro Ala Cys Ala Asp Ile Pro Ser Pro Lys Leu

1

5

10

15

Gly Leu Pro Lys Ser Ser Glu Ser Ala Leu Lys Cys Arg Trp His Leu
 20 25 30
 Ala Val Thr Lys Thr Gln Pro Gln Ala Ala Cys Lys Pro Val Arg Pro
 35 40 45
 Ser Gly Ala Ala Glu Gln Lys Tyr Val Glu Lys Phe Leu Arg Val His
 50 55 60
 Gly Ile Ser Leu Gln Glu Thr Thr Arg Ala Glu Thr Gly Met Ala Tyr
 65 70 75 80
 Arg Asn Leu Gly Lys Ser Gly Leu Arg Val Ser Cys Leu Gly Leu Gly
 85 90 95
 Thr Trp Val Thr Phe Gly Gly Gln Ile Ser Asp Glu Val Ala Glu Arg
 100 105 110
 Leu Met Thr Ile Ala Tyr Glu Ser Gly Val Asn Leu Phe Asp Thr Ala
 115 120 125
 Glu Val Tyr Ala Ala Gly Lys Ala Glu Val Ile Leu Gly Ser Ile Ile
 130 135 140
 Lys Lys Lys Gly Trp Arg Arg Ser Ser Leu Val Ile Thr Thr Lys Leu
 145 150 155 160
 Tyr Trp Gly Gly Lys Ala Glu Thr Glu Arg Gly Leu Ser Arg Lys His
 165 170 175
 Ile Ile Glu Gly Leu Lys Gly Ser Leu Gln Arg Leu Gln Leu Glu Tyr
 180 185 190
 Val Asp Val Val Phe Ala Asn Arg Pro Asp Ser Asn Thr Pro Met Glu
 195 200 205
 Glu Ile Val Arg Ala Met Thr His Val Ile Asn Gln Gly Met Ala Met
 210 215 220
 Tyr Trp Gly Thr Ser Arg Trp Ser Ala Met Glu Ile Met Glu Ala Tyr
 225 230 235 240
 Ser Val Ala Arg Gln Phe Asn Met Ile Pro Pro Val Cys Glu Gln Ala
 245 250 255
 Glu Tyr His Leu Phe Gln Arg Glu Lys Val Glu Val Gln Leu Pro Glu
 260 265 270
 Leu Tyr His Lys Ile Gly Val Gly Ala Met Thr Trp Ser Pro Leu Ala
 275 280 285
 Cys Gly Ile Ile Ser Gly Lys Tyr Gly Asn Gly Val Pro Glu Ser Ser
 290 295 300
 Arg Ala Ser Leu Lys Cys Tyr Gln Trp Leu Lys Glu Arg Ile Val Ser
 305 310 315 320
 Glu Glu Gly Arg Lys Gln Gln Asn Lys Leu Lys Asp Leu Ser Pro Ile
 325 330 335
 Ala Glu Arg Leu Gly Cys Thr Leu Pro Gln Leu Ala Val Ala Trp Cys
 340 345 350
 Leu Arg Asn Glu Gly Val Ser Ser Val Leu Leu Gly Ser Ser Thr Pro
 355 360 365
 Glu Gln Leu Ile Glu Asn Leu Gly Ala Ile Gln Val Leu Pro Lys Met
 370 375 380
 Thr Ser His Val Val Asn Glu Ile Asp Asn Ile Leu Arg Asn Lys Pro
 385 390 395 400
 Tyr Ser Lys Lys Asp Tyr Arg Ser
 405

<210> 106

<211> 3103

<212> DNA

<213> Homo sapiens

<400> 106

ttcagattac tttgatgaca gtgacttcca gtcttctctg aaagatctcc acgatgctgg 60


```

cagccccggac agggggcagcg gggagtcaga tctcagagga gaacaccaag ttaaggagac 120
agtctggggtt ttctgtagca gggaaagaca aatctcccaa gaaagcctca gaaaacgcta 180
aagacagcgag ccttagtccc tcaggggaaa gccagctcag ggcgcgtaaa ctggctctgc 240
tgcgcgaaagt ggagatgaac tggtagctaa agctctgcga cctgtccagc gagcacacca 300
ccgtctgcac cacaggcatg ccgcacagga atcttgaaaa atcaggactc agagttttctt 360
gcttgggtct tggaaacatgg gtgacatttg gaggtcaaat ttcagatgag gttgctgaac 420
ggctgatgac catcgcctat gaaagtgggtg ttaacctctt tgatactgcc gaagtctatg 480
ctgctggaaa ggctgaagtg attctgggga gcatcatcaa gaagaaaggc tggaggagggt 540
ccagtctggt cataacaacc aaactctact ggggtggaaa agctgaaaca gaaagagggc 600
tgtcaagaaa gcatattatt gaaggattga agggctccct ccagaggctg cagctcgagt 660
atgtggatgt ggtcttttga aatcgaccgg acagtaacac tcccatggaa gaaattgtcc 720
gagccatgac acatgtgata aaccaaggca tggcgatgta ctggggcacc tcgagatgga 780
gtgctatgga gatcatggaa gcctattctg tagcaagaca gttcaatatg atcccaccgg 840
tctgtgaaca agctgagtag catcttttcc agagagagaa agtggagggtc cagctgccag 900
agctctacca caaaataggt gttggcgcaa tgacatggtc tccacttgcc tgtggaatca 960
tctcagggaaa atacggaaac ggggtgcctg aaagtccag ggcttccactg aagtgtacc 1020
agtggttgaa agaaagaatt gtaagtgaag aaggggagaaa acagcaaaac aagctaaaag 1080
acctttcccc aattgctggag cgtctgggat gcacactacc tcagctagct gttgcgtggt 1140
gcctgagaaa tgaagggtgtg agttctgtgc tcctgggatc atccactcct gaacaactca 1200
ttgaaaacct tggtgccatt caggttctcc caaagatgac atcacatgtg gtaaatgaga 1260
ttgataacat actgcgcaac aagccctaca gcaagaaggc ctatagatca taaggcaatg 1320
catgaaccac agaagctgca tggttaaaat agcggcctgt gccagtaga gaaagggtgtt 1380
actaaccagt cttttgaatc acttagcagc ttgctcgtca acctctagt tccctccctg 1440
gattctttga ggtgtctgct gtcgctacca ctgtgcacat ctgaaaactc acaaccaaga 1500
aaatccattc tattttctta tcttggactg gagtcaccta ttcttgcat gctgtatata 1560
cctcatgctt atgcaatggg aagaatatgg gggccagggg gtgtggtact accttcaggc 1620
atthtgtaac tcaaagaagg ctgtacagat atattttttc aaaagaacaa aatccacaga 1680
tgcaatgtga gttgcgtaag aaacagagta gatagactaa attcagtga ggaaggaat 1740
tgagagattt ttcttagtaa atagattatt gtttaagtaaa tagttattaa aaatatct 1800
cactgcaaaa aaaaaagcag tatcttcact caaaagtctt gcttgaaga ataagcagaa 1860
agaattttat atattttttt tctattttca cattcatact aacaagtttt gttccatttg 1920
ttattcaata aaacaaaaat ttctaggtat ttgctttatt acctttcaaa tattttactgt 1980
tgcttggccc caagaatggc cttgtacaac ttatccagaa tgtctattag gattctaattg 2040
ttatgtccac ttacaagtag agaccgcaaa aggatgaata cccaatcttt agtgacaatg 2100
cagctgattt atgaaagaga gggctacact gctatggaaa cttagcttca aagaaaatgc 2160
aatgtatctg caattaggtg ttcatthttt actacatttt attaaaacct gctttatact 2220
ttcaactgct tgtaggcaca acttctgcaa gtttaaatat ttgagcttta caaataaaca 2280
tacacatgct gttttttaag taaacctgta aaatacccag gaaggcaaat gttcattggt 2340
taattagcac tgggatttta taatataatg tttgggtatt ttgaggcatt gttacatga 2400
aagtcaacca ctggctttgt gaaaaatgct atgtcactat tcagaatatg ctgggtaaat 2460
taacttgcct agtgaaaagc aaaatgttaa agaaagaact tctggttcta taatcatatt 2520
atatgcacta aactatatgc atgaaagtgc tttgcatgga ttaatggggc ttacccttgt 2580
tgcaactcgaa atctgaggtg tatctagccc tgccactatt ggctacttac cctcattaat 2640
atcccacttg agaaaaattg tgagactata ctgtgtcaat atctgtaaaa agagagaaaa 2700
catgtttttt tttttgaagg ggggtggtgt ggagtggccc ttttaactcta tttggctatc 2760
tgaggatgta caaaattctc atttaatttt ctggtcagca agttccccac acagaaatca 2820
ctctgaggtt tacagaagaa ctgtaatat attttaaaa gcgattttct gtcattagtt 2880
ctagatatgt acttcatggt taaattctaa atctgaaaat gctagtggga gatatacaga 2940
aatthttctt ttgattacta gtacctgtat tctaacagag agtttgaatt ttttgccgt 3000
gttatcagaa tgatggaaat tgatcatttt cagttgttca ttgtgtattc aatccagcga 3060
actgctgtat gtatagagga gctgaggtgc tgtctaattg gaa 3103

```

<210> 107

<211> 419

<212> PRT

<213> Homo sapiens

<400> 107

Met Leu Ala Ala Arg Thr Gly Ala Ala Gly Ser Gln Ile Ser Glu Glu

1	5	10	15
Asn Thr Lys	Leu Arg Arg Gln Ser Gly	Phe Ser Val Ala Gly	Lys Asp
	20	25	30
Lys Ser Pro	Lys Lys Ala Ser Glu Asn	Ala Lys Asp Ser Ser	Leu Ser
	35	40	45
Pro Ser Gly	Glu Ser Gln Leu Arg Ala Arg	Gln Leu Ala Leu Leu	Arg
	50	55	60
Glu Val Glu	Met Asn Trp Tyr Leu Lys Leu	Cys Asp Leu Ser Ser	Glu
	65	70	75
His Thr Thr	Val Cys Thr Thr Gly Met Pro	His Arg Asn Leu Gly	Lys
	85	90	95
Ser Gly Leu	Arg Val Ser Cys Leu Gly Leu	Gly Thr Trp Val Thr	Phe
	100	105	110
Gly Gly Gln	Ile Ser Asp Glu Val Ala Glu	Arg Leu Met Thr Ile	Ala
	115	120	125
Tyr Glu Ser	Gly Val Asn Leu Phe Asp Thr	Ala Glu Val Tyr Ala	Ala
	130	135	140
Gly Lys Ala	Glu Val Ile Leu Gly Ser Ile Ile	Lys Lys Lys Gly	Trp
	145	150	155
Arg Arg Ser	Ser Leu Val Ile Thr Thr Lys	Leu Tyr Trp Gly Gly	Lys
	165	170	175
Ala Glu Thr	Glu Arg Gly Leu Ser Arg Lys	His Ile Ile Glu Gly	Leu
	180	185	190
Lys Gly Ser	Leu Gln Arg Leu Gln Leu Glu	Tyr Val Asp Val Val	Phe
	195	200	205
Ala Asn Arg	Pro Asp Ser Asn Thr Pro Met	Glu Glu Ile Val Arg	Ala
	210	215	220
Met Thr His	Val Ile Asn Gln Gly Met Ala	Met Tyr Trp Gly Thr	Ser
	225	230	235
Arg Trp Ser	Ala Met Glu Ile Met Glu Ala	Tyr Ser Val Ala Arg	Gln
	245	250	255
Phe Asn Met	Ile Pro Pro Val Cys Glu Gln	Ala Glu Tyr His Leu	Phe
	260	265	270
Gln Arg Glu	Lys Val Glu Val Gln Leu Pro	Glu Leu Tyr His Lys	Ile
	275	280	285
Gly Val Gly	Ala Met Thr Trp Ser Pro Leu	Ala Cys Gly Ile Ile	Ser
	290	295	300
Gly Lys Tyr	Gly Asn Gly Val Pro Glu Ser	Ser Arg Ala Ser Leu	Lys
	305	310	315
Cys Tyr Gln	Trp Leu Lys Glu Arg Ile Val	Ser Glu Glu Gly Arg	Lys
	325	330	335
Gln Gln Asn	Lys Leu Lys Asp Leu Ser Pro	Ile Ala Glu Arg Leu	Gly
	340	345	350
Cys Thr Leu	Pro Gln Leu Ala Val Ala Trp	Cys Leu Arg Asn Glu	Gly
	355	360	365
Val Ser Ser	Val Leu Leu Gly Ser Ser Thr	Pro Glu Gln Leu Ile	Glu
	370	375	380
Asn Leu Gly	Ala Ile Gln Val Leu Pro Lys	Met Thr Ser His Val	Val
	385	390	395
Asn Glu Ile	Asp Asn Ile Leu Arg Asn Lys	Pro Tyr Ser Lys Lys	Asp
	405	410	415
Tyr Arg Ser			

<210> 108
 <211> 2620
 <212> DNA
 <213> Homo sapiens

<400> 108

```

agggaccgtg cgctgcctgg ggaagcaatg caagtctcca tagcctgcac agagcacaat 60
ttgaagagtc ggaatggtga ggaccgactt ctgagcaagc agagctccac cgtccccaat 120
gtggtgaacg cagcccgggc caaattccgc acggtcgcta tcatcgcgcg cagcctgggg 180
acgttcacgc ctcagcatca cttttctctc aaagagtcca ccgcaaagca gactggcatg 240
aaatatagga atcttggaat atcaggactc agagtttctt gcttgggtct tggaaacatgg 300
gtgacatttg gaggtcaaat ttcagatgag gttgctgaac ggctgatgac catcgccctat 360
gaaagtgggtg ttaacctctt tgatactgcc gaagtctatg ctgctggaaa ggctgaagtg 420
attctgggga gcatcatcaa gaagaaaggc tggaggagggt ccagtctggt cataacaacc 480
aaactctact ggggtggaat agctgaaaca gaaagagggc tgtcaagaaa gcatattatt 540
gaaggattga agggctccct ccagaggctg cagctcgagt atgtggatgt ggtctttgca 600
aatcgaccgg acagtaaacac tcccatggaa gaaattgtcc gagccatgac acatgtgata 660
aaccaaggca tggcgatgta ctggggcacc tcgagatgga gtgctatgga gatcatggaa 720
gcctattctg tagcaagaca gttcaatatg atcccaccgg tctgtgaaca agctgagtag 780
catcttttcc agagagagaa agtggaggct cagctgccag agctctacca caaaataggt 840
gttggcgcaa tgacatggct tccacttgcc tgtggaatca tctcaggaaa ataccgaaac 900
ggggtgcctg aaagttccag ggcttcaactg aagtgtacc agtgggtgaa agaaagaatt 960
gtaagtgaag aaggagaaaa acagcaaaac aagctaaaaag acctttcccc aattgctggag 1020
cgtctgggat gcacactacc tcagctagct gttgcgtggt gcctgagaaa tgaagggtgtg 1080
agttctgtgc tctctgggatc atccactcct gaacaactca ttgaaaacct tggtgccatt 1140
caggttctcc caaagatgac atcacatgtg gtaaatgaga ttgataacat actgcgcaac 1200
aagccctaca gcaagaagga ctatagatca taaggcaatg catgaaccac agaagctgca 1260
tggttaaaat agcggcctgt gccagtaga gaaagggtgt actaaccagt cttttgaatc 1320
acttagcagc ttgctcgta acctctagt tccctccctg gattctttga ggtgtctgct 1380
gtcgctacca ctgtgcacat ctgaaaactc acaaccaaga aaatccattc tttttctta 1440
tcttgactg gagtcacctt ttcttgcat gctgtataca cctcatgctt atgcaatggg 1500
aagaatatgg gggccagggg gtgtggtact accttcaggc atttggtaac tcaaagaagg 1560
ctgtacagat atattttttc aaaaagaaca aaatccacag atgcaatgtg agttgcgtaa 1620
gaaacagagt agatagacta aattcagtga aggaaaggaa ttgagagatt tttcttagta 1680
aatagattat tgttaagtaa atagttatta aaaatatatc tcaactgcaa aaaaaaaaaa 1740
gcagtatctt cactcaaaag tcttgcttgg aagaataagc agaaagaatt ttatatattt 1800
tttttctatt ttcacattca tactaacaag ttttgttcca tttgttattc aataaaacaa 1860
aaattttctag gtattttgctt tattaccttt caaatattta ctgttgcttg gccccaaaga 1920
tggtccttga caacttatcc agaattgtct ttaggattct aatgttatgt ccacttacaa 1980
gtagagacag taaaaggatg aatacccaat ctttagtgac aatgcagctg atttatgaaa 2040
gagagggcta cactgctatg gaaacttagc ttcaaagaaa atgcaatgta tctgcaatta 2100
ggtgttcatt ttttactaca ttttattaaa acctgcttta tactttcaac tgctttagg 2160
cacaacttct gcaagtttaa atatttgagc tttacaaata aacatacaca tgctgttttt 2220
taagtaaac tgtaaaatac ccagggaaggc aaatgttcat tgtttaatta gcaactggg 2280
tttataatat aatgtttggt atttttgagg cattgttaac atgaaagtca accactggct 2340
ttgtgaaaaa tgctatgtca ctattcagaa tatgctgggt aaattaactt gcctagtga 2400
aagcaaaatg ttaaagaaag aacttctggt tctataatca tattatatgc actaaactat 2460
atgcatgaaa gttctttgca tggattaatg gggcttacc ttgttgcaact cgaaatctga 2520
ggtgtatcta gccctgccac tattggctac ttaccctcat taatatccca cttgagaaaa 2580
attgtgagac tatactgtgt caatatctgt aaaaagagag 2620

```

<210> 109

<211> 401

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Gln Val Ser Ile Ala Cys Thr Glu His Asn Leu Lys Ser Arg Asn
 1             5             10             15
Gly Glu Asp Arg Leu Leu Ser Lys Gln Ser Ser Thr Ala Pro Asn Val
      20             25             30
Val Asn Ala Ala Arg Ala Lys Phe Arg Thr Val Ala Ile Ile Ala Arg
      35             40             45

```

Ser	Leu	Gly	Thr	Phe	Thr	Pro	Gln	His	His	Ile	Ser	Leu	Lys	Glu	Ser
50						55					60				
Thr	Ala	Lys	Gln	Thr	Gly	Met	Lys	Tyr	Arg	Asn	Leu	Gly	Lys	Ser	Gly
65					70					75					80
Leu	Arg	Val	Ser	Cys	Leu	Gly	Leu	Gly	Thr	Trp	Val	Thr	Phe	Gly	Gly
				85					90					95	
Gln	Ile	Ser	Asp	Glu	Val	Ala	Glu	Arg	Leu	Met	Thr	Ile	Ala	Tyr	Glu
			100					105					110		
Ser	Gly	Val	Asn	Leu	Phe	Asp	Thr	Ala	Glu	Val	Tyr	Ala	Ala	Gly	Lys
		115					120					125			
Ala	Glu	Val	Ile	Leu	Gly	Ser	Ile	Ile	Lys	Lys	Lys	Gly	Trp	Arg	Arg
		130				135					140				
Ser	Ser	Leu	Val	Ile	Thr	Thr	Lys	Leu	Tyr	Trp	Gly	Gly	Lys	Ala	Glu
145					150				155						160
Thr	Glu	Arg	Gly	Leu	Ser	Arg	Lys	His	Ile	Ile	Glu	Gly	Leu	Lys	Gly
				165					170					175	
Ser	Leu	Gln	Arg	Leu	Gln	Leu	Glu	Tyr	Val	Asp	Val	Val	Phe	Ala	Asn
			180					185					190		
Arg	Pro	Asp	Ser	Asn	Thr	Pro	Met	Glu	Glu	Ile	Val	Arg	Ala	Met	Thr
		195					200					205			
His	Val	Ile	Asn	Gln	Gly	Met	Ala	Met	Tyr	Trp	Gly	Thr	Ser	Arg	Trp
		210				215					220				
Ser	Ala	Met	Glu	Ile	Met	Glu	Ala	Tyr	Ser	Val	Ala	Arg	Gln	Phe	Asn
225					230				235						240
Met	Ile	Pro	Pro	Val	Cys	Glu	Gln	Ala	Glu	Tyr	His	Leu	Phe	Gln	Arg
				245					250					255	
Glu	Lys	Val	Glu	Val	Gln	Leu	Pro	Glu	Leu	Tyr	His	Lys	Ile	Gly	Val
			260					265					270		
Gly	Ala	Met	Thr	Trp	Ser	Pro	Leu	Ala	Cys	Gly	Ile	Ile	Ser	Gly	Lys
		275					280					285			
Tyr	Gly	Asn	Gly	Val	Pro	Glu	Ser	Ser	Arg	Ala	Ser	Leu	Lys	Cys	Tyr
		290				295					300				
Gln	Trp	Leu	Lys	Glu	Arg	Ile	Val	Ser	Glu	Glu	Gly	Arg	Lys	Gln	Gln
305					310					315					320
Asn	Lys	Leu	Lys	Asp	Leu	Ser	Pro	Ile	Ala	Glu	Arg	Leu	Gly	Cys	Thr
				325					330					335	
Leu	Pro	Gln	Leu	Ala	Val	Ala	Trp	Cys	Leu	Arg	Asn	Glu	Gly	Val	Ser
			340					345					350		
Ser	Val	Leu	Leu	Gly	Ser	Ser	Thr	Pro	Glu	Gln	Leu	Ile	Glu	Asn	Leu
			355				360					365			
Gly	Ala	Ile	Gln	Val	Leu	Pro	Lys	Met	Thr	Ser	His	Val	Val	Asn	Glu
		370				375					380				
Ile	Asp	Asn	Ile	Leu	Arg	Asn	Lys	Pro	Tyr	Ser	Lys	Lys	Asp	Tyr	Arg
385					390					395					400
Ser															

<210> 110
 <211> 3944
 <212> DNA
 <213> Homo sapiens

<400> 110
 cttcaaacct tcacagctaa tcaaagacct ggccaaagag atccggctca gtgagaatgc 60
 ctccaaagcc gtccgaccgg aagtgaatac tgtcgctcgc tcagatgagg tgtgtgacgg 120
 ggaccgggag aaggaggagc ccccgctctc cattgaggcc accccgcctc aatccctcct 180
 ggagaaagtg tccaaaaaaa agactcccaa aactgtgaag atgcccaagc catccaaaat 240
 ccccaagccc ccgaagcccc ctaagcccc aaggccccc aaaacgctga agctcaaaga 300

tggaggcaag	aagaaagga	agaagtccc	ggagtcagcc	tcacccacca	tccccaacct	360
ggacctgtc	gaagcccaca	ccaaggaggc	actgaccaag	atggagccgc	ccaagaaggg	420
caaggccaca	aagagtgtcc	tgagtgtgcc	caacaaagat	gtgggtcaca	tgcagaatga	480
tgtggagagg	ctggaaattc	gagagcaaac	caagagcaag	tcagaggcca	agtggaagta	540
caagaacagc	aaacctgact	ccttactgaa	gatggaagag	gagcagaagc	tagagaagtc	600
gcctctagct	ggaaacaaa	acaataagtt	ctctttttct	ttctccaaca	agaaactcct	660
cggtccaag	gctctcaggc	ccccgacgag	ccctgggtgtg	ttcggggcct	tgcagaactt	720
caaggaggac	aagcccaagc	ccgtgcggga	tgagtatgag	tacgtgtcgg	atgacggtga	780
gctcaagatc	gacgagtttc	ccatcaggag	gaagaaaaac	gccccgaaaa	gggacttgtc	840
cttcttggtg	gataagaagg	ctgtgctgcc	cacgcctgtc	acgaagccaa	agctggactc	900
ggcagcgtac	aagcagagt	atgactcctc	ggacgagggt	tcgctgcaca	tcgacacaga	960
caccaagccc	ggccgcaatg	ccagagtcaa	gaaggagagt	gggagctcgg	cagctggcat	1020
cttggacctg	ctgcaggcca	gtgaggaggt	tggcgcgctg	gagtacaacc	ccagcagcca	1080
gcccccgcc	tccccagca	cacaggaagc	cattcaggga	atgctgtcca	tggccaacct	1140
gcaggcctcc	gactcctgcc	tgcagaccac	gtggggagct	ggccaggcca	aggggagctc	1200
gctggctgcc	catggtgccc	ggaagaatgg	gggtggcagt	ggcaagagt	caggcaaacg	1260
actgctgaag	agggtcgcca	agaacagtgt	cgacctggac	gactacgagg	aagagcagga	1320
ccacctggat	gcctgcttca	aggactcaga	ctacgtttac	ccctcactgg	agtcagatga	1380
agacaacccc	atctttaagt	cccggtcgaa	gaaaaggaaa	ggctcagacg	acgctcccta	1440
cagoccaaaca	gcaagggctg	gcccacgggt	gccaagacag	gacaggcctg	tgcgtgaggg	1500
tacacgggtg	gcttccatcg	agaccgggct	ggcggtgct	gcagctaagt	tgtcccagca	1560
ggaggagcag	aaaagcaaga	aaaaaaagag	tgccaagagg	aagctgactc	ctaaccacc	1620
ctcctctcc	acctccacct	ccatctctgc	cggcaccacc	tccacctcca	ccacgccagc	1680
ctctaccacc	cctgcctcca	ccacaccggc	ctccaccacc	ccggcctcca	ccagcacggc	1740
cagcagccag	gcctcgcagg	agggcagctc	gccagagccc	ccgcctgagt	cgcatagcag	1800
cagcctggcg	gaccatgagt	acacagccgc	tggcaccttc	accggggccc	aggtggccg	1860
cacctccagc	cccatggccc	ctggggtctt	tctcacacag	aggcgccct	ccgcctcgtc	1920
tccaaacaac	aacaccgctg	ccaaaggaaa	acgtacgaaa	aagggcattg	cgaccgctca	1980
gcagaggctt	gggaaaattt	tgaaaattca	tcggaacggg	aaactactcc	tttaagattt	2040
ggaaagccag	gatcctttctg	ctccgctcag	gacccccgga	gccccgcgaa	aacatctgcc	2100
tcccaggagg	gtgccgagct	gcctcaccag	ggagggcctt	gcctcttccc	ggctgccatc	2160
tccccaaaca	gcgtctgtcc	cttcagccgg	cagagcgagc	ccagcgtggc	ccctcaattt	2220
gaaaatggac	gtctttttctc	aagttgctaa	gagtgatctg	tcccagaaaa	gcggccctgc	2280
aagtttgagg	accgcttatt	ccactttaag	gacagccttc	aggccccctg	agcgtgggtg	2340
tgattgcagc	gcctctgcag	ctctgctgag	agcatgagtc	cttcaaggaa	gacagagtga	2400
gccagtgtc	accagcccca	gagtcagagc	tggccacagg	ctggcagcct	ccaggggctt	2460
aaaaaaaaag	gcaagaaca	cgaaaagagg	aggagcaagt	gggatgttta	tgtccccctt	2520
tctcttctcg	agtgaattctc	agccaagtcc	agacagtgtc	cggcggtga	ggaagggtct	2580
gccccgagct	ttctgggttg	caggtggcag	caggatggtg	ggtgttcagc	ctgaatgccc	2640
aggagcattt	ctggggggca	gctaagactg	gcagctgggt	tgggtgtgta	gcgggcaggg	2700
gagccattgt	ggggtcccca	ggaaagggca	agggctcagc	cacatcttgg	ggtctgggag	2760
gccaggcta	agccatgtgg	cagggaccgt	cttgccctgc	tggccacact	ctggagaagc	2820
acttctcagc	caaggcaccc	ctgccctggg	actggcaggg	caggggcagg	ggcagggaca	2880
gtggacaggc	ggcccgagga	cttacggctg	gcacttctct	gttctcccgt	gtcagcgtgt	2940
ggtgtcgct	gcattgggtg	tacctggatg	gtgtgtccac	catcgacacg	gaggggctgg	3000
atttgtttct	caggcaatcc	tgtattttta	ttttagatgt	atttcctgaa	gcataatttt	3060
catagaatgt	agcgtgtaaa	tagcttttta	aataacttct	tttttataag	agtaaaagta	3120
tcttttaggaa	tttcttttcta	tagagtctct	cattaacatt	tatacagatt	ttttgctgag	3180
tcagatggac	agttgggttc	tgatgctttt	tccttctcct	ttccttttat	tattattatt	3240
tttttctttt	agaactaag	gtattgcctg	aaaaacaagt	gatgtctgtg	cagccttaca	3300
ctctgtcttt	acagaagcaa	atagtacaca	aaagatctat	ttcagacaca	ttttgaagat	3360
gaatcttcaa	ctttaatacc	agctctttgt	tttccttgta	tgatgagggg	attgggggat	3420
acagttattt	tactagcacc	ttgtgaagtg	ttccgtgtt	ttgtgatgct	gtaattttat	3480
aatgtttgta	cttttttata	tttgtacatt	tcttatgagc	tttgtttata	taccattac	3540
ctggatgttt	ttgtccactg	ggagaggcag	cttgggtggag	gccttatcca	ctccactttg	3600
tcctgttttg	agggacgcag	tccctagggc	ccgagactgg	gtgggagagg	gggagtctca	3660
cggggcccca	ggcttattca	gaactggtgt	ttttaaagtt	tcctttaccc	tgccttgttt	3720
gaacatttat	ataatctaac	ctggacatca	agctgttctc	tctctctctt	ttttttaatt	3780
ttattattat	tatttttgga	acatgtacat	ttctaacaaa	gtttatcgtg	gctattaaag	3840

tggttttattt cccaattcat attactcttg tatcgagtcc atgaggtcta aggcaactta 3900
 gatcaaagtt ttaaaaaagt aaaaatattt caggttttgt acag 3944

<210> 111
 <211> 677
 <212> PRT
 <213> Homo sapiens

<400> 111
 Phe Lys Pro Ser Gln Leu Ile Lys Asp Leu Ala Lys Glu Ile Arg Leu
 1 5 10 15
 Ser Glu Asn Ala Ser Lys Ala Val Arg Pro Glu Val Asn Thr Val Ala
 20 25 30
 Ser Ser Asp Glu Val Cys Asp Gly Asp Arg Glu Lys Glu Glu Pro Pro
 35 40 45
 Ser Pro Ile Glu Ala Thr Pro Pro Gln Ser Leu Leu Glu Lys Val Ser
 50 55 60
 Lys Lys Lys Thr Pro Lys Thr Val Lys Met Pro Lys Pro Ser Lys Ile
 65 70 75 80
 Pro Lys Pro Pro Lys Pro Pro Lys Pro Pro Arg Pro Pro Lys Thr Leu
 85 90 95
 Lys Leu Lys Asp Gly Gly Lys Lys Lys Gly Lys Lys Ser Arg Glu Ser
 100 105 110
 Ala Ser Pro Thr Ile Pro Asn Leu Asp Leu Leu Glu Ala His Thr Lys
 115 120 125
 Glu Ala Leu Thr Lys Met Glu Pro Pro Lys Lys Gly Lys Ala Thr Lys
 130 135 140
 Ser Val Leu Ser Val Pro Asn Lys Asp Val Val His Met Gln Asn Asp
 145 150 155 160
 Val Glu Arg Leu Glu Ile Arg Glu Gln Thr Lys Ser Lys Ser Glu Ala
 165 170 175
 Lys Trp Lys Tyr Lys Asn Ser Lys Pro Asp Ser Leu Leu Lys Met Glu
 180 185 190
 Glu Glu Gln Lys Leu Glu Lys Ser Pro Leu Ala Gly Asn Lys Asp Asn
 195 200 205
 Lys Phe Ser Phe Ser Phe Ser Asn Lys Lys Leu Leu Gly Ser Lys Ala
 210 215 220
 Leu Arg Pro Pro Thr Ser Pro Gly Val Phe Gly Ala Leu Gln Asn Phe
 225 230 235 240
 Lys Glu Asp Lys Pro Lys Pro Val Arg Asp Glu Tyr Glu Tyr Val Ser
 245 250 255
 Asp Asp Gly Glu Leu Lys Ile Asp Glu Phe Pro Ile Arg Arg Lys Lys
 260 265 270
 Asn Ala Pro Lys Arg Asp Leu Ser Phe Leu Leu Asp Lys Lys Ala Val
 275 280 285
 Leu Pro Thr Pro Val Thr Lys Pro Lys Leu Asp Ser Ala Ala Tyr Lys
 290 295 300
 Gln Ser Asp Asp Ser Ser Asp Glu Gly Ser Leu His Ile Asp Thr Asp
 305 310 315 320
 Thr Lys Pro Gly Arg Asn Ala Arg Val Lys Lys Glu Ser Gly Ser Ser
 325 330 335
 Ala Ala Gly Ile Leu Asp Leu Leu Gln Ala Ser Glu Glu Val Gly Ala
 340 345 350
 Leu Glu Tyr Asn Pro Ser Ser Gln Pro Pro Ala Ser Pro Ser Thr Gln
 355 360 365
 Glu Ala Ile Gln Gly Met Leu Ser Met Ala Asn Leu Gln Ala Ser Asp
 370 375 380
 Ser Cys Leu Gln Thr Thr Trp Gly Ala Gly Gln Ala Lys Gly Ser Ser
 385 390 395 400

Leu Ala Ala His Gly Ala Arg Lys Asn Gly Gly Gly Ser Gly Lys Ser
 405 410 415
 Ala Gly Lys Arg Leu Leu Lys Arg Ala Ala Lys Asn Ser Val Asp Leu
 420 425 430
 Asp Asp Tyr Glu Glu Glu Gln Asp His Leu Asp Ala Cys Phe Lys Asp
 435 440 445
 Ser Asp Tyr Val Tyr Pro Ser Leu Glu Ser Asp Glu Asp Asn Pro Ile
 450 455 460
 Phe Lys Ser Arg Ser Lys Lys Arg Lys Gly Ser Asp Asp Ala Pro Tyr
 465 470 475 480
 Ser Pro Thr Ala Arg Val Gly Pro Ser Val Pro Arg Gln Asp Arg Pro
 485 490 495
 Val Arg Glu Gly Thr Arg Val Ala Ser Ile Glu Thr Gly Leu Ala Ala
 500 505 510
 Ala Ala Ala Lys Leu Ser Gln Gln Glu Glu Gln Lys Ser Lys Lys Lys
 515 520 525
 Lys Ser Ala Lys Arg Lys Leu Thr Pro Asn Thr Thr Ser Pro Ser Thr
 530 535 540
 Ser Thr Ser Ile Ser Ala Gly Thr Thr Ser Thr Thr Thr Pro Ala
 545 550 555 560
 Ser Thr Thr Pro Ala Ser Thr Thr Pro Ala Ser Thr Thr Pro Ala Ser
 565 570 575
 Thr Ser Thr Ala Ser Ser Gln Ala Ser Gln Glu Gly Ser Ser Pro Glu
 580 585 590
 Pro Pro Pro Glu Ser His Ser Ser Ser Leu Ala Asp His Glu Tyr Thr
 595 600 605
 Ala Ala Gly Thr Phe Thr Gly Ala Gln Ala Gly Arg Thr Ser Gln Pro
 610 615 620
 Met Ala Pro Gly Val Phe Leu Thr Gln Arg Arg Pro Ser Ala Ser Ser
 625 630 635 640
 Pro Asn Asn Asn Thr Ala Ala Lys Gly Lys Arg Thr Lys Lys Gly Met
 645 650 655
 Ala Thr Ala Lys Gln Arg Leu Gly Lys Ile Leu Lys Ile His Arg Asn
 660 665 670
 Gly Lys Leu Leu
 675

<210> 112

<211> 5433

<212> DNA

<213> Homo sapiens

<400> 112

atgggatggc tgtggatcctt tggggcagcc ctggggcagc gtctgggcta cagttcacag 60
 cagcaaaggg tgccatttct tcagcctccc ggtcaaagtc aactgcaagc gagttatgtg 120
 gagtttagac ccagccaggg ttgtagccct ggatactatc gggatcataa aggcttgtat 180
 accggacggg gtgttcctct caattgcaac ggacattcaa atcaatgcca ggatggctca 240
 ggcatatgtg ttaactgtca gcacaacacc gcgggagagc actgtgaacg ctgccaggag 300
 ggctactatg gcaacgcctt ccacggatcc tgcagggcct gcccatgtcc tcacactaac 360
 agctttgcca ctggctgtgt ggtgaatggg ggagacgtgc ggtgctcctg caaagctggg 420
 tacacaggaa cacagtgtga aaggtgtgca ccgggatatt tcgggaatcc ccagaaattc 480
 ggaggtagct gccaaccatg cagttgtaac agcaatggcc agctgggcag ctgtcatccc 540
 ctgactggag actgcataaa ccaagaaccc aaagatagca gccctgcaga agaattgtat 600
 gattgcgaca gctgtgtgat gacctcctg aacgacctgg ccaccatggg cgagcagctc 660
 cgcttggtca agtctcagct gcagggcctg agtgccagcg cagggttctt ggagcagatg 720
 aggcacatgg agaccaggc caaggacctg aggaatcagt tgctcaacta ccgttctgcc 780
 atttcaaata atggatcaaa aatagaaggc ctggaaagag aactgactga tttgaatcaa 840
 gaatttgaga ctttgcaaga aaaggctcaa gtaaattcca gaaaagcaca aacattaaac 900

aacaatgtta	atcgggcaac	acaaagcgca	aaagaactgg	atgtgaagat	taaaaatgtc	960
atccgggaatg	tgcacattct	tttaaagcag	atctctgga	cagatggaga	gggaaacaac	1020
gtgccttcag	gtgacttttc	cagagagtgg	gctgaagccc	agcgcatgat	gaggggaactg	1080
cggaacagga	actttggaaa	gcacctcaga	gaagcagaag	ctgataaaaag	ggagtcgcag	1140
ctcttgctga	accggataag	gacctggcag	aaaaccacc	agggggagaa	caatgggctt	1200
gctaacagta	tccgggattc	tttaaataaa	tacgaagcca	aactcagtga	ccttcgtgct	1260
cggctgcagg	aggcagctgc	ccaagccaag	caggcaaatg	gcttgaacca	agaaaacgag	1320
agagcttttg	gagccattca	gagacaagtg	aaagaaataa	attccctgca	gagtgatttc	1380
accaagtatc	taaccactgc	agactcatct	ttgttgcaaa	ccaacattgc	gctgcagctg	1440
atggagaaaa	gccagaagga	atatgaaaaa	ttagctgcca	gtttaaatga	agcaagacaa	1500
gaactaagtg	acaaagtaag	agaactttcc	agatctgctg	gcaaaacatc	ccttgtggag	1560
gaggcagaaa	agcacgcgcg	gtccttacaa	gagctggcaa	agcagctgga	agagatcaag	1620
agaaacgcca	gcggggatga	gctggtgcgc	tgtgctgtgg	atgccgccac	cgctacgag	1680
aacatcctca	atgccatcaa	agcggccgag	gacgcagcca	acagggctgc	cagtgcattct	1740
gaatctgccc	tccagacagt	gataaaggaa	gatctgccaa	gaaaagctaa	aaccctgagt	1800
tccaacagtg	ataaactgtt	aaatgaagcc	aagatgacac	aaaagaagct	aaagcaagaa	1860
gtcagtccag	ctctcaacaa	cctacagcaa	accctgaata	ttgtgacagt	tcagaaagaa	1920
gtgatagaca	ccaatctcac	aactctccga	gatggtcttc	atgggataca	gagaggtgat	1980
attgatgcta	tgatcagtag	tgcaaagagc	atggtcagaa	aggccaacga	catcacagat	2040
gaggtctctg	atgggtctaa	ccccatccag	acagatgtgg	aaagaattaa	ggacacctat	2100
gggaggacac	agaacgaaga	cttcaaaaag	gctctgactg	atgcagataa	ctcggtgaat	2160
aagttaacca	acaaactacc	tgatcttttg	cgcaagattg	aaagtatcaa	ccaacagctg	2220
ttgcccttgg	gaaacatctc	tgacaacatg	gacagaatac	gagaactaat	tcagcaggcc	2280
agagatgctg	ccagttaagg	tgctgtcccc	atgaggttca	atggtaaatac	tggagtgcga	2340
gtccgactgc	caaatagacct	ggaagatttg	aaaggatata	catctctgtc	cttgtttctc	2400
caaaggccca	actcaagaga	aaatgggggt	actgagaata	tgtttgtgat	gtaccttga	2460
aataaagatg	cctcccggga	ctacatcggc	atggcagttg	tggatggcca	gtcacctgt	2520
gtctacaacc	tgggggaccg	tgaggctgaa	ctccaagtgg	accagatctt	gaccaagagt	2580
gagactaagg	aggcagttat	ggatcgggtg	aaatttcaga	gaatttatca	gtttgcaagg	2640
cttaattaca	ccaaaggagc	cacatccagt	aaaccagaaa	caccccgagt	ctatgacatg	2700
gatggtagaa	atagcaatac	actccttaat	ttggatcctg	aaaatgttgt	attttatgtt	2760
ggaggttacc	cacctgattt	taaacttccc	agtcgactaa	gtttccctcc	atacaaagg	2820
tgtattgaat	tagatgacct	caatgaaaat	gttctgagct	tgtacaactt	caaaaaaaca	2880
ttcaatctca	acacaactga	agtggagcct	tgtagaagga	ggaagggaaga	gtcagacaaa	2940
aattattttg	aaggtacggg	ctatgctcga	gttccaactc	aaccacatgc	tcccatccca	3000
accctttggc	agacaattca	gaccaccgtg	gatagaggct	tgctgttctt	tgcagaaaac	3060
ggggatcgct	tcatatctct	aaatatagaa	gatggcaagc	tcattggtgag	atacaaacctg	3120
aattcagagc	tacaaaaaga	gagaggagtt	ggagacgcca	taaaacaacg	cagagacctat	3180
tcgattcaga	tcaaaattgg	aaaactccaa	aagcgtatgt	ggataaatgt	ggacgttcaa	3240
aacactataa	ttgatggtga	agtatttgat	ttcagcacat	attatctggg	aggaattcca	3300
attgcaatca	gggaaagatt	taacatttct	acgcctgctt	tccgaggctg	catgaaaaat	3360
ttgaagaaaa	ccagtgggtg	cgttagattg	aatgatactg	tgggagtaac	caaaaagtgc	3420
tcggaagact	ggaagcttgt	gcgatctgcc	tcattctcca	gaggaggaca	attgagtttc	3480
actgattttg	gcttaccacc	tactgaccac	ctccaggcct	cattttggatt	tcagaccttt	3540
caaccagtg	gcataattat	agatcatcag	acatggacaa	ggaacctgca	ggtcactctg	3600
gaagatgggt	acattgaatt	gagcaccagc	gatagcggcg	gccaattttt	taaatctcca	3660
cagacgtata	tggatgggtt	actgcattat	gtatctgtaa	taagcgacaa	ctctggaacta	3720
cggcttctca	tcgatgacca	gcttctgaga	aatagcaaaa	ggotaaaaca	catttcaagt	3780
tcccggcagt	ctctgcgtct	gggcgggagc	aattttgagg	gttgtattag	caatgttttt	3840
gtccagaggt	tatcactgag	tcctgaagtc	ctagatttga	ccagtaactc	tctcaagaga	3900
gatgtgtccc	tgggaggctg	cagtttaaac	aaaccacctt	ttctaattgt	gcttaaagg	3960
tctaccaggt	ttaacaagac	caagactttt	cgtatcaacc	agctgttgca	ggacacacca	4020
gtggcctccc	caaggagcgt	gaagggtgtg	caagatgctt	gctcaccact	tcccaagacc	4080
caggccaatc	atggagccct	ccagtttggg	gacattccca	ccagccactt	gctattcaag	4140
cttcctcagg	agctgctgaa	accaggtgca	cagtttgcgt	tggacatgca	gacaacatcc	4200
tccagaggac	tgggtgtttca	cacgggcact	aagaactcct	ttatggctct	ttatctttca	4260
aaaggacgtc	tgggtctttgc	actggggaca	gatgggaaaa	aattgaggat	caaaaagcaag	4320
gagaaatgca	atgatgggaa	atggcacacg	gtggtgtttg	gccatgatgg	ggaaaagggg	4380
cgcttggttg	tggatggact	gagggcccg	gaggggaagt	tgcttgga	ctccaccatc	4440


```

agcatcagag cgccagtttta cctgggatca cctccatcag ggaaacccaaa gagcctcccc 4500
acaaacagct ttgtgggatg cctgaagaac ttccagctgg attcaaaacc cttgtatacc 4560
ccttcttcaa gcttcggggg gtcttcctgc ttgggtgggc ctttgagaga aggcatttat 4620
ttctctgaag aaggagggtca tgtcgtcttg gctcactctg tattgttggg gccagaatth 4680
aagcttgtht tcagcatccg cccaagaagt ctactggga tcctaataca catcggaagt 4740
cagcccggga agcacttatg tgtttacctg gaggcaggaa aggtcacggc ctctatggac 4800
agtggggcag gtgggacctc aacgtcgggc acaccaaagc agtctctgtg tgatggacag 4860
tggcactcgg tggcagtcac cataaaacaa cacatcctgc acctggaact ggacacagac 4920
agtagctaca cagctggaca gatccccctc ccacctgcca gcaactcaaga gccactacac 4980
cttgagggtg ctccagccaa tttagacgaca ctgaggatcc ctgtgtggaa atcattctth 5040
ggctgtctga ggaatattca tgtcaatcac atccctgtcc ctgtcactga agccttggaa 5100
gtccaggggc ctgtcagttc gaatggttgt cctgaccagt aacccaagcc tatttcacag 5160
caaggaaatt caccttcaaa agcactgatt acccaatgca cctccctccc cagctcgaga 5220
tcattcttca attaggacac aaaccagaca ggtttaatag cgaatctaath tttgaattct 5280
gaccatggat acccatcact ttggcattca gtgctacatg tgtattttat ataaaaatcc 5340
catttcttga agataaaaaa attgtttatt aaattgttat gcacagaatg tttttggtaa 5400
tattaatttc cactaaaaaa ttaaatgtct ttt 5433

```

<210> 113

<211> 1713

<212> PRT

<213> Homo sapiens

<400> 113

```

Met Gly Trp Leu Trp Ile Phe Gly Ala Ala Leu Gly Gln Cys Leu Gly
 1          5          10          15
Tyr Ser Ser Gln Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln
 20          25          30
Ser Gln Leu Gln Ala Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys
 35          40          45
Ser Pro Gly Tyr Tyr Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys
 50          55          60
Val Pro Cys Asn Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser
 65          70          75          80
Gly Ile Cys Val Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu
 85          90          95
Arg Cys Gln Glu Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg
100          105          110
Ala Cys Pro Cys Pro His Thr Asn Ser Phe Ala Thr Gly Cys Val Val
115          120          125
Asn Gly Gly Asp Val Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr
130          135          140
Gln Cys Glu Arg Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe
145          150          155          160
Gly Gly Ser Cys Gln Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly
165          170          175
Ser Cys His Pro Leu Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp
180          185          190
Ser Ser Pro Ala Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr
195          200          205
Leu Leu Asn Asp Leu Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys
210          215          220
Ser Gln Leu Gln Gly Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met
225          230          235          240
Arg His Met Glu Thr Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn
245          250          255
Tyr Arg Ser Ala Ile Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu
260          265          270
Arg Glu Leu Thr Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys

```

275	280	285
Ala Gln Val Asn Ser Arg Lys	Ala Gln Thr Leu Asn	Asn Asn Val Asn
290	295	300
Arg Ala Thr Gln Ser Ala Lys	Glu Leu Asp Val Lys	Ile Lys Asn Val
305	310	315
Ile Arg Asn Val His Ile Leu	Leu Lys Gln Ile Ser	Gly Thr Asp Gly
325	330	335
Glu Gly Asn Asn Val Pro Ser	Gly Asp Phe Ser Arg	Glu Trp Ala Glu
340	345	350
Ala Gln Arg Met Met Arg Glu	Leu Arg Asn Arg Asn	Phe Gly Lys His
355	360	365
Leu Arg Glu Ala Glu Ala Asp	Lys Arg Glu Ser Gln	Leu Leu Leu Asn
370	375	380
Arg Ile Arg Thr Trp Gln Lys	Thr His Gln Gly Glu	Asn Asn Gly Leu
385	390	395
Ala Asn Ser Ile Arg Asp Ser	Leu Asn Glu Tyr Glu	Ala Lys Leu Ser
405	410	415
Asp Leu Arg Ala Arg Leu Gln	Glu Ala Ala Gln Ala	Lys Gln Ala
420	425	430
Asn Gly Leu Asn Gln Glu Asn	Glu Arg Ala Leu Gly	Ala Ile Gln Arg
435	440	445
Gln Val Lys Glu Ile Asn Ser	Leu Gln Ser Asp Phe	Thr Lys Tyr Leu
450	455	460
Thr Thr Ala Asp Ser Ser Leu	Leu Gln Thr Asn Ile	Ala Leu Gln Leu
465	470	475
Met Glu Lys Ser Gln Lys Glu	Tyr Glu Lys Leu Ala	Ala Ser Leu Asn
485	490	495
Glu Ala Arg Gln Glu Leu Ser	Asp Lys Val Arg Glu	Leu Ser Arg Ser
500	505	510
Ala Gly Lys Thr Ser Leu Val	Glu Glu Ala Glu Lys	His Ala Arg Ser
515	520	525
Leu Gln Glu Leu Ala Lys Gln	Leu Glu Glu Ile Lys	Arg Asn Ala Ser
530	535	540
Gly Asp Glu Leu Val Arg Cys	Ala Val Asp Ala Ala	Thr Ala Tyr Glu
545	550	555
Asn Ile Leu Asn Ala Ile Lys	Ala Ala Glu Asp Ala	Ala Asn Arg Ala
565	570	575
Ala Ser Ala Ser Glu Ser Ala	Leu Gln Thr Val Ile	Lys Glu Asp Leu
580	585	590
Pro Arg Lys Ala Lys Thr Leu	Ser Ser Asn Ser Asp	Lys Leu Leu Asn
595	600	605
Glu Ala Lys Met Thr Gln Lys	Lys Leu Lys Gln Glu	Val Ser Pro Ala
610	615	620
Leu Asn Asn Leu Gln Gln Thr	Leu Asn Ile Val Thr	Val Gln Lys Glu
625	630	635
Val Ile Asp Thr Asn Leu Thr	Thr Leu Arg Asp Gly	Leu His Gly Ile
645	650	655
Gln Arg Gly Asp Ile Asp Ala	Met Ile Ser Ser Ala	Lys Ser Met Val
660	665	670
Arg Lys Ala Asn Asp Ile Thr	Asp Glu Val Leu Asp	Gly Leu Asn Pro
675	680	685
Ile Gln Thr Asp Val Glu Arg	Ile Lys Asp Thr Tyr	Gly Arg Thr Gln
690	695	700
Asn Glu Asp Phe Lys Lys Ala	Leu Thr Asp Ala Asp	Asn Ser Val Asn
705	710	715
Lys Leu Thr Asn Lys Leu Pro	Asp Leu Trp Arg Lys	Ile Glu Ser Ile
725	730	735
Asn Gln Gln Leu Leu Pro Leu	Gly Asn Ile Ser Asp	Asn Met Asp Arg
740	745	750

Ile	Arg	Glu	Leu	Ile	Gln	Gln	Ala	Arg	Asp	Ala	Ala	Ser	Lys	Val	Ala		
		755					760					765					
Val	Pro	Met	Arg	Phe	Asn	Gly	Lys	Ser	Gly	Val	Glu	Val	Arg	Leu	Pro		
		770				775					780						
Asn	Asp	Leu	Glu	Asp	Leu	Lys	Gly	Tyr	Thr	Ser	Leu	Ser	Leu	Phe	Leu		
785					790					795					800		
Gln	Arg	Pro	Asn	Ser	Arg	Glu	Asn	Gly	Gly	Thr	Glu	Asn	Met	Phe	Val		
				805					810					815			
Met	Tyr	Leu	Gly	Asn	Lys	Asp	Ala	Ser	Arg	Asp	Tyr	Ile	Gly	Met	Ala		
			820					825					830				
Val	Val	Asp	Gly	Gln	Leu	Thr	Cys	Val	Tyr	Asn	Leu	Gly	Asp	Arg	Glu		
		835					840					845					
Ala	Glu	Leu	Gln	Val	Asp	Gln	Ile	Leu	Thr	Lys	Ser	Glu	Thr	Lys	Glu		
		850				855					860						
Ala	Val	Met	Asp	Arg	Val	Lys	Phe	Gln	Arg	Ile	Tyr	Gln	Phe	Ala	Arg		
865					870					875					880		
Leu	Asn	Tyr	Thr	Lys	Gly	Ala	Thr	Ser	Ser	Lys	Pro	Glu	Thr	Pro	Gly		
				885					890					895			
Val	Tyr	Asp	Met	Asp	Gly	Arg	Asn	Ser	Asn	Thr	Leu	Leu	Asn	Leu	Asp		
			900					905					910				
Pro	Glu	Asn	Val	Val	Phe	Tyr	Val	Gly	Gly	Tyr	Pro	Pro	Asp	Phe	Lys		
		915					920					925					
Leu	Pro	Ser	Arg	Leu	Ser	Phe	Pro	Pro	Tyr	Lys	Gly	Cys	Ile	Glu	Leu		
		930				935					940						
Asp	Asp	Leu	Asn	Glu	Asn	Val	Leu	Ser	Leu	Tyr	Asn	Phe	Lys	Lys	Thr		
945					950					955					960		
Phe	Asn	Leu	Asn	Thr	Glu	Val	Glu	Pro	Cys	Arg	Arg	Arg	Lys	Glu			
				965				970					975				
Glu	Ser	Asp	Lys	Asn	Tyr	Phe	Glu	Gly	Thr	Gly	Tyr	Ala	Arg	Val	Pro		
			980					985					990				
Thr	Gln	Pro	His	Ala	Pro	Ile	Pro	Thr	Phe	Gly	Gln	Thr	Ile	Gln	Thr		
		995				1000						1005					
Thr	Val	Asp	Arg	Gly	Leu	Leu	Phe	Phe	Ala	Glu	Asn	Gly	Asp	Arg	Phe		
		1010				1015					1020						
Ile	Ser	Leu	Asn	Ile	Glu	Asp	Gly	Lys	Leu	Met	Val	Arg	Tyr	Lys	Leu		
1025					1030					1035					1040		
Asn	Ser	Glu	Leu	Pro	Lys	Glu	Arg	Gly	Val	Gly	Asp	Ala	Ile	Asn	Asn		
				1045					1050					1055			
Gly	Arg	Asp	His	Ser	Ile	Gln	Ile	Lys	Ile	Gly	Lys	Leu	Gln	Lys	Arg		
			1060					1065					1070				
Met	Trp	Ile	Asn	Val	Asp	Val	Gln	Asn	Thr	Ile	Ile	Asp	Gly	Glu	Val		
		1075					1080					1085					
Phe	Asp	Phe	Ser	Thr	Tyr	Tyr	Leu	Gly	Gly	Ile	Pro	Ile	Ala	Ile	Arg		
	1090				1095						1100						
Glu	Arg	Phe	Asn	Ile	Ser	Thr	Pro	Ala	Phe	Arg	Gly	Cys	Met	Lys	Asn		
1105					1110					1115					1120		
Leu	Lys	Lys	Thr	Ser	Gly	Val	Val	Arg	Leu	Asn	Asp	Thr	Val	Gly	Val		
				1125					1130					1135			
Thr	Lys	Lys	Cys	Ser	Glu	Asp	Trp	Lys	Leu	Val	Arg	Ser	Ala	Ser	Phe		
			1140					1145					1150				
Ser	Arg	Gly	Gly	Gln	Leu	Ser	Phe	Thr	Asp	Leu	Gly	Leu	Pro	Pro	Thr		
		1155					1160					1165					
Asp	His	Leu	Gln	Ala	Ser	Phe	Gly	Phe	Gln	Thr	Phe	Gln	Pro	Ser	Gly		
	1170					1175					1180						
Ile	Leu	Leu	Asp	His	Gln	Thr	Trp	Thr	Arg	Asn	Leu	Gln	Val	Thr	Leu		
1185					1190					1195					1200		
Glu	Asp	Gly	Tyr	Ile	Glu	Leu	Ser	Thr	Ser	Asp	Ser	Gly	Gly	Pro	Ile		
				1205					1210					1215			
Phe	Lys	Ser	Pro	Gln	Thr	Tyr	Met	Asp	Gly	Leu	Leu	His	Tyr	Val	Ser		

Val	Ile	Ser	Asp	Asn	Ser	Gly	Leu	Arg	Leu	Leu	Ile	Asp	Asp	Gln	Leu	1220	1225	1230
			1235						1240									1245
Leu	Arg	Asn	Ser	Lys	Arg	Leu	Lys	His	Ile	Ser	Ser	Ser	Arg	Gln	Ser			
		1250					1255					1260						
Leu	Arg	Leu	Gly	Gly	Ser	Asn	Phe	Glu	Gly	Cys	Ile	Ser	Asn	Val	Phe	1265	1270	1275
Val	Gln	Arg	Leu	Ser	Leu	Ser	Pro	Glu	Val	Leu	Asp	Leu	Thr	Ser	Asn			1280
			1285						1290									1295
Ser	Leu	Lys	Arg	Asp	Val	Ser	Leu	Gly	Gly	Cys	Ser	Leu	Asn	Lys	Pro			
		1300							1305				1310					
Pro	Phe	Leu	Met	Leu	Leu	Lys	Gly	Ser	Thr	Arg	Phe	Asn	Lys	Thr	Lys	1315	1320	1325
Thr	Phe	Arg	Ile	Asn	Gln	Leu	Leu	Gln	Asp	Thr	Pro	Val	Ala	Ser	Pro	1330	1335	1340
Arg	Ser	Val	Lys	Val	Trp	Gln	Asp	Ala	Cys	Ser	Pro	Leu	Pro	Lys	Thr	1345	1350	1355
Gln	Ala	Asn	His	Gly	Ala	Leu	Gln	Phe	Gly	Asp	Ile	Pro	Thr	Ser	His		1365	1370
																		1375
Leu	Leu	Phe	Lys	Leu	Pro	Gln	Glu	Leu	Leu	Lys	Pro	Arg	Ser	Gln	Phe	1380	1385	1390
Ala	Val	Asp	Met	Gln	Thr	Thr	Ser	Ser	Arg	Gly	Leu	Val	Phe	His	Thr	1395	1400	1405
Gly	Thr	Lys	Asn	Ser	Phe	Met	Ala	Leu	Tyr	Leu	Ser	Lys	Gly	Arg	Leu	1410	1415	1420
Val	Phe	Ala	Leu	Gly	Thr	Asp	Gly	Lys	Lys	Leu	Arg	Ile	Lys	Ser	Lys	1425	1430	1435
Glu	Lys	Cys	Asn	Asp	Gly	Lys	Trp	His	Thr	Val	Val	Phe	Gly	His	Asp		1445	1450
																		1455
Gly	Glu	Lys	Gly	Arg	Leu	Val	Val	Asp	Gly	Leu	Arg	Ala	Arg	Glu	Gly	1460	1465	1470
Ser	Leu	Pro	Gly	Asn	Ser	Thr	Ile	Ser	Ile	Arg	Ala	Pro	Val	Tyr	Leu	1475	1480	1485
Gly	Ser	Pro	Pro	Ser	Gly	Lys	Pro	Lys	Ser	Leu	Pro	Thr	Asn	Ser	Phe	1490	1495	1500
Val	Gly	Cys	Leu	Lys	Asn	Phe	Gln	Leu	Asp	Ser	Lys	Pro	Leu	Tyr	Thr	1505	1510	1515
Pro	Ser	Ser	Ser	Phe	Gly	Val	Ser	Ser	Cys	Leu	Gly	Gly	Pro	Leu	Glu		1525	1530
																		1535
Lys	Gly	Ile	Tyr	Phe	Ser	Glu	Glu	Gly	Gly	His	Val	Val	Leu	Ala	His	1540	1545	1550
Ser	Val	Leu	Leu	Gly	Pro	Glu	Phe	Lys	Leu	Val	Phe	Ser	Ile	Arg	Pro	1555	1560	1565
Arg	Ser	Leu	Thr	Gly	Ile	Leu	Ile	His	Ile	Gly	Ser	Gln	Pro	Gly	Lys	1570	1575	1580
His	Leu	Cys	Val	Tyr	Leu	Glu	Ala	Gly	Lys	Val	Thr	Ala	Ser	Met	Asp	1585	1590	1595
Ser	Gly	Ala	Gly	Gly	Thr	Ser	Thr	Ser	Val	Thr	Pro	Lys	Gln	Ser	Leu		1605	1610
																		1615
Cys	Asp	Gly	Gln	Trp	His	Ser	Val	Ala	Val	Thr	Ile	Lys	Gln	His	Ile	1620	1625	1630
Leu	His	Leu	Glu	Leu	Asp	Thr	Asp	Ser	Ser	Tyr	Thr	Ala	Gly	Gln	Ile	1635	1640	1645
Pro	Phe	Pro	Pro	Ala	Ser	Thr	Gln	Glu	Pro	Leu	His	Leu	Gly	Gly	Ala	1650	1655	1660
Pro	Ala	Asn	Leu	Thr	Thr	Leu	Arg	Ile	Pro	Val	Trp	Lys	Ser	Phe	Phe	1665	1670	1675
Gly	Cys	Leu	Arg	Asn	Ile	His	Val	Asn	His	Ile	Pro	Val	Pro	Val	Thr		1685	1690
																		1695

Glu Ala Leu Glu Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp
 1700 1705 1710
 Gln

<210> 114
 <211> 5175
 <212> DNA
 <213> Homo sapiens

<400> 114
 acagcggagc gcagagttag aaccaccaac cgaggcgccg ggcagcgacc cctgcagcgg 60
 agacagagac tgagcggccc ggcaccgccca tgcctgcgct ctggctgggc tgcctgcctct 120
 gcttctcgct cctcctgccc gcagcccggg ccacctccag gaggggaagtc tgtgattgca 180
 atgggaagtc caggcagtgat atctttgatc gggaaacttca cagacaaaact ggtaattgat 240
 tccgctgcct caactgcaat gacaacactg atggcattca ctgcgagaag tgcaagaatg 300
 gcttttaccg gcacagagaa agggaccgct gtttgccctg caattgtaac tccaaagggt 360
 ctcttagtgc tcgatgtgac aactctggag ggtgcagctg taaaccagggt gtgacaggag 420
 ccgatgcga ccgatgtctg ccaggcttcc acatgctcac ggatgcgggg tgcacccaag 480
 accagagact gctagactcc aagtgtgact gtgaccagc tggcatcgca gggccctgtg 540
 acgcgggccg ctgtgtctgc aagccagctg ttactggaga acgctgtgat aggtgtcgat 600
 caggttacta taatctggat ggggggaacc ctgagggctg taccagtgat ttctgctatg 660
 ggcattcagc cagctgcgc agctctgcag aatacagtgat ccataagatc acctctacct 720
 ttcattcaaga tgttgatggc tgggaaggctg tccaacgaaa tgggtctcct gcaaagctcc 780
 aatggtcaca gcgccatcaa gatgtgttta gctcagccca acgactagac cctgtctatt 840
 ttgtggctcc tgccaaatct cttgggaatc aacaggtgag ctatgggcaa agcctgtcct 900
 ttgactaccg tgtggacaga ggaggcagac acccatctgc ccatgatgtg attctggaag 960
 gtgctggctc acggatcaca gctcccttga tggcacttgg caagacactg ccttgtgggc 1020
 tcaccaagac ttacacattc aggttaaatg agcatccaag caataattgg agccccagc 1080
 tgagttactt tgagtatcga aggttactgc ggaatctcac agccctccgc atccgagcta 1140
 catatggaga atacagtact ggggtacattg acaatgtgac cctgatttca gccgcacctg 1200
 tctctggagc ccagcagccc tgggttgaac agtgtatatg tcctgttggg tacaaggggc 1260
 aattctgcca ggattgtgct tctggctaca agagagattc agcgagactg gggccttttg 1320
 gcacctgtat tccttghtaac tgtcaagggg gaggggcctg tgatccagac acaggagatt 1380
 gttattcagg ggatgagaat cctgacattg agtgtgctga ctgcccattt ggtttctaca 1440
 acgatccgca cgacccccgc agctgcaagc catgtcccctg tcataacggg ttcagctgct 1500
 cagtgatgcc ggagacggag gaggtgggtg gcaataactg ccctcccggg gtcaccgggtg 1560
 cccgctgtga gctctgtgct gatggctact ttggggaccc ctttgggtgaa catggcccag 1620
 tgaggccttg tcagccctgt caatgcaaca acaatgtgga cccagtgcc tctgggaatt 1680
 gtgaccggct gacaggcagg tgtttgaagt gtatccacaa cacagccggc atctactgcy 1740
 accagtgcaa agcaggctac ttcggggacc cattggctcc caaccagca gacaagtgtc 1800
 gagcttgcaa ctgtaacccc atgggctcag agcctgtagg atgtcgaagt gatggcacct 1860
 gtgtttgcaa gccaggatctt ggtggcccca actgtgagca tggagcattc agctgtccag 1920
 cttgctataa tcaagtgaag attcagatgg atcagtttat gcagcagctt cagagaatgg 1980
 - aggcctgat ttcaaaggct cagggtggtg atggagtagt acctgatata gagctggaag 2040
 gcaggatgca gcaggctgag caggcccttc aggcattct gagagatgcc cagatttcag 2100
 aagggtgctag cagatccctt ggtctccagt tggccaagggt gaggagccaa gagaacagct 2160
 accagagccg cctggatgac ctcaagatga ctgtggaag agttcgggct ctgggaagtc 2220
 agtaccagaa ccgagttcgg gatactcaca ggctcatcac tcagatgcag ctgagcctgg 2280
 cagaaagtga agcttccctg ggaaacacta acattccctg ctacagaccac tacgtggggc 2340
 caaatggctt taaaagtctg gctcaggagg ccacaagatt agcagaaaagc cacgttgagt 2400
 cagccagtaa catggagcaa ctgacaagggt aaactgagga ctattccaaa caagccctct 2460
 cactggtgcy caaggccctg catgaaggag tcggaagcgg aagcggtagc ccggacgggtg 2520
 ctgtggtgca agggcttgtg gaaaaattgg agaaaaccaa gtccctggcc cagcagttga 2580
 caagggagcc cactcaagcg gaaattgaag cagataggct ttatcagcac agtctccgcc 2640
 tcctggattc agtgtctcgg cttcaggggag tcagtgatca gtccctttcag gtggaagaag 2700
 caaagaggat caaacaacaaa gcggattcac tctcaacgct ggtaaccagg catatggatg 2760
 agttcaagcg tacacaaaag aatctgggaa actggaaaga agaagcacag cagctcttac 2820

```

agaatggaaa aagtgggaga gagaaatcag atcagctgct ttcccgtgcc aatcttgcta 2880
aaagcagagc acaagaagca ctgagtatgg gcaatgccac tttttatgaa gttgagagca 2940
tccttaaaaa cctcagagag tttgacctgc aggtggacaa cagaaaagca gaagctgaag 3000
aagccatgaa gagactctcc tacatcagcc agaaggtttc agatgccagt gacaagaccc 3060
agcaagcaga aagagccctg gggagcgtg ctgctgatgc acagagggca aagaatgggg 3120
ccggggaggc cctggaaatc tccagtgaga ttgaacagga gattgggagt ctgaacttgg 3180
aagccaatgt gacagcagat ggagccttgg ccatggaaaa gggactggcc tctctgaaga 3240
gtgagatgag ggaagtggaa ggagagctgg aaaggaagga gctggagttt gacacgaata 3300
tggatgcagt acagatggtg attacagaag cccagaaggt tgataccaga gccaagaacg 3360
ctggggttac aatccaagac aactcaaca cattagacgg cctcctgcat ctgatggacc 3420
agcctctcag tgtagatgaa gaggggctg tcttactgga gcagaagctt tcccagacca 3480
agaccagat caacagccaa ctgcggccca tgatgtcaga gctggaagag agggcacgtc 3540
agcagagggg ccacctccat ttgctggaga caagcataga tgggattctg gctgatgtga 3600
agaacttgga gaacattagg gacaacctgc cccaggctg ctacaatacc caggctcttg 3660
agcaacagtg aagctgccat aaatatctt caactgaggt tcttgggata cagatctcag 3720
ggctcgggag ccatgtcatg tgagtgggtg ggatggggac atttgaacat gtttaatggg 3780
tatgctcagg tcaactgacc tgacccatt cctgatccca tggccagggt gttgtcttat 3840
tgcaccatac tcttgcttc ctgatgctg gcaatgaggc agatagcact ggggtgtgaga 3900
atgatcaagg atctggagcc caaagaatg actgtagga aagacaaact gcacaggcag 3960
atgtttgcct cataatagtc gtaagtggag tcttggatt tggacaagtg ctgttgggtg 4020
atagtcaact tattctttga gtaatgtgac taaagaaaa aactttgact ttgccaggc 4080
atgaaattct tctaattgtc agaacagagt gcaaccagt cacactgtgg ccagtaaaat 4140
actattgcct catattgtcc tctgcaagct tcttgctgat cagagttcct cctacttaca 4200
accagggtg tgaacatgtt ctccattttc aagctggaag aagtgagcag tgttggagtg 4260
aggacctgta aggcaggccc attcagagct atggtgcttg ctggtgcctg ccaccttcaa 4320
gttctggacc tgggcatgac atcctttctt ttaatgatgc catggcaact tagagattgc 4380
atttttatta aagcatttcc taccagcaaa gcaaatgttg ggaaagtatt tactttttcg 4440
gtttcaaagt gatagaaaag tgtggcttgg gcattgaaag aggtaaaatt ctctagattt 4500
attagtctta attcaatcct acttttcgaa caccaaaaat gatgcgcata aatgtatttt 4560
atcttatttt ctcaatctcc tctctcttcc ctccaccat aataagagaa tgttctact 4620
cacacttcag ctgggtcaca tccatccctc cattcatcct tccatccatc tttccatcca 4680
ttacctccat ccactcctcc aacatatatt tattgagtac ctactgtgtg ccaggggctg 4740
gtgggacagt ggtgacatag tctctgccct catagagttg attgtctagt gaggaagaca 4800
agcattttta aaaaataaat ttaaacttac aaactttgtt tgtcacaagt ggtgtttatt 4860
gcaataaccg cttggtttgc aacctctttg ctcaacagaa catatgttgc aagaccctcc 4920
catgggggca cttgagtttt ggcaaggctg acagagctct gggttgtgca catttctttg 4980
cattccagct gtcactctgt gcctttctac aactgattgc aacagactgt tgagttatga 5040
taacaccagt gggaattgct ggaggaacca gaggcacttc caccttggct gggaagacta 5100
tggtgctgcc ttgcttctgt atttccttgg attttcttga aagtgttttt aaataaagaa 5160
caattgttag atgcc 5175

```

<210> 115

<211> 1193

<212> PRT

<213> Homo sapiens

<400> 115

```

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
 1           5           10           15
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
 20           25           30
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
 35           40           45
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
 50           55           60
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
 65           70           75           80
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
 85           90           95

```

Asp	Asn	Ser	Gly	Arg	Cys	Ser	Cys	Lys	Pro	Gly	Val	Thr	Gly	Ala	Arg	100	105	110
Cys	Asp	Arg	Cys	Leu	Pro	Gly	Phe	His	Met	Leu	Thr	Asp	Ala	Gly	Cys	115	120	125
Thr	Gln	Asp	Gln	Arg	Leu	Leu	Asp	Ser	Lys	Cys	Asp	Cys	Asp	Pro	Ala	130	135	140
Gly	Ile	Ala	Gly	Pro	Cys	Asp	Ala	Gly	Arg	Cys	Val	Cys	Lys	Pro	Ala	145	150	155
Val	Thr	Gly	Glu	Arg	Cys	Asp	Arg	Cys	Arg	Ser	Gly	Tyr	Tyr	Asn	Leu	165	170	175
Asp	Gly	Gly	Asn	Pro	Glu	Gly	Cys	Thr	Gln	Cys	Phe	Cys	Tyr	Gly	His	180	185	190
Ser	Ala	Ser	Cys	Arg	Ser	Ser	Ala	Glu	Tyr	Ser	Val	His	Lys	Ile	Thr	195	200	205
Ser	Thr	Phe	His	Gln	Asp	Val	Asp	Gly	Trp	Lys	Ala	Val	Gln	Arg	Asn	210	215	220
Gly	Ser	Pro	Ala	Lys	Leu	Gln	Trp	Ser	Gln	Arg	His	Gln	Asp	Val	Phe	225	230	235
Ser	Ser	Ala	Gln	Arg	Leu	Asp	Pro	Val	Tyr	Phe	Val	Ala	Pro	Ala	Lys	245	250	255
Phe	Leu	Gly	Asn	Gln	Gln	Val	Ser	Tyr	Gly	Gln	Ser	Leu	Ser	Phe	Asp	260	265	270
Tyr	Arg	Val	Asp	Arg	Gly	Gly	Arg	His	Pro	Ser	Ala	His	Asp	Val	Ile	275	280	285
Leu	Glu	Gly	Ala	Gly	Leu	Arg	Ile	Thr	Ala	Pro	Leu	Met	Pro	Leu	Gly	290	295	300
Lys	Thr	Leu	Pro	Cys	Gly	Leu	Thr	Lys	Thr	Tyr	Thr	Phe	Arg	Leu	Asn	305	310	315
Glu	His	Pro	Ser	Asn	Asn	Trp	Ser	Pro	Gln	Leu	Ser	Tyr	Phe	Glu	Tyr	325	330	335
Arg	Arg	Leu	Leu	Arg	Asn	Leu	Thr	Ala	Leu	Arg	Ile	Arg	Ala	Thr	Tyr	340	345	350
Gly	Glu	Tyr	Ser	Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Ile	Ser	Ala	355	360	365
Arg	Pro	Val	Ser	Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Gln	Cys	Ile	Cys	370	375	380
Pro	Val	Gly	Tyr	Lys	Gly	Gln	Phe	Cys	Gln	Asp	Cys	Ala	Ser	Gly	Tyr	385	390	395
Lys	Arg	Asp	Ser	Ala	Arg	Leu	Gly	Pro	Phe	Gly	Thr	Cys	Ile	Pro	Cys	405	410	415
Asn	Cys	Gln	Gly	Gly	Gly	Ala	Cys	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Tyr	420	425	430
Ser	Gly	Asp	Glu	Asn	Pro	Asp	Ile	Glu	Cys	Ala	Asp	Cys	Pro	Ile	Gly	435	440	445
Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys	450	455	460
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Met	Pro	Glu	Thr	Glu	Glu	Val	Val	465	470	475
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys	485	490	495
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg	500	505	510
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Asn	Asn	Val	Asp	Pro	Ser	Ala	Ser	515	520	525
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn	530	535	540
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp	545	550	555
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn	560		

				565					570					575			
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys	Val		
			580					585					590				
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe	Ser		
		595					600					605					
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe	Met		
	610					615					620						
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly	Gly		
625					630					635					640		
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Glu	Gly	Arg	Met	Gln	Gln	Ala		
				645					650						655		
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu	Gly		
			660					665					670				
Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu		
		675					680					685					
Asn	Ser	Tyr	Gln	Ser	Arg	Leu	Asp	Asp	Leu	Lys	Met	Thr	Val	Glu	Arg		
	690					695					700						
Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Arg	Val	Arg	Asp	Thr	His		
705					710					715					720		
Arg	Leu	Ile	Thr	Gln	Met	Gln	Leu	Ser	Leu	Ala	Glu	Ser	Glu	Ala	Ser		
				725					730						735		
Leu	Gly	Asn	Thr	Asn	Ile	Pro	Ala	Ser	Asp	His	Tyr	Val	Gly	Pro	Asn		
			740					745					750				
Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Leu	Ala	Glu	Ser	His		
		755					760						765				
Val	Glu	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Thr	Arg	Glu	Thr	Glu	Asp		
	770					775					780						
Tyr	Ser	Lys	Gln	Ala	Leu	Ser	Leu	Val	Arg	Lys	Ala	Leu	His	Glu	Gly		
785					790					795					800		
Val	Gly	Ser	Gly	Ser	Gly	Ser	Pro	Asp	Gly	Ala	Val	Val	Gln	Gly	Leu		
			805						810					815			
Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg		
			820					825						830			
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser		
		835					840						845				
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Arg	Leu	Gln	Gly	Val	Ser	Asp	Gln		
	850					855					860						
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser		
865					870					875					880		
Leu	Ser	Thr	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln		
				885					890					895			
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn		
		900						905					910				
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn		
		915					920						925				
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr		
	930					935					940						
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu		
945					950					955					960		
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu		
				965					970					975			
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln		
			980					985					990				
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys		
		995					1000						1005				
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu		
	1010					1015					1020						
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu		
1025					1030					1035					1040		

Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val
1045 1050 1055
Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp
1060 1065 1070
Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala
1075 1080 1085
Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly
1090 1095 1100
Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu
1105 1110 1115 1120
Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser
1125 1130 1135
Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln
1140 1145 1150
Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala
1155 1160 1165
Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys
1170 1175 1180
Tyr Asn Thr Gln Ala Leu Glu Gln Gln
1185 1190

<210> 116
<211> 749
<212> DNA
<213> Homo sapiens

<400> 116
atggcggcta acgctactac caaccggtcg cagctgctgc cgtagagact tgtggacaaa 60
tgtataggat caagaattca catcgtgatg aagagtgata aggaaattgt tggtagctctt 120
ctaggatttg atgactttgt caatatggta ctggaagatg tcaactgagtt tgaaatcaca 180
ccagaaggaa gaaggattac taaattagat cagattttgc taaatggaaa taatataaca 240
atgctgggttc ctggaggaga aggacctgaa gtgtgaatga gtttccttga cttacactag 300
attttgtttt ggcttataat gacaagaaaa tgggaattttt tttccactt tctaattgtt 360
aaatcccata aagctaagtt tcccgttaaa gggaagtgtt ttgaagatgt gtacccattt 420
ttgtaagtta atcatgatta tcctggaaaa agaagaaaag aacttcttct tttgcagatg 480
aaaataaagg tgttttttgt taactgtcat tttgtttatt ctactgcagt agccagtgga 540
acaaagtttg tagttatttt gccacttact tttctgtcat tatatgctta tttgttttgt 600
catttacgtg accatttgat tctcaacaaa aagttgttcc aaacaaaatg atgaactttg 660
atgtgaacag gtgcatttaa acaaccggaa atgatcactt agaaaattca attaaaatgc 720
tgttgttttg taaaaaaaaa aaaaaaaaaa 749

<210> 117
<211> 91
<212> PRT
<213> Homo sapiens

<400> 117
Met Ala Ala Asn Ala Thr Thr Asn Pro Ser Gln Leu Leu Pro Leu Glu
1 5 10 15
Leu Val Asp Lys Cys Ile Gly Ser Arg Ile His Ile Val Met Lys Ser
20 25 30
Asp Lys Glu Ile Val Gly Thr Leu Gly Phe Asp Asp Phe Val Asn
35 40 45
Met Val Leu Glu Asp Val Thr Glu Phe Glu Ile Thr Pro Glu Gly Arg
50 55 60
Arg Ile Thr Lys Leu Asp Gln Ile Leu Leu Asn Gly Asn Asn Ile Thr
65 70 75 80
Met Leu Val Pro Gly Gly Glu Gly Pro Glu Val

85

90

<210> 118
 <211> 1717
 <212> DNA
 <213> Homo sapiens

<400> 118
 gtggattcctt gtccatagtg catctgcttt aagaattaac gaaagcagtg tcaagacagt 60
 aaggattcaa accatttgcc aaaaatgagt ctaagtgcac ttactctctt cctggcattg 120
 attggtggtg ccagtggtgcca gtactatgat tatgatcttc ccctatcaat ttatgggcaa 180
 tcatcaccaa actgtgcacc agaatgtaac tgccctgaaa gctacccaag tgccatgtac 240
 tgtgatgagc tgaaattgaa aagtgtacca atgggtgcctc ctggaatcaa gtatctttac 300
 cttaggaata accagattga ccatattgat gaaaaggcct ttgagaatgt aactgatctg 360
 cagtggctca ttctagatca caaccttcta gaaaactcca agataaaaagg gagagttttc 420
 tctaaattga aacaactgaa gaagctgcat ataaaccaca acaacctgac agagtctgtg 480
 ggcccacttc ccaaatctct ggaggatctg cagcttactc ataacaagat cacaagctg 540
 ggctcttttg aaggattggt aaacctgacc ttcatccatc tccagcacia tcggctgaaa 600
 gaggatgctg tttcagctgc ttttaaagggt cttaaatcac tccaatacct tgacttgagc 660
 ttcaatcaga tagccagact gccttctggt ctccctgtct ctcttctaac tctctactta 720
 gacaacaata agatcagcaa catccctgat gagtatttca agcgttttaa tgcattgcag 780
 tatctgcgtt tatctcacia cgaactggct gatagtggaa tacctggaaa ttctttcaat 840
 gtgtcatccc tggttgagct ggatctgtcc tataacaagc ttaaaaacat accaactgtc 900
 aatgaaaacc ttgaaaacta ttacctggag gtcaatcaac ttgagaagtt tgacataaag 960
 agcttctgca agatcctggg gccattatcc tactccaaga tcaagcattt gcgtttggat 1020
 ggcaatcgca tctcagaaac cagtcttcca ccggaatgt atgaatgtct acgtgttgct 1080
 aacgaagtca ctcttaatta atatctgtat cctggaacaa tattttatgg ttatgttttt 1140
 ctgtgtgtca gttttcatag tatccatatt ttattactgt ttattacttc catgaatttt 1200
 aaaatctgag ggaaatgttt tgtaaacatt tatttttttt aaagaaaaga tgaaaggcag 1260
 gcctatttca tcacaagaac acacacatat acacgaatag acatcaaact caatgcttta 1320
 tttgtaaatt tagtggtttt ttatttctac tgtcaaatga tgtgcaaaac cttttactgg 1380
 ttgcatggaa atcagccaag ttttataatc cttaaatctt aatgttcctc aaagcttgga 1440
 ttaaatacat atggatgtta ctctcttgca ccaaattatc ttgatacatt caaatttgct 1500
 tggtaaaaaa ataggtggta gatattgagg ccaagaatat tgcaaaatac atgaagcttc 1560
 atgcacttaa agaagtattt ttagaataag aatttgcata cttacctagt gaaacttttc 1620
 tagaattatt tttcactcta agtcatgtat gtttctcttt gattatattg atgttatgtt 1680
 taataagcta ctagcaaaat aaaacatagc aaatggc 1717

<210> 119
 <211> 338
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
 1 5 10 15
 Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
 20 25 30
 Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
 35 40 45
 Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val
 50 55 60
 Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His
 65 70 75 80
 Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile
 85 90 95
 Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe
 100 105 110

Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu
 115 120 125
 Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu
 130 135 140
 Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn
 145 150 155 160
 Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val
 165 170 175
 Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
 180 185 190
 Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu
 195 200 205
 Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr
 210 215 220
 Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu
 225 230 235 240
 Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu
 245 250 255
 Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val
 260 265 270
 Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys
 275 280 285
 Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser
 290 295 300
 Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser
 305 310 315 320
 Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr
 325 330 335
 Leu Asn

<210> 120
 <211> 1334
 <212> DNA
 <213> Homo sapiens

<400> 120
 gcagaccccc atcatgggca gccagagctc caaggctccc cggggcgacg tgaccgccga 60
 ggaggcagca ggcgttccc ccgcgaaggc caacggccag gagaatggcc acgtgaaaag 120
 caatggagac ttatccccca aggggtgaagg ggagtcgccc cctgtgaacg gaacagatga 180
 ggcagccggg gccactggcg atgccatcga gccagcacc cctagccagg gtgctgaggc 240
 caagggggag gtccccccca aggagacccc caagaagaag aagaaattct ctttcaagaa 300
 gcctttcaaa ttgagcggcc tgtccttcaa gagaaatcgg aaggagggtg ggggtgattc 360
 ttctgcctcc tcaccacacag aggaagagca ggagcagggg gagatcgggt cctgcagcga 420
 cgagggcact gctcaggaag ggaaggccgc agccaccct gagagccagg aaccacaggc 480
 caagggggca gaggctagt cagcctcaga agaagaggca gggcccagg ctacagagcc 540
 atccactccc tcggggccgg agagtggccc tacaccagcc agcgtgagc agaatgagta 600
 gctaggtagg ggcaggtgg tgatctctaa gctgcaaaaa ctgtgctgtc cttgtgaggt 660
 cactgcctgg acctggtgcc ctggctgcct tcctgtgccc agaaaggaag gggctattgc 720
 ctctctccag ccacgttccc ttctctctc tcctctctgt ggattctccc atcagccatc 780
 tggttctcct cttaaggcca gttgaagatg gtcccttaca gcttcccaag ttaggttagt 840
 gatgtgaaat gctcctgtcc ctggccctac ctcccttccc gtccccaccc ctgcataagg 900
 cagttgttg ttttcttccc caattctttt ccaagtagg tttgtttacc ctactccca 960
 aatccctgag ccagaagtgg ggtgcttata ctcccaaacc ttgagtgtcc agccttcccc 1020
 tgttgttttt agtctcttgt gctgtgccta gtggcacctg ggctggggag gacactgccc 1080
 cgtctagggt tttataaatg tcttactcaa gttcaaacct ccagcctgtg aatcaactgt 1140
 gtctcttttt tgacttggt agcaagtatt aggcttggg gtggggggag gtctgtaatt 1200
 tgaaacaact tcttgtcttt ttttctocca ctgttgtaaa taacttttaa tggccaaacc 1260

ccagatttgt actttttttt tttttctaac tgctaaaacc attctcttcc acctgggttt 1320
actgtaacat ttgg 1334

<210> 121
<211> 195
<212> PRT
<213> Homo sapiens

<400> 121
Met Gly Ser Gln Ser Ser Lys Ala Pro Arg Gly Asp Val Thr Ala Glu
1 5 10 15
Glu Ala Ala Gly Ala Ser Pro Ala Lys Ala Asn Gly Gln Glu Asn Gly
20 25 30
His Val Lys Ser Asn Gly Asp Leu Ser Pro Lys Gly Glu Gly Glu Ser
35 40 45
Pro Pro Val Asn Gly Thr Asp Glu Ala Ala Gly Ala Thr Gly Asp Ala
50 55 60
Ile Glu Pro Ala Pro Pro Ser Gln Gly Ala Glu Ala Lys Gly Glu Val
65 70 75 80
Pro Pro Lys Glu Thr Pro Lys Lys Lys Lys Phe Ser Phe Lys Lys
85 90 95
Pro Phe Lys Leu Ser Gly Leu Ser Phe Lys Arg Asn Arg Lys Glu Gly
100 105 110
Gly Gly Asp Ser Ser Ala Ser Ser Pro Thr Glu Glu Glu Gln Glu Gln
115 120 125
Gly Glu Ile Gly Ala Cys Ser Asp Glu Gly Thr Ala Gln Glu Gly Lys
130 135 140
Ala Ala Ala Thr Pro Glu Ser Gln Glu Pro Gln Ala Lys Gly Ala Glu
145 150 155 160
Ala Ser Ala Ala Ser Glu Glu Glu Ala Gly Pro Gln Ala Thr Glu Pro
165 170 175
Ser Thr Pro Ser Gly Pro Glu Ser Gly Pro Thr Pro Ala Ser Ala Glu
180 185 190
Gln Asn Glu
195

<210> 122
<211> 1081
<212> DNA
<213> Homo sapiens

<400> 122
attgcaactt ggtctcacag tggcttaggc caggggtggga gcagtgaacg gagtcacaaa 60
agaaattttt cagctgtcct ctctgacacc acccggcct gcctctttgt tgccatgaga 120
gtgcctacc tcttctgct attcctgcct gcaggcttgc tggctcaggg ccagtatgat 180
ctggaccgc tgcgcgctt ccctgaccac gtccagtaca ccactatag cgaccagatc 240
gacaaccag actactatga ttatcaagag gtgactctc ggccctccga ggaacagttc 300
cagttccagt ccagcagca agtccaacag gaagtcattc cagcccaac ccagaacca 360
ggaaatgcag agctggagcc cacagagcct gggcctcttg actgccgtga ggaacagtac 420
ccgtgcaccc gcctctactc catacacagg ccttgcaaac agtgtctcaa cgaggctctgc 480
ttctacagcc tccgcgctgt gtacgtcatt aacaaggaga tctgtgttcg tacagtgtgt 540
gcccacgagg agctcctccg agctgacctc tgtcgggaca agttctcaa atgtggcgtg 600
atggccagca gcggcctgtg ccaatccgtg gcggcctcct gtgccaggag ctgtgggagc 660
tgctagggtg gtgctggcat cctgagtcct ggccctcctg ggatctgggg ccctcgggct 720
acctgacctg gtgctttttt ccccatcccc atgttccttt tattctgaaa aagttagtgg 780
actgcagccc tgggggttgc aggtgcggt gcctcaggcc cctccttcag cctgtggcca 840
cctctggggc acgatggggg ctccccactg ccagtcctgc ccctcgggtt gggggagtat 900
cccaggcctc tctgtgggac ctgggcctga cgggcccttc tcagcccggt ttgaggacag 960

```

acagtccccc gaggtaggct acatcccccc accccagctg gtctgcttgg atttcctaca 1020
gcccccggtgg gcatggacca cctttatattt atacaaaatt aaaaacaagt ttttacaaaa 1080
a                                                    1081

```

```

<210> 123
<211> 183
<212> PRT
<213> Homo sapiens

```

```

<400> 123
Met Arg Ala Ala Tyr Leu Phe Leu Leu Phe Leu Pro Ala Gly Leu Leu
 1           5           10           15
Ala Gln Gly Gln Tyr Asp Leu Asp Pro Leu Pro Pro Phe Pro Asp His
          20           25           30
Val Gln Tyr Thr His Tyr Ser Asp Gln Ile Asp Asn Pro Asp Tyr Tyr
          35           40           45
Asp Tyr Gln Glu Val Thr Pro Arg Pro Ser Glu Glu Gln Phe Gln Phe
 50           55           60
Gln Ser Gln Gln Gln Val Gln Gln Glu Val Ile Pro Ala Pro Thr Pro
65           70           75           80
Glu Pro Gly Asn Ala Glu Leu Glu Pro Thr Glu Pro Gly Pro Leu Asp
          85           90           95
Cys Arg Glu Glu Gln Tyr Pro Cys Thr Arg Leu Tyr Ser Ile His Arg
          100          105          110
Pro Cys Lys Gln Cys Leu Asn Glu Val Cys Phe Tyr Ser Leu Arg Arg
          115          120          125
Val Tyr Val Ile Asn Lys Glu Ile Cys Val Arg Thr Val Cys Ala His
          130          135          140
Glu Glu Leu Leu Arg Ala Asp Leu Cys Arg Asp Lys Phe Ser Lys Cys
145          150          155          160
Gly Val Met Ala Ser Ser Gly Leu Cys Gln Ser Val Ala Ala Ser Cys
          165          170          175
Ala Arg Ser Cys Gly Ser Cys
          180

```

```

<210> 124
<211> 1066
<212> DNA
<213> Homo sapiens

```

```

<400> 124
ggccaagggg cggctccggc gggcgggactc ggagcgggcg gcggagtgac ccggacagct 60
gtcctctctg acaccacccc ggccctgcctc tttgttgcca tgagagctgc ctacctcttc 120
ctgctatttc tgccctgcagg cttgctggct cagggccagt atgatctgga ccgctgccc 180
ccgttcocctg accacgtcca gtacacccac tatagcgacc agatcgacaa ccagactac 240
tatgattatc aagaggtgac tcctcggccc tccgaggaac agttccagtt ccagtcccag 300
cagcaagtcc aacaggaagt catcccagcc ccaaccccag aaccaggaaa tgcagagctg 360
gagcccacag agcctgggcc tcttgactgc cgtgaggaac agtaccctg caccgcctc 420
tactccatac acaggccttg caaacagtgt ctcaacgagg tctgcttcta cagcctccgc 480
cgtgtgtacg tcattaacaa ggagatctgt gttcgtacag tgtgtgcca cgaggagctc 540
ctccgagctg acctctgtcg ggacaagtgc tccaaatgtg gcgtgatggc cagcagcggc 600
ctgtgccaat ccgtggcggc ctccctgtgcc aggagctgtg ggagctgcta ggggtggtgct 660
ggcatcctga gtccctggccc tcctgggata tggggccctc gggctacctg acctggtgct 720
tttttcccca tcccatggtt ccttttattc tgaaaaagtt agtggactgc agccctgggg 780
gttgaggctc gcggtgcctc agggccctcc ttcagcctgt ggccacctct ggggacacgat 840
gggggctccc cactgcccag tctgcccctc ggggtggggg agtatcccag gcctctctgt 900
gggacctggg cctgacgggc ccttctcagc ccgttttgag gacagacagt ccccgagggt 960
aggctacatc cccccacccc agctggtctg cttggatttc ctacagcccc cgtgggcatg 1020

```

gaccaccttt attttataca aaatttaaaaa caagtttttta caaaaa

1066

<210> 125
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 125
 Met Arg Ala Ala Tyr Leu Phe Leu Leu Phe Leu Pro Ala Gly Leu Leu
 1 5 10 15
 Ala Gln Gly Gln Tyr Asp Leu Asp Pro Leu Pro Pro Phe Pro Asp His
 20 25 30
 Val Gln Tyr Thr His Tyr Ser Asp Gln Ile Asp Asn Pro Asp Tyr Tyr
 35 40 45
 Asp Tyr Gln Glu Val Thr Pro Arg Pro Ser Glu Glu Gln Phe Gln Phe
 50 55 60
 Gln Ser Gln Gln Gln Val Gln Gln Glu Val Ile Pro Ala Pro Thr Pro
 65 70 75 80
 Glu Pro Gly Asn Ala Glu Leu Glu Pro Thr Glu Pro Gly Pro Leu Asp
 85 90 95
 Cys Arg Glu Glu Gln Tyr Pro Cys Thr Arg Leu Tyr Ser Ile His Arg
 100 105 110
 Pro Cys Lys Gln Cys Leu Asn Glu Val Cys Phe Tyr Ser Leu Arg Arg
 115 120 125
 Val Tyr Val Ile Asn Lys Glu Ile Cys Val Arg Thr Val Cys Ala His
 130 135 140
 Glu Glu Leu Leu Arg Ala Asp Leu Cys Arg Asp Lys Phe Ser Lys Cys
 145 150 155 160
 Gly Val Met Ala Ser Ser Gly Leu Cys Gln Ser Val Ala Ala Ser Cys
 165 170 175
 Ala Arg Ser Cys Gly Ser Cys
 180

<210> 126
 <211> 1611
 <212> DNA
 <213> Homo sapiens

<400> 126
 acataatttc tggagccctg taccaacgtg tggccacata ttctgtcagg aaccctgtgt 60
 gatcatggtc tggatctgca acacggggcca ggccaaagtc acagatcttg agatcacagg 120
 tgggtgttgag cagcaggcag gcaggcaatc ggtccgagtg gctgtcggct cttcagctct 180
 ccgctcggcg tcttccttcc tctcccgtc agcgtcggcg gctgcaccgg cggcgggcag 240
 tcttgccgga ggggcgacaa gagctgagtc gcggccgccc agcgtcgagc tcagcgcggc 300
 ggaggcggcg gcggcccggc agccaacatg gcggcggcgg cggcggcggg cgcgggcccg 360
 gagatggtcc gcgggcaggt gttcgacgtg gggccgcgct acaccaacct ctgtacatc 420
 ggcgagggcg cctacggcat ggtgtgtctt gcttatgata atgtcaacaa agttcgagta 480
 gctatcaaga aaatcagccc ctttgagcac cagacctact gccagagAAC cctgagggag 540
 ataaaaatct tactgogctt cagacatgag aacatcattg gaatcaatga cattattcga 600
 gcaccaacca tcgagcaaat gaaagatgta tatatagtag aggacctcat ggaaacagat 660
 ctttacaagc tcttgaagac acaacacctc agcaatgacc atatctgcta tttctctac 720
 cagatcctca gaggggttaa atatatccat tcagctaacg ttctgcaccg tgacctcaag 780
 ccttccaacc tgctgctcaa caccacctgt gatctcaaga tctgtgactt tggcctggcc 840
 cgtgttgagc atccagacca tgatcacaca gggttcctga cagaatatgt ggccacacgt 900
 tggtagaggc ctcagaaat tatgttgat tccaagggtc acaccaagtc cattgatatt 960
 tggctctgtg gctgcattct ggcagaaatg ctttccaaca ggcccatctt tccagggaag 1020
 cattatcttg accagctgaa tcacattttg ggtattcttg gatccccatc acaagaagac 1080
 ctgaattgta taataaattt aaaagctagg aactatttgc tttctcttcc acacaaaaat 1140

```

aaggtgccat ggaacagget gttcccaa at gctgactcca aagctctgga cttattggac 1200
aaaatgttga cattcaaccc acacaagagg attgaagtag aacaggctct ggcccaccca 1260
tatctggagc agtattacga cccgagtgac gagcccatog ccgaagcacc attcaagttc 1320
gacatggaat tggatgactt gcctaaggaa aagctaaaag aactaatttt tgaagagact 1380
gctagattcc agccaggata cagatcttaa atttgtcagg acaagggtct agaggactgg 1440
acgtgctcag acatcggtgt tcttcttccc agttcttgac ccttggtcct gtctccagcc 1500
cgtcttggct tatccacttt gactcctttg agccgttttg aggggcggtt tctggtagtt 1560
gtggctttta tgctttcaaa gaatttcttc agtccagaga attcactggc c 1611

```

<210> 127

<211> 360

<212> PRT

<213> Homo sapiens

<400> 127

```

Met Ala Ala Ala Ala Ala Ala Gly Ala Gly Pro Glu Met Val Arg Gly
 1          5          10          15
Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly
      20          25          30
Glu Gly Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Val Asn Lys
      35          40          45
Val Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr
      50          55          60
Cys Gln Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His
      65          70          75          80
Glu Asn Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu
      85          90          95
Gln Met Lys Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu
      100         105         110
Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr
      115         120         125
Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn
      130         135         140
Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Thr Thr
      145         150         155         160
Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro
      165         170         175
Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp
      180         185         190
Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser
      195         200         205
Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn
      210         215         220
Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile
      225         230         235         240
Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile
      245         250         255
Asn Leu Lys Ala Arg Asn Tyr Leu Leu Ser Leu Pro His Lys Asn Lys
      260         265         270
Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp Ser Lys Ala Leu Asp
      275         280         285
Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His Lys Arg Ile Glu Val
      290         295         300
Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Ser
      305         310         315         320
Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe Asp Met Glu Leu Asp
      325         330         335
Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile Phe Glu Glu Thr Ala
      340         345         350

```

Arg Phe Gln Pro Gly Tyr Arg Ser
355 360

<210> 128
<211> 2917
<212> DNA
<213> Homo sapiens

<400> 128

```

ggaaaaaagc gacttggtggc ggtcgagcgt ggcgagggcg aatcctcggc actaagcaaa 60
tatggacctc gcggcgggcag cggagccggg cgccggcagc cagcacctgg aggtccgcga 120
cgaggtggcc gagaagtgcc agaaaactgtt cctggacttc ttggaggagt ttcagagcag 180
cgatggagaa attaaatact tgcaattagc agaggaactg attcgtcctg agagaaacac 240
attggtttgt agttttgtgg acctggaaca atttaaccag caactttcca ccaccattca 300
agaggagttc tatagagtgt acccttacct gtgtcgggcc ttgaaaacat tcgtcaaaga 360
ccgtaaagag atccctcttg ccaaggattt ttatggtgca ttccaagacc tgccaccag 420
acacaagatt cgagagctca cctcatccag aattggtttg ctactcgcga tcagtgggca 480
ggtggtgcgg actcaccagc ttcaccaga gcttgtagc ggaacttttc tgtgcttgga 540
ctgtcagaca gtgatcagg atgtagaaca gcagttcaaa tacacacagc caaacatctg 600
ccgaaatcca gtttgtgcc acaggaggag attcttactg gatacaaata aatcaagatt 660
tggttgattt caaaaggttc gtattcaaga gacccaagct gagcttcctc gagggagtat 720
ccccgcagc ttagaagtaa ttttaagggc tgaagctgtg gaatcagctc aagctggtga 780
caagtgtgac ttacaggga cactgattgt tgtgcctgac gtctccaagc ttagcacacc 840
aggagcacgt gcagaaacta attcccgtgt cagtgggtgt gatggatatg agacagaagg 900
cattcgagga ctccggggccc ttggtggttag ggacctttct tataggctgg tctttcttgc 960
ctgctgtgtt gcgccaaacca acccaagggt tggggggaaa gagctcagag atgaggaaca 1020
gacagctgag agcattaaga accaaatgac tgtgaaagaa tgggagaaag tgtttgagat 1080
gagtcagat aaaaatctat accacaatct ttgtaccagc ctgttccta ctatacatg 1140
caatgatgaa gtaaaacggg gtgtcctgct gatgctcttt ggtggcgttc caaagacaac 1200
aggagaaggg acctctcttc gaggggacat aaatgtttgc attggttggtg acccaagtac 1260
agctaagagc caatttctca agcacgtgga ggagttcagc ccagagctg tctacaccag 1320
tggtaaagcg tccagtgtct ctggcttaac agcagctgtt gtgagagatg aagaatctca 1380
tgagtttgtc attgaggctg gagctttgat gttggctgat aatggtgtgt gttgtattga 1440
tgaatttgat aagatggacg tgcgggatca agttgctatt catgaagcta tggaaacagca 1500
gaccataatc atcactaaag caggagtga ggtactctg aacgcccga cgtccatttt 1560
ggcagcagca aacccaatca gtggacacta tgacagatca aaatcattga aacagaatat 1620
aaatttgtca gctcccatca tgtcccgatt cgatctcttc tttatccttg tggatgaatg 1680
taatgaggtt acagattatg ccattgccag gcgcatagta gatttgcatt caagaattga 1740
ggaatcaatt gatcgtgtct attccctcga tgatatcaga agatatcttc tctttgcaag 1800
acagtttaaa ccaagattt ccaaagagtc agaggacttc attgtggagc aatataaaca 1860
tctccgccag agagatggtt ctggagtgc caagtcttca tggaggatta cagtgcgaca 1920
gcttgagagc atgattcgtc tctctgaagc tatggctcgg atgcactgct gtgatgaggt 1980
ccaacctaaa catgtgaagg aagctttccg gttactgaat aaatcaatca tccgtgtgga 2040
aacacctgat gtoaatctag atcaagagga agagatccag atggaggtag atgagggtgc 2100
tggtggcatc aatggtcatg ctgacagccc tgctcctgtg aacgggatca atggctacaa 2160
tgaagacata aatcaagagt ctgctcccaa agcctcctta aggctgggct tctctgagta 2220
ctgccgaatc tctaacctta ttgtgcttca cctcagaaag gtggaagaag aagaggacga 2280
gtcagcatta aagaggagcg agcttggtta ctggtacttg aaggaaatcg aatcagagat 2340
agactctgaa gaagaactta taaataaaaa aagaatcata gagaaagtta ttcactcgact 2400
cacacactat gatcatgttc taattgagct caccaggct ggattgaaag gctccacaga 2460
gggaagtgag agctatgaag aagatcccta cttggtagtt aaccctaact acttgctcga 2520
agattgagat agtgaaagta actgaccaga gctgaggaac tgtggcacag cacctcgtgg 2580
cctggagcct ggctggagct ctgctagggc cagaagtgtt tctggaagtg atgcttccag 2640
gatttgtttt cagaacaag aattgagttg atggtcctat gtgtcacatt catcacagg 2700
ttcataccaa cacaggcttc agcacttctt ttggtgtgtt tcctgtccca gtgaagtgtg 2760
aaccaaataa tgtgtagtct ctataaccaa tacctttgtt ttcattgtgt agaaaaggcc 2820
cattactttt aagggtatgt ctgtcctatt gagcaaataa ctttttttca attgccagct 2880
actgctttta ttcatacaaa taaaataact tgttctg 2917

```


<210> 129
 <211> 821
 <212> PRT
 <213> Homo sapiens

<400> 129

Met	Asp	Leu	Ala	Ala	Ala	Ala	Glu	Pro	Gly	Ala	Gly	Ser	Gln	His	Leu
1			5						10					15	
Glu	Val	Arg	Asp	Glu	Val	Ala	Glu	Lys	Cys	Gln	Lys	Leu	Phe	Leu	Asp
			20					25					30		
Phe	Leu	Glu	Glu	Phe	Gln	Ser	Ser	Asp	Gly	Glu	Ile	Lys	Tyr	Leu	Gln
		35					40					45			
Leu	Ala	Glu	Glu	Leu	Ile	Arg	Pro	Glu	Arg	Asn	Thr	Leu	Val	Val	Ser
		50				55					60				
Phe	Val	Asp	Leu	Glu	Gln	Phe	Asn	Gln	Gln	Leu	Ser	Thr	Thr	Ile	Gln
65					70					75					80
Glu	Glu	Phe	Tyr	Arg	Val	Tyr	Pro	Tyr	Leu	Cys	Arg	Ala	Leu	Lys	Thr
			85						90					95	
Phe	Val	Lys	Asp	Arg	Lys	Glu	Ile	Pro	Leu	Ala	Lys	Asp	Phe	Tyr	Val
			100					105					110		
Ala	Phe	Gln	Asp	Leu	Pro	Thr	Arg	His	Lys	Ile	Arg	Glu	Leu	Thr	Ser
			115				120					125			
Ser	Arg	Ile	Gly	Leu	Leu	Thr	Arg	Ile	Ser	Gly	Gln	Val	Val	Arg	Thr
			130			135					140				
His	Pro	Val	His	Pro	Glu	Leu	Val	Ser	Gly	Thr	Phe	Leu	Cys	Leu	Asp
145					150					155					160
Cys	Gln	Thr	Val	Ile	Arg	Asp	Val	Glu	Gln	Gln	Phe	Lys	Tyr	Thr	Gln
			165						170					175	
Pro	Asn	Ile	Cys	Arg	Asn	Pro	Val	Cys	Ala	Asn	Arg	Arg	Arg	Phe	Leu
			180					185					190		
Leu	Asp	Thr	Asn	Lys	Ser	Arg	Phe	Val	Asp	Phe	Gln	Lys	Val	Arg	Ile
			195				200					205			
Gln	Glu	Thr	Gln	Ala	Glu	Leu	Pro	Arg	Gly	Ser	Ile	Pro	Arg	Ser	Leu
			210			215					220				
Glu	Val	Ile	Leu	Arg	Ala	Glu	Ala	Val	Glu	Ser	Ala	Gln	Ala	Gly	Asp
225					230					235					240
Lys	Cys	Asp	Phe	Thr	Gly	Thr	Leu	Ile	Val	Val	Pro	Asp	Val	Ser	Lys
			245						250					255	
Leu	Ser	Thr	Pro	Gly	Ala	Arg	Ala	Glu	Thr	Asn	Ser	Arg	Val	Ser	Gly
			260				265						270		
Val	Asp	Gly	Tyr	Glu	Thr	Glu	Gly	Ile	Arg	Gly	Leu	Arg	Ala	Leu	Gly
		275					280					285			
Val	Arg	Asp	Leu	Ser	Tyr	Arg	Leu	Val	Phe	Leu	Ala	Cys	Cys	Val	Ala
		290				295					300				
Pro	Thr	Asn	Pro	Arg	Phe	Gly	Gly	Lys	Glu	Leu	Arg	Asp	Glu	Glu	Gln
305					310					315					320
Thr	Ala	Glu	Ser	Ile	Lys	Asn	Gln	Met	Thr	Val	Lys	Glu	Trp	Glu	Lys
			325						330					335	
Val	Phe	Glu	Met	Ser	Gln	Asp	Lys	Asn	Leu	Tyr	His	Asn	Leu	Cys	Thr
			340					345					350		
Ser	Leu	Phe	Pro	Thr	Ile	His	Gly	Asn	Asp	Glu	Val	Lys	Arg	Gly	Val
		355					360					365			
Leu	Leu	Met	Leu	Phe	Gly	Gly	Val	Pro	Lys	Thr	Thr	Gly	Glu	Gly	Thr
		370				375					380				
Ser	Leu	Arg	Gly	Asp	Ile	Asn	Val	Cys	Ile	Val	Gly	Asp	Pro	Ser	Thr
385					390					395					400
Ala	Lys	Ser	Gln	Phe	Leu	Lys	His	Val	Glu	Glu	Phe	Ser	Pro	Arg	Ala
			405						410					415	

Val	Tyr	Thr	Ser	Gly	Lys	Ala	Ser	Ser	Ala	Ala	Gly	Leu	Thr	Ala	Ala		
			420					425					430				
Val	Val	Arg	Asp	Glu	Glu	Ser	His	Glu	Phe	Val	Ile	Glu	Ala	Gly	Ala		
		435					440					445					
Leu	Met	Leu	Ala	Asp	Asn	Gly	Val	Cys	Cys	Ile	Asp	Glu	Phe	Asp	Lys		
	450					455					460						
Met	Asp	Val	Arg	Asp	Gln	Val	Ala	Ile	His	Glu	Ala	Met	Glu	Gln	Gln		
465					470					475					480		
Thr	Ile	Ser	Ile	Thr	Lys	Ala	Gly	Val	Lys	Ala	Thr	Leu	Asn	Ala	Arg		
			485						490						495		
Thr	Ser	Ile	Leu	Ala	Ala	Ala	Asn	Pro	Ile	Ser	Gly	His	Tyr	Asp	Arg		
			500					505					510				
Ser	Lys	Ser	Leu	Lys	Gln	Asn	Ile	Asn	Leu	Ser	Ala	Pro	Ile	Met	Ser		
		515					520					525					
Arg	Phe	Asp	Leu	Phe	Phe	Ile	Leu	Val	Asp	Glu	Cys	Asn	Glu	Val	Thr		
	530					535					540						
Asp	Tyr	Ala	Ile	Ala	Arg	Arg	Ile	Val	Asp	Leu	His	Ser	Arg	Ile	Glu		
545					550					555					560		
Glu	Ser	Ile	Asp	Arg	Val	Tyr	Ser	Leu	Asp	Asp	Ile	Arg	Arg	Tyr	Leu		
				565					570					575			
Leu	Phe	Ala	Arg	Gln	Phe	Lys	Pro	Lys	Ile	Ser	Lys	Glu	Ser	Glu	Asp		
			580					585					590				
Phe	Ile	Val	Glu	Gln	Tyr	Lys	His	Leu	Arg	Gln	Arg	Asp	Gly	Ser	Gly		
		595					600					605					
Val	Thr	Lys	Ser	Ser	Trp	Arg	Ile	Thr	Val	Arg	Gln	Leu	Glu	Ser	Met		
	610					615					620						
Ile	Arg	Leu	Ser	Glu	Ala	Met	Ala	Arg	Met	His	Cys	Cys	Asp	Glu	Val		
625					630					635					640		
Gln	Pro	Lys	His	Val	Lys	Glu	Ala	Phe	Arg	Leu	Leu	Asn	Lys	Ser	Ile		
				645					650					655			
Ile	Arg	Val	Glu	Thr	Pro	Asp	Val	Asn	Leu	Asp	Gln	Glu	Glu	Glu	Ile		
			660					665					670				
Gln	Met	Glu	Val	Asp	Glu	Gly	Ala	Gly	Gly	Ile	Asn	Gly	His	Ala	Asp		
		675					680						685				
Ser	Pro	Ala	Pro	Val	Asn	Gly	Ile	Asn	Gly	Tyr	Asn	Glu	Asp	Ile	Asn		
	690					695					700						
Gln	Glu	Ser	Ala	Pro	Lys	Ala	Ser	Leu	Arg	Leu	Gly	Phe	Ser	Glu	Tyr		
705					710					715					720		
Cys	Arg	Ile	Ser	Asn	Leu	Ile	Val	Leu	His	Leu	Arg	Lys	Val	Glu	Glu		
				725					730					735			
Glu	Glu	Asp	Glu	Ser	Ala	Leu	Lys	Arg	Ser	Glu	Leu	Val	Asn	Trp	Tyr		
			740					745					750				
Leu	Lys	Glu	Ile	Glu	Ser	Glu	Ile	Asp	Ser	Glu	Glu	Glu	Leu	Ile	Asn		
		755					760						765				
Lys	Lys	Arg	Ile	Ile	Glu	Lys	Val	Ile	His	Arg	Leu	Thr	His	Tyr	Asp		
	770					775					780						
His	Val	Leu	Ile	Glu	Leu	Thr	Gln	Ala	Gly	Leu	Lys	Gly	Ser	Thr	Glu		
785					790					795					800		
Gly	Ser	Glu	Ser	Tyr	Glu	Glu	Asp	Pro	Tyr	Leu	Val	Val	Asn	Pro	Asn		
				805					810					815			
Tyr	Leu	Leu	Glu	Asp													
			820														

<210> 130

<211> 786

<212> DNA

<213> Homo sapiens

<400> 130

```

cgggcgaagc agcgcggggca gcgagatgca gcaccgagggc ttctctctcc tcaccctcct 60
cgccctgctg gcgctcacct ccgcggtcgc caaaaagaaa gataagggtga agaagggcgg 120
cccggggagc gagtgcgctg agtgggcctg ggggccctgc acccccagca gcaaggattg 180
cggcgtgggt ttccgcgagg gcacctgcgg ggcccagacc cagcgcaccc ggtgcagggt 240
gccctgcaac tggaagaagg agtttgagc cgactgcaag tacaagtttg agaactgggg 300
tgcgtgtgat gggggcacag gcaccaaagt ccgccaaggg accctgaaga aggcgcgcta 360
caatgctcag tgccaggaga ccatccgcgt caccaagccc tgcaccccca agaccaaaagc 420
aaaggccaaa gccaaagaaag ggaagggaaa ggactagacg ccaagcctgg atgccaagga 480
gcccctgggt tcacatgggg cctggccacg ccctccctct cccaggcccg agatgtgacc 540
caccagtgcc ttctgtctgc tcgttagctt taatcaatca tgccctgcct tgtccctctc 600
actcccccag cccacccta agtgcccaa gtggggaggg acaagggatt ctgggaagct 660
tgagcctccc ccaaagcaat gtgagtccta gagccgctt ttgttcttcc ccacaattcc 720
attactaaga aacacatcaa ataaactgac tttttccccc caataaaaagc tcttcttttt 780
taatat
786

```

<210> 131

<211> 143

<212> PRT

<213> Homo sapiens

<400> 131

```

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1          5          10          15
Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
          20          25          30
Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
          35          40          45
Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
          50          55          60
Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
          65          70          75          80
Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
          85          90          95
Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
          100          105          110
Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
          115          120          125
Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
          130          135          140

```

<210> 132

<211> 603

<212> DNA

<213> Homo sapiens

<400> 132

```

cgtgctgcta cacaagaacc ctgagactga cctgcaggac gaaaccatga agagcctgat 60
ccttcttgcc atcctggccg ccttagcggt agtaactttg tgttatgaat cacatgaaag 120
catggaatct tatgaactta atcccttcat taacaggaga aatgcaaata ccttcatatc 180
ccctcagcag agatgggagag ctaaagtcca agagaggatc cgagaacgct ctaagcctgt 240
ccacgagctc aataggggaag cctgtgatga ctacagactt tgccaacgct acgccatgg 300
ttatggatac aatgctgcct ataatcgcta cttcaggaag cgccgagggg ccaaagaga 360
ctgaggggaag aaaaaaaatc tctttttttc tggaggctgg cacctgattt tgtatcccc 420
tgtagcagca ttactgaaat acataggctt atatacaatg cttctttcct gtatattctc 480
ttgtctggct gcaccccttt ttcccgcctt cagattgata agtaatgaaa gtgcactgca 540
gtgaggggtc aaggagagtc aacatatgtg attgttccat aataaaacttc tgggtgtgata 600
ctt
603

```

<210> 133
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 133
 Met Lys Ser Leu Ile Leu Leu Ala Ile Leu Ala Ala Leu Ala Val Val
 1 5 10 15
 Thr Leu Cys Tyr Glu Ser His Glu Ser Met Glu Ser Tyr Glu Leu Asn
 20 25 30
 Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln
 35 40 45
 Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro
 50 55 60
 Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu
 65 70 75 80
 Arg Tyr Ala Met Val Tyr Gly Tyr Asn Ala Ala Tyr Asn Arg Tyr Phe
 85 90 95
 Arg Lys Arg Arg Gly Ala Lys
 100

<210> 134
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 134
 tagaagttta caatgaagtt tcttctaata ctgctcctgc aggcactgc ttctggagct 60
 ctccccctga acagctctac aagcctggaa aaaaataatg tgctatttgg tgagagatac 120
 ttagaaaaat tttatggcct tgagataaac aaacttccag tgacaaaaat gaaatatagt 180
 ggaaacttaa tgaaggaaaa aatccaagaa atgcagcact tcttgggtct gaaagtgacc 240
 gggcaactgg acacatctac cctggagatg atgcacgcac ctcgatgtgg agtccccgat 300
 ctccatcatt tcagggaagt gccagggggg ccgctatgga ggaaacatta tatcacctac 360
 agaataaata attacacacc tgacatgaac cgtgaggatg ttgactacgc aatccggaaa 420
 gctttccaag tatggagtaa tgttaccocc ttgaaattca gcaagattaa cacaggcatg 480
 gctgacattt tgggtggttt tggccgtgga gctcatggag acttccatgc ttttgatggc 540
 aaaggtggaa tcctagccca tgccttttga cctggatctg gcattggagg ggatgcacat 600
 ttcgatgagg acgaattctg gactacacat tcaggaggca caaacttggt cctcactgct 660
 gttcacgaga ttggccattc cttaggtctt ggccattcta gtgatccaaa ggctgtaattg 720
 ttccccacct acaaatatgt cgacatcaac acatttcgcc tctctgctga tgacatacgt 780
 ggcattcagt ccctgtatgg agacccaaaa gagaaccaac gcttgccaaa tcctgacaat 840
 tcagaaccag ctctctgtga ccccaatttg agttttgatg ctgtcactac cgtgggaaat 900
 aagatctttt tcttcaaaga caggttcttc tggctgaagg tttctgagag accaaagacc 960
 agtgtaatt taatttcttc cttatggcca acctgccc atggcattga agctgcttat 1020
 gaaattgaag ccagaaatca agtttttctt tttaaagatg acaaatactg gtttaattagc 1080
 aatttaagac cagagccaaa ttatcccaag agcatacatt ctttttggtt tcctaacttt 1140
 gtgaaaaaaaa ttgatgcagc tgttttttaac ccacgttttt ataggaccta cttcttttga 1200
 gataaccagt attggaggta tgatgaaagg agacagatga tggaccctgg ttatcccaaa 1260
 ctgattacca agaacttcca aggaatcggg cctaaaattg atgcagtctt ctattctaaa 1320
 aacaaatact actatttctt ccaaggatct aaccaatttg aatatgactt cctactccaa 1380
 cgtatcacca aaacactgaa aagcaatagc tggtttggtt gttagaaatg gtgtaattaa 1440
 tggtttttgt tagttcactt cagcttaata agtatttatt gcataatttg tatgtcctca 1500
 gtgtaccact acttagagat atgtatcata aaaataaaat ctgtaaacca taggtaattga 1560
 ttatataaaa tacataatat ttttcaattt tgaaaactct aattgtccat tcttgcttga 1620
 ctctactatt aagtttgaaa atagttacct tcaaagcaag ataattctat ttgaagcatg 1680
 ctctgtaagt tgcttcctaa catccttgga ctgagaaatt atacttactt ctggcataac 1740
 taaaattaag tatatatatt ttggctcaaa taaaattg 1778

<400>	135														
Met	Lys	Phe	Leu	Leu	Ile	Leu	Leu	Leu	Gln	Ala	Thr	Ala	Ser	Gly	Ala
1				5					10					15	
Leu	Pro	Leu	Asn	Ser	Ser	Thr	Ser	Leu	Glu	Lys	Asn	Asn	Val	Leu	Phe
			20					25					30		
Gly	Glu	Arg	Tyr	Leu	Glu	Lys	Phe	Tyr	Gly	Leu	Glu	Ile	Asn	Lys	Leu
		35					40					45			
Pro	Val	Thr	Lys	Met	Lys	Tyr	Ser	Gly	Asn	Leu	Met	Lys	Glu	Lys	Ile
	50					55					60				
Gln	Glu	Met	Gln	His	Phe	Leu	Gly	Leu	Lys	Val	Thr	Gly	Gln	Leu	Asp
65				70					75					80	
Thr	Ser	Thr	Leu	Glu	Met	Met	His	Ala	Pro	Arg	Cys	Gly	Val	Pro	Asp
			85						90				95		
Leu	His	His	Phe	Arg	Glu	Met	Pro	Gly	Gly	Pro	Val	Trp	Arg	Lys	His
			100					105					110		
Tyr	Ile	Thr	Tyr	Arg	Ile	Asn	Asn	Tyr	Thr	Pro	Asp	Met	Asn	Arg	Glu
		115					120					125			
Asp	Val	Asp	Tyr	Ala	Ile	Arg	Lys	Ala	Phe	Gln	Val	Trp	Ser	Asn	Val
	130					135					140				
Thr	Pro	Leu	Lys	Phe	Ser	Lys	Ile	Asn	Thr	Gly	Met	Ala	Asp	Ile	Leu
145				150						155					160
Val	Val	Phe	Ala	Arg	Gly	Ala	His	Gly	Asp	Phe	His	Ala	Phe	Asp	Gly
			165						170					175	
Lys	Gly	Gly	Ile	Leu	Ala	His	Ala	Phe	Gly	Pro	Gly	Ser	Gly	Ile	Gly
			180					185					190		
Gly	Asp	Ala	His	Phe	Asp	Glu	Asp	Glu	Phe	Trp	Thr	Thr	His	Ser	Gly
		195					200					205			
Gly	Thr	Asn	Leu	Phe	Leu	Thr	Ala	Val	His	Glu	Ile	Gly	His	Ser	Leu
	210					215					220				
Gly	Leu	Gly	His	Ser	Ser	Asp	Pro	Lys	Ala	Val	Met	Phe	Pro	Thr	Tyr
225				230						235					240
Lys	Tyr	Val	Asp	Ile	Asn	Thr	Phe	Arg	Leu	Ser	Ala	Asp	Asp	Ile	Arg
			245						250					255	
Gly	Ile	Gln	Ser	Leu	Tyr	Gly	Asp	Pro	Lys	Glu	Asn	Gln	Arg	Leu	Pro
		260						265					270		
Asn	Pro	Asp	Asn	Ser	Glu	Pro	Ala	Leu	Cys	Asp	Pro	Asn	Leu	Ser	Phe
		275					280						285		
Asp	Ala	Val	Thr	Thr	Val	Gly	Asn	Lys	Ile	Phe	Phe	Phe	Lys	Asp	Arg
	290					295					300				
Phe	Phe	Trp	Leu	Lys	Val	Ser	Glu	Arg	Pro	Lys	Thr	Ser	Val	Asn	Leu
305				310						315					320
Ile	Ser	Ser	Leu	Trp	Pro	Thr	Leu	Pro	Ser	Gly	Ile	Glu	Ala	Ala	Tyr
			325						330					335	
Glu	Ile	Glu	Ala	Arg	Asn	Gln	Val	Phe	Leu	Phe	Lys	Asp	Asp	Lys	Tyr
			340												

Leu Ile Thr Lys Asn Phe Gln Gly Ile Gly Pro Lys Ile Asp Ala Val
 420 425 430
 Phe Tyr Ser Lys Asn Lys Tyr Tyr Tyr Phe Phe Gln Gly Ser Asn Gln
 435 440 445
 Phe Glu Tyr Asp Phe Leu Leu Gln Arg Ile Thr Lys Thr Leu Lys Ser
 450 455 460
 Asn Ser Trp Phe Gly Cys
 465 470

<210> 136
 <211> 1821
 <212> DNA
 <213> Homo sapiens

<400> 136
 acaaggaggc aggcaagaca gcaaggcata gagacaacat agagctaagt aaagccagtg 60
 gaaatgaaga gtcttccaat cctactgttg ctgtgcgtgg cagtttgctc agcctatcca 120
 ttggatggag ctgcaagggg tgaggacacc agcatgaacc ttgttcagaa atatctagaa 180
 aactactacg acctcaaaaa agatgtgaaa cagtttggtta ggagaaaagga cagtggctcct 240
 gttgttaaaaa aaatccgaga aatgcagaag ttccttggat tggaggtgac ggggaagctg 300
 gactccgaca ctctggagggt gatgcgcaag ccaggtgtg gagttcctga tgttggtcac 360
 ttcagaacct ttcctggcat cccgaagtgg aggaaaaccc accttacata caggattgtg 420
 aattatacac cagatttgcc aaaagatgct gttgattctg ctgttgagaa agctctgaaa 480
 gtctgggaag aggtgactcc actcacattc tccaggctgt atgaaggaga ggctgatata 540
 atgatctctt ttgcagttag agaacatgga gacttttacc cttttgatgg acctggaaat 600
 gttttggccc atgcctatgc ccctgggcca gggattaatg gagatgccc ctttgatgat 660
 gatgaacaat ggacaaagga tacaacaggg accaatttat ttctcgttgc tgctcatgaa 720
 attggccact ccctgggtct ctttactca gccaacactg aagctttgat gtacccactc 780
 tactactcac tcacagacct gactcgggtc cgctgtctc aagatgatat aaatggcatt 840
 cagtcacctc atggacctcc ccctgactcc cctgagaccc ccctgggtacc cacggaacct 900
 gtccctccag aacctgggac gccagccaac tgtgatcctg ctttgtcctt tgatgctgtc 960
 agcactctga ggggagaaat cctgatcttt aaagacaggc acttttggcg caaatccctc 1020
 aggaagcttg aacctgaatt gcatttgatc tcttcatttt ggccatctct tccttcaggc 1080
 gtggatgccg catatgaagt tactagcaag gacctcgttt tcatttttaa aggaaatcaa 1140
 ttctgggcca tcagaggaaa tgaggtaaga gctggatacc caagaggcat ccacacccta 1200
 ggtttccctc caaccgtgag gaaaatcgat gcagccattt ctgataagga aaagaacaaa 1260
 acatatttct ttgtagagga caaatactgg agatttgatg agaagagaaa ttccatggag 1320
 ccaggctttc ccaagcaaat agctgaagac tttccaggga ttgactcaaa gattgatgct 1380
 gtttttgaag aatttggggt cttttatttc tttactggat cttcacagtt ggagtttgac 1440
 ccaaatgcaa agaaagtgac acacactttg aagagtaaca gctggcttaa ttgttgaaag 1500
 agatatgtag aaggcacaat atgggcactt taaatgaagc taataattct tcacctaaat 1560
 ctctgtgaat tgaaatgttc gttttctcct gcctgtgctg tgactcgagt cacactcaag 1620
 ggaacttgag cgtgaatctg tatcttgccg gtcattttta tgttattaca gggcattcaa 1680
 atgggctgct gcttagcttg caccttgatc catagagtga tctttcccaa gagaagggga 1740
 agcactcgtg tgcaacagac aagtgactgt atctgtgtag actatttgct tatttaataa 1800
 agacgatttg tcagttgttt t 1821

<210> 137
 <211> 477
 <212> PRT
 <213> Homo sapiens

<400> 137
 Met Lys Ser Leu Pro Ile Leu Leu Leu Leu Cys Val Ala Val Cys Ser
 1 5 10 15
 Ala Tyr Pro Leu Asp Gly Ala Ala Arg Gly Glu Asp Thr Ser Met Asn
 20 25 30
 Leu Val Gln Lys Tyr Leu Glu Asn Tyr Tyr Asp Leu Lys Lys Asp Val

<210> 138
<211> 1127

<212> DNA

<213> Homo sapiens

<400> 138

```

accaaatacaa ccataggtcc aagaacaatt gtctctggac ggcagctatg cgactcacgg 60
tgctgtgtgc tgtgtgcctg ctgcctggca gcttggccct gccgctgcct caggaggcgg 120
gaggcatgag tgagctacag tgggaacagg ctccaggacta tctcaagaga ttttatctct 180
atgactcaga aacaaaaaat gccaacagtt tagaagccaa actcaaggag atgcaaaaaat 240
tctttggcct acctataact ggaatgttaa actcccgcgt catagaaata atgcagaagc 300
ccagatgtgg agtgccagat gttgcagaat actcactatt tccaaatagc ccaaaatgga 360
cttccaaagt ggtcacctac aggatcgat catatactcg agacttaccg catattacag 420
tggatcgatt agtgtcaaag gctttaaaca tgtggggcaa agagatcccc ctgcatttca 480
ggaaagtgtg atggggaaact gctgacatca tgattggcct tgcgcgagga gctcatgggg 540
actcctaccc atttgatggg ccaggaaaca cgctggctca tgcctttgcg cctgggacag 600
gtctcggagg agatgctcac ttgatgagg atgaacgctg gacggatggg agcagtctag 660
ggattaactt cctgtatgct gcaactcatg aacttggcca ttctttgggt atgggacatt 720
cctctgatcc taatgcagtg atgtatccaa cctatggaaa tggagatccc caaaatttta 780
aactttccca ggatgatatt aaaggcattc agaaactata tggaaagaga agtaattcaa 840
gaaagaaata gaaacttcag gcagaacatc cattcattca ttcattggat tgtatatcat 900
tggtgcacaa tcagaattga taagcactgt tcctccactc catttagcaa ttatgtcacc 960
cttttttatt gcagttgggt tttgaatgtc tttcactcct tttattgggt aaactccttt 1020
atggtgtgac tgtgtcttat tccatctatg agctttgtca gtgcgcgtag atgtcaataa 1080
atgttacata cacaataaaa taaaatgttt attccatggt aaatttta 1127

```

<210> 139

<211> 267

<212> PRT

<213> Homo sapiens

<400> 139

```

Met Arg Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu
1      5      10      15
Ala Leu Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp
20      25      30
Glu Gln Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu
35      40      45
Thr Lys Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys
50      55      60
Phe Phe Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu
65      70      75      80
Ile Met Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser
85      90      95
Leu Phe Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg
100     105     110
Ile Val Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu
115     120     125
Val Ser Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe
130     135     140
Arg Lys Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg
145     150     155     160
Gly Ala His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu
165     170     175
Ala His Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe
180     185     190
Asp Glu Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe
195     200     205
Leu Tyr Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His
210     215     220
Ser Ser Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp

```


225		230		235		240									
Pro	Gln	Asn	Phe	Lys	Leu	Ser	Gln	Asp	Asp	Ile	Lys	Gly	Ile	Gln	Lys
				245					250					255	
Leu	Tyr	Gly	Lys	Arg	Ser	Asn	Ser	Arg	Lys	Lys					
			260					265							

<210> 140

<211> 1078

<212> DNA

<213> Homo sapiens

<400> 140

```

aagaacaatt gtctctggac ggcagctatg cgactcacgg tgctgtgtgc tgtgtgcctg 60
ctgcctggca gcctggccct gccgctgcct caggaggcgg gaggcattgag tgagctacag 120
tgggaacagg ctccaggacta tctcaagaga ttttatctct atgactcaga acaaaaaaat 180
gccaacagtt tagaagccaa actcaaggag atgcaaaaaat tctttggcct acctataact 240
ggaatgttaa actcccgct catagaaata atgcagaagc ccagatgtgg agtgccagat 300
gttgcagaat actcactatt tccaaatagc ccaaaatgga ctcccaaagt ggtcacctac 360
aggatcgtat catatactcg agacttacgg catattacag tggatcgatt agtgtcaaag 420
gctttaaaca tgtggggcaa agagatcccc ctgcatttca ggaaagtgt atggggaact 480
gotgacatca tgattggctt tgcgcgagga gctcatgggg actcctaccc atttgatggg 540
ccaggaaaca cgctggctca tgcctttgct cctgggacag gtctcggagg agatgctcac 600
ttcgatgagg atgaacgctg gacggatggt agcagctctag ggattaactt cctgtatgct 660
gcaactcatg aacttggcca ttctttgggt atgggacatt cctctgatcc taatgcagt 720
atgtatccaa cctatggaaa tggagatccc caaaatttta aactttccca ggatgatatt 780
aaaggcaftc agaaactata tggaaagaga agtaattcaa gaaagaaata gaaacttcag 840
gcagaacatc cattcattca ttcatgggat tgtatatcat tgttgcaaa tcagaattga 900
taagcactgt tctccactc catttagcaa ttatgtcaac cttttttatt gcagttgggt 960
tttgaatgtc tttcactcct tttattgggt aaactccttt atgggtgtgac tgtgtcttat 1020
tccatctatg agctttgtca gtgcgcgtag atgtcaataa atgttacata cacaaata 1078

```

<210> 141

<211> 2334

<212> DNA

<213> Homo sapiens

<400> 141

```

agacacctct gccctcacca tgagcctctg gcagccctg gtcctggtgc tccctggtgct 60
gggctgctgc tttgtgccc ccagacagcg ccagtcacc cttgtgctct tccctggaga 120
cctgagaacc aatctcacgg acaggcagct ggcagaggaa tacctgtacc gctatggta 180
cactcgggtg gcagagatgc gtggagagtc gaaatctctg gggcctgcgc tgcctgtct 240
ccagaagcaa ctgtccctgc ccgagaccgg tgagctggat agcgccacgc tgaaggccat 300
gcgaacccca cggcgcgggg tcccagacct gggcagattc caaacctttg agggcgacct 360
caagtggcac caccacaaca tcacctattg gatccaaaac tactcggaag acttgccgcg 420
ggcggtgatt gacgacgct ttgcccgcgc ctctgcactg tggagcgcgg tgacgcgcgt 480
caccttcact cgcgtgtaca gccgggacgc agacatcgtc atccagtttg gtgtcgcgga 540
gcacggagac gggatatcct tcgacgggaa ggacgggctc ctggcacacg cctttcctcc 600
tggccccggc attcaggag acgcccattt cgacgatgac gagttgtggt ccctgggcaa 660
gggcgtcgtg gttccaactc ggtttggaac cgcagatggc gcggcctgcc acttcccctt 720
catcttcgag ggccgctcct actctgcctg caccaccgac ggtcgtctcc acggcttgcc 780
ctggtgcagt accacggcca actacgacac cgacgaccgg tttggcttct gccccagcga 840
gagactctac acccgggacg gcaatgctga tgggaaaccc tgccagtttc cattcatctt 900
ccaaggccaa tctactcgg cctgcaccac ggacggctgc tccgacggct accgctggtg 960
cgccaccacc gccaaactac accgggacaa gctcttcggc ttctgcccga cccgagctga 1020
ctcgacggtg atggggggca actcggcggg ggagctgtgc gtcttccct tcaacttctc 1080
gggtaaggag tactcgacct gtaccagcga gggccgcgga gatgggcgcc tctggtgcgc 1140
taccacctcg aactttgaca gcgacaagaa gtggggcttc tgcccggacc aaggatacag 1200
tttgttctc gtggcggcgc atgagttcgg ccacgcgctg ggcttagatc attcctcagt 1260

```

```

gccggaggcg ctcattgtacc ctatgtaccg cttcactgag gggccccct tgcataagga 1320
cgacgtgaat ggcattccggc acctctatgg tcctcgccct gaacctgagc caccgcctcc 1380
aaccaccacc acaccgcagc ccacggctcc cccgacggtc tgccccaccg gacccccac 1440
tgtccacccc tcagagcgcc ccacagctgg cccacacagg cccccctcag ctggccccac 1500
aggtccccc actgctggcc cttctacggc cactactgtg cctttgagtc cgggtggacga 1560
tgcctgcaac gtgaacatct tcgacgccat cgcggagatt gggaaccagc tgtattttgt 1620
caaggatggg aagtactggc gattctctga gggcaggggg agccggccgc agggcccctt 1680
ccttatcgcc gacaagtggc ccgcgctgcc ccgcaagctg gactcggctt ttgaggagcc 1740
gctctccaag aagcttttct tcttctctgg gcgccagggt tgggtgtaca caggcgcgtc 1800
ggtgctgggc ccgaggcgtc tggacaagct gggcctggga gccgacgtgg ccaggtgac 1860
cggggccctc cggagtggca gggggaagat gctgctgttc agcgggcggc gcctctggag 1920
gttcgacgtg aaggcgca tggtgatcc ccgagcgcc agcgaggtgg accgatgtt 1980
ccccgggtg cctttggaca cgcacgacgt cttccagtac cgagagaaag cctatttctg 2040
ccaggaccgc ttctactggc gcgtgagttc ccgagtgag ttgaaccagg tggaccaagt 2100
gggctacgtg acctatgaca tcctgcagtg ccctgaggac tagggctccc gtcctgcttt 2160
gcagtgccat gtaaatcccc actgggacca accctgggga aggagccagt ttgccggata 2220
caaactggtg ttctgttctg gaggaaggg aggagtgag gtgggctggg ccctctcttc 2280
tcacctttgt tttttgttg agtgtttcta ataaacttgg attctctaac cttt 2334

```

<210> 142

<211> 707

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys
1          5          10          15
Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro
20          25          30
Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
35          40          45
Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
50          55          60
Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
65          70          75          80
Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
85          90          95
Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
100         105         110
Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
115         120         125
Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
130         135         140
Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145         150         155         160
Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
165         170         175
Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
180         185         190
Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
195         200         205
Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
210         215         220
Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225         230         235         240
Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
245         250         255
Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
260         265         270

```

```

Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys
      275      280      285
Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr
      290      295      300
Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr
305      310      315      320
Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
      325      330      335
Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
      340      345      350
Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
      355      360      365
Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
      370      375      380
Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
385      390      395      400
His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
      405      410      415
Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
      420      425      430
Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
      435      440      445
Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
      450      455      460
Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
465      470      475      480
Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
      485      490      495
Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
      500      505      510
Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly
      515      520      525
Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
      530      535      540
Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
545      550      555      560
Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser
      565      570      575
Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
      580      585      590
Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
      595      600      605
Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
      610      615      620
Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
625      630      635      640
Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
      645      650      655
Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
      660      665      670
Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
      675      680      685
Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys
      690      695      700
Pro Glu Asp
705

```

<211> 2217
 <212> DNA
 <213> Homo sapiens

<400> 143
 ggccggccac tcccgtctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60
 cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120
 tcctgtggga cccccgccct cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180
 cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcaccctt ggacggagtc 240
 ctggccaacc cacctaaccat ttccagcctc tcccctcgcc aactccttgg cttcccgtgt 300
 gcggaggtgt ccggcctgag cacggagcgt gtccggggagc tggctgtggc cttggcacag 360
 aagaatgtca agctctcaac agagcagctg cgctgtctgg ctaccggct ctctgagccc 420
 cccgaggacc tggacgccct ccatttggac ctgctgctat tcctcaaccc agatgcgttc 480
 tcggggcccc aggcctgcac ccgtttcttc tcccgcatca cgaaggccaa tgtggacctg 540
 ctcccagggg gggctcccgga gcgacagcgg ctgctgcctg cggctctggc ctgctggggg 600
 gtgcgggggt ctctgctgag cgaggctgat gtgcggggctc tgggaggcct ggcttgcgac 660
 ctgcctgggc gctttgtggc cgagtcggcc gaagtgtctg taccctggct ggtgagctgc 720
 ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
 cccccctacg gccccccgtc gacatggtct gtctccacga tggacgctct gcggggcctg 840
 ctgcccgtgc tgggccagcc catcatccgc agcatccgc agggcatcgt ggccgcgtgg 900
 cggcaacgct cctctcggga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
 cggttcgggc ggaagtggga gaagacagcc tgtccttcag gcaagaaggc ccgcggcata 1020
 gacgagagcc tcattcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
 ctggccaccc agatggaccg cgtgaacgcc atccccctca cctacgagca gctggacgtc 1140
 ctaaagcata aactggatga gctctaccca caaggttacc ccgagtctgt gatccagcac 1200
 ctgggctacc tcttcctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
 ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggct 1320
 cctcggcggc ccctcccaca ggtggccacc ctgatcgacc gctttgtgaa gggaaggggc 1380
 cagctagaca aagacaccct agacaccctg accgccttct accctgggta cctgtgctcc 1440
 ctacgccccg aggagctgag ctccgtgcc ccagcagca tctgggcggc caggccccag 1500
 gacctggaca cgtgtgaccc aaggcagctg gacgtcctct atcccaaggc ccgccttgct 1560
 ttccagaaca tgaacgggtc cgaatacttc gtgaagatcc agtccttctt ggggtggggc 1620
 cccacggagg atttgaaggc gctcagtcag cagaatgtga gcatggactt ggccacgttc 1680
 atgaagctgc ggacggatgc ggtgctgcc ttgactgtgg ctgaggtgca gaaacttctg 1740
 ggacccacag tggagggcct gaaggcggag gagcggcacc gcccggtgcg ggactggatc 1800
 ctacggcagc ggcaggacga cctggacacg ctggggctgg ggctacaggg cggcatcccc 1860
 aacggctacc tggctcctaga cctcagcgtg caaggtgggc ggggcggcca ggccagggct 1920
 gggggcagag ctgggggcgt ggaggtgggc gctctgagtc accctctct ctgtagaggc 1980
 cctctcgggg acgccctgcc tcctaggacc tggacctgtt ctcaccgtcc tggcaactgc 2040
 cctagcctcc accctggcct gagggcccca ctcccttgct ggccccagcc ctgctgggga 2100
 tccccgcctg gccaggagca ggcacgggtg atccccgttc caccccaaga gaactgcgc 2160
 tcagtaaacg ggaacatgcc ccctgcagac acgtaaaaaa aaaaaaaaaa aaaaaaa 2217

<210> 144
 <211> 702
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
 1 5 10 15
 Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
 20 25 30
 Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
 35 40 45
 Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
 50 55 60
 Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
 65 70 75 80

Arg	Val	Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu
				85					90					95	
Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro
			100					105					110		
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro
		115					120					125			
Asp	Ala	Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile
	130					135					140				
Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln
	145				150					155					160
Arg	Leu	Leu	Pro	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu	
				165				170					175		
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu
			180					185					190		
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu
		195					200					205			
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg
	210					215					220				
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp
	225				230					235					240
Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly
				245					250					255	
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg
		260						265					270		
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile
		275					280					285			
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser
	290					295					300				
Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys
	305				310					315					320
Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met
			325					330						335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu
			340					345					350		
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val
		355					360					365			
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile
	370					375					380				
Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu
	385				390					395					400
Val	Asn	Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Ala	Pro	Arg	Arg	Pro	Leu
			405						410					415	
Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp	Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln
			420					425					430		
Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr	Leu	Thr	Ala	Phe	Tyr	Pro	Gly	Tyr
		435					440					445			
Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu	Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser
	450					455					460				
Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp	Leu	Asp	Thr	Cys	Asp	Pro	Arg	Gln
	465				470					475					480
Leu	Asp	Val	Leu	Tyr	Pro	Lys	Ala	Arg	Leu	Ala	Phe	Gln	Asn	Met	Asn
			485					490						495	
Gly	Ser	Glu	Tyr	Phe	Val	Lys	Ile	Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro
		500						505					510		
Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser	Gln	Gln	Asn	Val	Ser	Met	Asp	Leu
		515					520					525			
Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr	Asp	Ala	Val	Leu	Pro	Leu	Thr	Val
	530					535					540				
Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly	Pro	His	Val	Glu	Gly	Leu	Lys	Ala

545		550		555		560
Glu Glu Arg His Arg	Pro Val Arg Asp Trp	Ile Leu Arg Gln Arg	Gln			
	565	570	575			
Asp Asp Leu Asp Thr	Leu Gly Leu Gly	Leu Gln Gly Gly	Ile Pro Asn			
	580	585	590			
Gly Tyr Leu Val Leu	Asp Leu Ser Val	Gln Gly Gly Arg	Gly Gly Gln			
	595	600	605			
Ala Arg Ala Gly Gly	Arg Ala Gly Gly	Val Glu Val Gly	Ala Leu Ser			
	610	615	620			
His Pro Ser Leu Cys	Arg Gly Pro Leu	Gly Asp Ala Leu	Pro Pro Arg			
	625	630	635			640
Thr Trp Thr Cys Ser	His Arg Pro Gly	Thr Ala Pro Ser	Leu His Pro			
	645	650	655			
Gly Leu Arg Ala Pro	Leu Pro Cys Trp	Pro Gln Pro Cys	Trp Gly Ser			
	660	665	670			
Pro Pro Gly Gln Glu	Gln Ala Arg Val	Ile Pro Val Pro	Pro Gln Glu			
	675	680	685			
Asn Ser Arg Ser Val	Asn Gly Asn Met	Pro Pro Ala Asp	Thr			
	690	695	700			

<210> 145
 <211> 2135
 <212> DNA
 <213> Homo sapiens

<400> 145

ggccggccac	tcccgtctgc	tgtgacgcgc	ggacagagag	ctaccggtgg	acccacgggtg	60
cctccctccc	tgggatctac	acagaccatg	gccttgccaa	cggctcgacc	cctggttgggg	120
tctgttgga	ccccgcctt	cggcagcctc	ctgttcctgc	tcttcagcct	cggatgggtg	180
cagccctcga	ggaccctggc	tggagagaca	gggcaggagg	ctgcaccctt	ggacggagtc	240
ctggccaacc	cacctaacat	ttccagcctc	tcccctcgcc	aactccttgg	cttcccgtgt	300
gcggaggtgt	ccggcctgag	cacggagcgt	gtccgggagc	tggctgtggc	cttggcacag	360
aagaatgtca	agctctcaac	agagcagctg	cgctgtctgg	ctcaccggct	ctctgagccc	420
cccagggacc	tggacgcctt	cccattggac	ctgctgctat	tcctcaaccc	agatgcgttc	480
tcggggcccc	aggcctgcac	ccgtttcttc	tcccgcacat	cgaaggccaa	tgtggacctg	540
ctcccagggg	gggctcccga	gcgacagcgg	ctgctgcctg	cggctctggc	ctgctgggggt	600
gtgcgggggt	ctctgctgag	cgaggctgat	gtgcgggctc	tgggaggcct	ggcttgcgac	660
ctgcctgggc	gctttgtggc	cgagtgcggc	gaagtgcctg	taccccggtt	ggtgagctgc	720
ccgggacccc	tggaccagga	ccagcaggag	gcagccaggg	cggctctgca	gggaggggga	780
ccccctacg	gcccccgctc	gacatggtct	gtctccacga	tggacgctct	gcggggcctg	840
ctgcccgtgc	tgggccagcc	catcatccgc	agcatccgcg	agggcatcgt	ggccgcgttg	900
cggcaacget	cctctcgga	cccatacctg	cggcagcctg	aacggaccat	cctccggccg	960
cgttccggc	gggaagtgga	gaagacagcc	tgtccttcag	gcaagaaggc	ccgcgagata	1020
gacgagagcc	tcattctcta	caagaagtgg	gagctggaag	cctgcgtgga	tgcggccctg	1080
ctggccaccc	agatggaccg	cgtgaacgcc	atccccctta	cctacgagca	gctggacgtc	1140
ctaaagcata	aactggatga	gctctaccca	caaggttacc	ccgagtctgt	gatccagcac	1200
ctgggctacc	tcttcctcaa	gatgagocct	gaggacattc	gcaagtggaa	tgtgacgtcc	1260
ctggagaccc	tgaaggcttt	gcttgaagtc	aacaaagggc	acgaaatgag	tcctcaggct	1320
cctcggcggc	ccctcccaca	ggtggccacc	ctgatcgacc	gctttgtgaa	gggaaggggc	1380
cagctagaca	aagacaccct	agacaccctg	accgccttct	accctgggta	cctgtgctcc	1440
ctcagccccg	aggagctgag	ctccgtgccc	cccagcagca	tctgggcggt	caggccccag	1500
gacctggaca	cgtgtgaccc	aaggcagctg	gacgtcctct	atcccaaggc	ccgccttgct	1560
ttccagaaca	tgaacgggtc	cgaatacttc	gtgaagatcc	agtccttctt	gggtggggcc	1620
cccacggagg	atttgaaggc	gctcagtcag	cagaatgtga	gcatggactt	ggccacgttc	1680
atgaagctgc	ggacggatgc	gtgctgcag	ttgactgtgg	ctgaggtgca	gaaacttttc	1740
ggacccacg	tggaggccct	gaaggcggag	gagcggcacc	gcccgggtgc	ggactggatc	1800
ctacggcagc	ggcaggacga	cctggacacg	ctggggctgg	ggctacaggg	cggcatcccc	1860
aacggctacc	tggtcctaga	cctcagcgtg	caagaggccc	tctcggggac	gccctgcctc	1920

```

ctaggacctg gacctgttct caccgtcctg gcactgctcc tagcctocac cctggcctga 1980
gggccccact cccttgctgg cccagccct gctggggatc cccgcctggc caggagcagg 2040
cacgggtgat ccccgttcca cccaagaga actcgcgctc agtaaacggg aacatgcccc 2100
ctgcagacac gtaaaaaaaaa aaaaaaaaaa aaaaa 2135

```

<210> 146
 <211> 630
 <212> PRT
 <213> Homo sapiens

<400> 146

Met	Ala	Leu	Pro	Thr	Ala	Arg	Pro	Leu	Leu	Gly	Ser	Cys	Gly	Thr	Pro
1				5				10						15	
Ala	Leu	Gly	Ser	Leu	Leu	Phe	Leu	Leu	Phe	Ser	Leu	Gly	Trp	Val	Gln
			20					25					30		
Pro	Ser	Arg	Thr	Leu	Ala	Gly	Glu	Thr	Gly	Gln	Glu	Ala	Ala	Pro	Leu
		35					40					45			
Asp	Gly	Val	Leu	Ala	Asn	Pro	Pro	Asn	Ile	Ser	Ser	Leu	Ser	Pro	Arg
	50				55						60				
Gln	Leu	Leu	Gly	Phe	Pro	Cys	Ala	Glu	Val	Ser	Gly	Leu	Ser	Thr	Glu
65					70					75					80
Arg	Val	Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu
				85					90					95	
Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro
			100					105					110		
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro
	115						120					125			
Asp	Ala	Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile
	130					135					140				
Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln
145					150					155					160
Arg	Leu	Leu	Pro	Ala	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu
				165					170					175	
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu
			180					185					190		
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu
	195						200						205		
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg
	210					215					220				
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp
225					230					235					240
Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly
				245					250					255	
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg
		260						265					270		
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile
	275						280					285			
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser
	290					295					300				
Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys
305					310					315					320
Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met
				325					330					335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu
			340					345					350		
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val
	355						360					365			
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile
	370					375						380			

Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu
385					390					395					400
Val	Asn	Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Ala	Pro	Arg	Arg	Pro	Leu
			405						410					415	
Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp	Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln
		420						425					430		
Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr	Leu	Thr	Ala	Phe	Tyr	Pro	Gly	Tyr
	435						440					445			
Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu	Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser
	450					455					460				
Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp	Leu	Asp	Thr	Cys	Asp	Pro	Arg	Gln
465					470					475					480
Leu	Asp	Val	Leu	Tyr	Pro	Lys	Ala	Arg	Leu	Ala	Phe	Gln	Asn	Met	Asn
			485						490					495	
Gly	Ser	Glu	Tyr	Phe	Val	Lys	Ile	Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro
		500						505					510		
Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser	Gln	Gln	Asn	Val	Ser	Met	Asp	Leu
	515						520					525			
Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr	Asp	Ala	Val	Leu	Pro	Leu	Thr	Val
	530					535					540				
Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly	Pro	His	Val	Glu	Gly	Leu	Lys	Ala
545					550					555					560
Glu	Glu	Arg	His	Arg	Pro	Val	Arg	Asp	Trp	Ile	Leu	Arg	Gln	Arg	Gln
			565					570						575	
Asp	Asp	Leu	Asp	Thr	Leu	Gly	Leu	Gly	Leu	Gln	Gly	Gly	Ile	Pro	Asn
		580						585					590		
Gly	Tyr	Leu	Val	Leu	Asp	Leu	Ser	Val	Gln	Glu	Ala	Leu	Ser	Gly	Thr
	595					600						605			
Pro	Cys	Leu	Leu	Gly	Pro	Gly	Pro	Val	Leu	Thr	Val	Leu	Ala	Leu	Leu
	610					615					620				
Leu	Ala	Ser	Thr	Leu	Ala										
625					630										

<210> 147

<211> 2105

<212> DNA

<213> Homo sapiens

<400> 147

```

ggccggccac tcccgtctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60
cctccctccc tgggatctac acagaccatg gccttgccaa cggtctgacc cctgttgagg 120
tcctgtggga ccccgccctc cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180
cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcaccctt ggacggagtc 240
ctggccaacc cacctaacat ttccagcctc tcccctcgcc aactccttgg cttcccgtgt 300
gcggaggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
aagaatgtca agctctcaac agagcagctg cgctgtctgg ctaccggct ctctgagccc 420
cccgaggacc tggacgcctt cccattggac ctgctgctat tcctcaaccc agatgcgttc 480
tcggggcccc aggcctgcac ccgtttcttc tccgcacatc cgaaggccaa tgtggacctg 540
ctcccagagg gggctcccga gcgacagcgg ctgctgcctg cggctctggc ctgctgggggt 600
gtgcgggggg ctctgctgag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660
ctgcctgggc gctttgtggc cgagtcggcc gaagtgcctg taccceggct ggtgagctgc 720
ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
ccccctacg gcccccgctc gacatggtct gtctccacga tggacgctct gcggggcctg 840
ctgcccctgc tgggccagcc catcatccgc agcatccgc agggcatcgt ggccgcgtgg 900
cggcaacgct cctctcggga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
cggttcgggc gggaagtggg gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140

```



```

ctaaagcata aactggatga gctctaccca caaggttacc ccgagtctgt gatccagcac 1200
ctgggctaacc tcttcctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagacccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggct 1320
cctcggcggc ccctcccaca ggtggccacc ctgatcgacc gctttgtgaa gggaaggggc 1380
cagctagaca aagacaccct agacaccctg accgccttct accctgggta cctgtgctcc 1440
ctcagccccg aggagctgag ctccgtgccc cccagcagca tctgggcggg caggccccag 1500
gacctggaca cgtgtgaccc aaggcagctg gacgtcctct atcccaaggc ccgccttgct 1560
ttccagaaca tgaacgggtc cgaatacttc gtgaagatcc agtccttctt ggggtggggcc 1620
cccacggagg atttgaaggc gctcagtcag cagaatgtga gcatggactt ggccacgttc 1680
atgaagctgc ggacggatgc ggtgctgccg ttgactgtgg ctgagggtga gaaacttctg 1740
ggacccccag tggagggcct gaaggcggag gacgggcacc gcccggtgcg ggactggatc 1800
ctacggcagc ggcaggacga cctggacacg ctggggctgg ggctacaggg cggcattccc 1860
aacggctacc tggtcctaga cctcagcgtg caaggacctg gacctgttct caccgtcctg 1920
gcactgctcc tagcctccac cctggcctga gggccccact cccttgctgg ccccagccct 1980
gctggggatc cccgcctggc caggagcagg cacgggtgat ccccgttcca cccaagaga 2040
actcgcgctc agtaaacggg aacatgcccc ctgcagacac gtaaaaaaaaa aaaaaaaaaa 2100
aaaaa 2105

```

<210> 148

<211> 620

<212> PRT

<213> Homo sapiens

<400> 148

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
 1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
          20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
          35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
          50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
          65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
          85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
          100          105          110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
          115          120          125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
          130          135          140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
          145          150          155          160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
          165          170          175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
          180          185          190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
          195          200          205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
          210          215          220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
          225          230          235          240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
          245          250          255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
          260          265          270
Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile

```

275	280	285
Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser		
290	295	300
Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys		
305	310	315
Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met		
325	330	335
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu		
340	345	350
Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val		
355	360	365
Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile		
370	375	380
Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu		
385	390	395
Val Asn Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu		
405	410	415
Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln		
420	425	430
Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr		
435	440	445
Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser		
450	455	460
Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln		
465	470	475
Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn		
485	490	495
Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro		
500	505	510
Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu		
515	520	525
Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val		
530	535	540
Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala		
545	550	555
Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln		
565	570	575
Asp Asp Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn		
580	585	590
Gly Tyr Leu Val Leu Asp Leu Ser Val Gln Gly Pro Gly Pro Val Leu		
595	600	605
Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala		
610	615	620

<210> 149

<211> 2193

<212> DNA

<213> Homo sapiens

<400> 149

```

ggccggccac tcccgctctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60
cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120
tctgttggga ccccgccct cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180
cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcaccctt ggacggagtc 240
ctggccaacc cacctaacat ttccagcctc tcccctcgcc aactccttgg cttcccggtg 300
gcggaggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
aagaatgtca agctctcaac agagcagctg cgctgtctgg ctcaccggct ctctgagccc 420
cccgaggacc tggacgccct cccattggac ctgctgctat tcctcaacc agatgcgttc 480

```

```

tcggggcccc aggcctgcac ccgtttcttc tcccgcata cgaaggccaa tgtggacctg 540
ctcccagagg gggctcccga gcgacagcgg ctgctgcctg cggctctggc ctgctggggg 600
gtgcgggggt ctctgctgag cgaggctgat gtgcggggtc tgggaggcct ggcttgcgac 660
ctgcctgggc gctttgtggc cgagtcggcc gaagtgtgtc taccocggct ggtgagctgc 720
ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
ccccctacg gcccccgctc gacatggtct gtctccacga tggacgtctc gcggggcctg 840
ctgcccgtgc tgggccagcc catcatccgc agcatccgc agggcatcgt ggccgcgtgg 900
cggcaacgct cctctcggga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
cggttccggc gggaagtggg gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
ctggccaccc agatggaccg cgtgaacgcc atccccctca cctacgagca gctggacgtc 1140
ctaaagcata aactggatga gctctaccca caaggttacc cggagtctgt gatccagcac 1200
ctgggctacc tcttcctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagaccc tgaaggcttt gctgaagtc aacaaagggc acgaaatgag tcctcaggtg 1320
gccaccctga tcgaccgctt tgtgaaggga aggggccagc tagacaaaga caccctagac 1380
accctgaccg ccttctaccc tgggtacctg tgcctccctc gccccgagga gctgagctcc 1440
gtgcccccca gcagcatctg ggcggtcagg ccccaggacc tggacacgtg tgaccaagg 1500
cagctggacg tctctatcc caaggcccg cttgctttcc agaactgaa cgggtccgaa 1560
tacttcgtga agatccagtc cttcctgggt ggggccccca cggaggattt gaaggcgctc 1620
agtgcagca atgtgagcat ggacttgcc acgttcatga agctgcggac ggatgcgggtg 1680
ctgcccgtga ctgtggctga ggtgcagaaa cttctgggac cccacgtgga gggcctgaag 1740
goggaggagc ggcaccgccc ggtgcgggac tggatcctac ggcagcggca ggacgacctg 1800
gacacgctgg ggtggggct acagggcggc atccccaaag gctacctggt cctagacctc 1860
agcgtgcaag gtgggcgggg cggccaggcc agggctgggg gcagagctgg gggcgtggag 1920
gtgggcgctc tgagtcaccc ctctctctgt agaggccctc tcggggacgc cctgcctcct 1980
aggacctgga cctgttctca ccgtcctggc actgctccta gcctocaccc tggcctgagg 2040
gccccactcc cttgctggcc ccagccctgc tggggatccc cgccctggca ggagcaggca 2100
cgggtgatcc ccgttccacc ccaagagaac tcgcgctcag taaacgggaa catgccccct 2160
gcagacacgt aaaaaaaaaa aaaaaaaaaa aaa 2193

```

<210> 150

<211> 694

<212> PRT

<213> Homo sapiens

<400> 150

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
100         105         110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
115         120         125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
130         135         140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
145         150         155         160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
165         170         175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu

```

Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu
		195					200					205			
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg
	210					215					220				
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp
225					230					235					240
Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly
				245					250					255	
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg
			260					265					270		
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile
		275					280					285			
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser
	290					295					300				
Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys
305					310					315					320
Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met
			325					330						335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu
			340					345					350		
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val
		355					360					365			
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile
	370					375					380				
Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu
385					390					395					400
Val	Asn	Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp
			405					410						415	
Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln	Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr
			420					425					430		
Leu	Thr	Ala	Phe	Tyr	Pro	Gly	Tyr	Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu
		435				440						445			
Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser	Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp
	450					455					460				
Leu	Asp	Thr	Cys	Asp	Pro	Arg	Gln	Leu	Asp	Val	Leu	Tyr	Pro	Lys	Ala
465				470						475					480
Arg	Leu	Ala	Phe	Gln	Asn	Met	Asn	Gly	Ser	Glu	Tyr	Phe	Val	Lys	Ile
			485					490						495	
Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser
			500					505					510		
Gln	Gln	Asn	Val	Ser	Met	Asp	Leu	Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr
		515				520						525			
Asp	Ala	Val	Leu	Pro	Leu	Thr	Val	Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly
	530														

Trp Pro Gln Pro Cys Trp Gly Ser Pro Pro Gly Gln Glu Gln Ala Arg
 660 665 670
 Val Ile Pro Val Pro Pro Gln Glu Asn Ser Arg Ser Val Asn Gly Asn
 675 680 685
 Met Pro Pro Ala Asp Thr
 690

<210> 151
 <211> 2081
 <212> DNA
 <213> Homo sapiens

<400> 151
 ggccggccac tcccgctctgc tgtgacgcgc ggacagagag ctaccgggtgg acccacgggtg 60
 cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120
 tcctgtggga ccccgccct cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180
 cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcacccct ggacggagtc 240
 ctggccaacc cacctaacat ttccagcctc tcccctcgcc aactccttgg cttcccgtgt 300
 gcggaggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
 aagaatgtca agctctcaac agagcagctg cgctgtctgg ctaccggct ctctgagccc 420
 ccgaggacc tggacgcct cccattggac ctgctgctat tctcaaccc agatgcgttc 480
 tgggggcccc aggcctgcac ccgtttcttc tccgcacatca cgaaggccaa tgtggacctg 540
 ctcccgaggg gggctcccga gcgacagcgg ctgctgcctg cggctctggc ctgctgggg 600
 gtgcggggggt ctctgctgag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660
 ctgectgggc gctttgtggc cgagtcggcc gaagtgtctg taccocggct ggtgagctgc 720
 ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
 cccccctacg gccccccgct gacatggtct gtctccacga tggacgtctt gcggggcctg 840
 ctgcccgtgc tgggccagcc catcatccgc agcatcccgc agggcatcgt ggccgcgtgg 900
 cggcaacyct cctctcgga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
 cggttccggc gggaagtggga gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
 gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
 ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140
 ctaaagcata aactggatga gctctaccca caaggttacc ccgagtctgt gatccagcac 1200
 ctgggctaoc tcttctccta gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
 ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tctcaggtg 1320
 gccaccctga tgcaccgctt tgtgaaggga aggggccagc tagacaaaga caccctagac 1380
 accctacagg ccttctaccc tgggtacctg tgctccctca gcccogagga gctgagctcc 1440
 gtgcccccca gcagcatctg ggcggtcagg ccccaggacc tggacacgtg tgaccacaagg 1500
 cagctggagc tctctatcc caaggccgc cttgctttcc agaacatgaa cgggtccgaa 1560
 tacttcgtga agatccagtc cttcctgggt ggggccccca cggaggattt gaaggcgctc 1620
 agtcagcaga atgtgagcat ggacttggcc acgttcatga agctgcggac ggatgcgggtg 1680
 ctgcccgttga ctgtggctga ggtgcagaaa cttctgggac cccacgtgga gggcctgaag 1740
 gcggaggagc ggcaccgccc ggtgcgggac tggatcctac ggcagcggca ggacgacctg 1800
 gacacgtctg ggtggggct acagggcggc atcccacacg gctacctggt cctagacctc 1860
 agcgtgcaag gacctggacc tgttctcacc gtcttggcac tgctcctagc ctccaccctg 1920
 gcctgagggc ccactccct tgctggcccc agccctgctg gggatccccg cctggccagg 1980
 agcaggcaag ggtgatcccc gttccacccc aagagaactc gcgtcagta aacgggaaca 2040
 tgccccctgc agacacgtaa aaaaaaaaaa aaaaaaaaaa a 2081

<210> 152
 <211> 612
 <212> PRT
 <213> Homo sapiens

<400> 152
 Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
 1 5 10 15
 Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln

Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser
			500					505					510		
Gln	Gln	Asn	Val	Ser	Met	Asp	Leu	Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr
		515					520					525			
Asp	Ala	Val	Leu	Pro	Leu	Thr	Val	Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly
	530					535					540				
Pro	His	Val	Glu	Gly	Leu	Lys	Ala	Glu	Glu	Arg	His	Arg	Pro	Val	Arg
545					550					555					560
Asp	Trp	Ile	Leu	Arg	Gln	Arg	Gln	Asp	Asp	Leu	Asp	Thr	Leu	Gly	Leu
			565					570						575	
Gly	Leu	Gln	Gly	Gly	Ile	Pro	Asn	Gly	Tyr	Leu	Val	Leu	Asp	Leu	Ser
		580						585					590		
Val	Gln	Gly	Pro	Gly	Pro	Val	Leu	Thr	Val	Leu	Ala	Leu	Leu	Leu	Ala
	595						600					605			
Ser	Thr	Leu	Ala												
			610												

<210> 153
 <211> 2111
 <212> DNA
 <213> Homo sapiens

<400> 153
 ggccggccac tcccggtctgc tgtgacgcgc ggacagagag ctaccgggtgg acccacgggtg 60
 cctccctccc tgggatctac acagaccatg gccttgccaa cggtctgacc cctggtgggg 120
 tctgtgga ccccgccct cggcagcctc ctgttctctgc tcttcagcct cggatgggtg 180
 cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcacccct ggacggagtc 240
 ctggccaacc cacctaaccat ttccagcctc tcccctcgcc aactccttgg cttcccggtg 300
 gcggaggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
 aagaatgtca agctctcaac agagcagctg cgctgtctgg ctacccggct ctctgagccc 420
 cccgaggacc tggacgcct cccattggac ctgctgctat tctcaaccc agatgcgttc 480
 tcggggcccc aggcctgcac ccgtttcttc tcccgcatca cgaaggccaa tgtggacctg 540
 ctcccgaggg gggtcccca ggcacagcgg ctgctgcctg cggctctggc ctgctgggg 600
 gtgcgggggt ctctgctgag cgaggtgat gtgcgggctc tgggaggcct ggcttgcgac 660
 ctgctgggc gcttctgtggc cgagtcggcc gaagtgtgc taccctggct ggtgagctgc 720
 ccgggacccc tggaccagga ccagcaggg gcagccagg cggtctgca gggcggggga 780
 cccccctacg gcccccgctc gacatggtct gtctccacga tggacgctct gcggggcctg 840
 ctgcccgtgc tgggccagcc catcatccgc agcatccgc agggcatcgt ggccgcgtgg 900
 cggcaacgct cctctcgga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
 cgggtccggc gggaagtga gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
 gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
 ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140
 ctaaagcata aactggatga gctctacca caaggttacc ccgagtctgt gatccagcac 1200
 ctgggtacc tcttctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
 ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tctcaggtg 1320
 gccaccctga tcgacgctt tgtgaaggga aggggccagc tagacaaaga caccctagac 1380
 accctgaccg ccttctaccc tgggtacctg tgtccttca gccccgagga gctgagctcc 1440
 gtgccccca gcagcatctg ggcggtcagg cccagacc tggacacgtg tgacccaagg 1500
 cagctggacg tctctatcc caaggcccg cttgctttcc agaactgaa cgggtccgaa 1560
 tacttctgta agatccagtc ctctctgggt ggggccccca cggaggattt gaaggcgtc 1620
 agtcagcaga atgtgagcat ggacttggcc acgttcatga agctgcggac ggatgcggtg 1680
 ctgccgttga ctgtggctga ggtgcagaaa cttctgggac cccacgtgga gggcctgaag 1740
 gcggaggagc ggcaccgccc ggtgcgggac tggatcctac ggcagcggca ggacgacctg 1800
 gacagcgtg agctggggt acaggcgcc atcccaacg gctacctggt cctagacctc 1860
 agcgtgcaag aggcctctc ggggacgccc tgcctcctag gacctggacc tgttctcacc 1920
 gtcttggcac tgcctctagc ctccaacctg gcctgagggc cccactccct tgcctggccc 1980
 agccctgctg gggatcccc cctggccagg agcaggcac ggtgatcccc gttccacccc 2040
 aagagaactc gcgctcagta aacgggaaca tgccccctgc agacacgtaa aaaaaaaaaa 2100

aaaaaaaaa a

2111

<210> 154

<211> 622

<212> PRT

<213> Homo sapiens

<400> 154

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
 1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
 20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
 35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
 50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
 65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
 85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
100          105          110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
115          120          125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
130          135          140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
145          150          155          160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
165          170          175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
180          185          190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
195          200          205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
210          215          220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
225          230          235          240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
245          250          255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
260          265          270
Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile
275          280          285
Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser
290          295          300
Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys
305          310          315          320
Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met
325          330          335
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu
340          345          350
Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val
355          360          365
Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile
370          375          380
Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu
385          390          395          400
Val Asn Lys Gly His Glu Met Ser Pro Gln Val Ala Thr Leu Ile Asp

```


<400>	155						
gaattccctg	gctgcttgaa	tctgtttctgc	cccccccca	cccatttcac	caccaccatg	60	
acaccgggca	cccagttctcc	tttctttcctg	ctgctgctcc	tcacagtgct	tacagttggt	120	
acaggttctg	gtcatgcaag	ctctacccca	ggtggagaaa	aggagacttc	ggctaccagg	180	
agaagttcag	tgcccagctc	tactgagaag	aatgctgtga	gtatgaccag	cagcgtactc	240	
tccagccaca	gccccgggtc	aggctctctc	accactcagg	gacaggatgt	cactctggcc	300	
ccggccacgg	aaccagcttc	aggttcagct	gccacctggg	gacaggatgt	cacctcggtc	360	
ccagtcacca	ggccagccct	gggtctcacc	accccggcag	cccacgatgt	cacctcagcc	420	
ccggacaaca	agccagcccc	gggtctcacc	gcccccccag	cccacgggtg	cacctcggcc	480	
ccggacacca	ggccgcccc	gggtctcacc	gcccccccag	cccacgggtg	cacctcggcc	540	
ccggacacca	ggccgcccc	gggtctcacc	gcccccccag	cccacgggtg	cacctcggcc	600	
ccggacacca	ggccgcccc	gggtctcacc	gcccccccag	cccacgggtg	cacctcggcc	660	
ccggacaaca	ggcccgccct	gggtctcacc	gcccccccag	cccacgggtg	cacctcggcc	720	
tcaggctctg	catcaggctc	agcttctact	ctggtgcaca	acggcacctc	tgccagggtct	780	
accacaaccc	cagccagcaa	gagcaactca	ttctcaattc	ccagccacca	ctctgatact	840	
cctaccaccc	ttgccagcca	tagcaaccaag	actgatgcca	gtagcactca	ccatagcacg	900	
gtacctctct	tcacctctct	caatcacagc	acttctcccc	agttgtctac	tgggggtctct	960	
ttcttttttc	tgtctttttc	catttcaaac	ctccagttta	attcctctct	ggaagatccc	1020	
agcaccgact	actaccaaga	gctgcagaga	gacatttctg	aaatgttttt	gcagattttat	1080	
aaacaagggg	gtttttctggg	cctctccaat	attaagttca	ggccagggatc	tgtgggtggt	1140	
caattgactc	tggccttcgc	agaaggtacc	atcaatgtcc	acgacgtgga	gacacagttc	1200	
aatcagtata	aaaccggaag	agcctctcga	tataacctga	cgatctcaga	cgtcagcgtg	1260	
agtcatgtgc	catttccctt	ctctgccag	tctggggctg	gggtgccagg	ctggggccatc	1320	
gcgctgctgg	tgctgggtctg	tggtctgggt	gcgctggcca	ttgtctatct	cattggccttg	1380	
gctgtctgtc	agtgccgcgc	aaagaactac	gggcagctgg	acatcttttc	agcccgggat	1440	

```

acctaccatc ctatgagcga gtaccccacc taccacaccc atggggcgcta tgtgccccct 1500
agcagtaccg atcgtagccc ctatgagaag gtttctgcag gtaatgggtgg cagcagcctc 1560
tcttacacaa acccagcagt ggcagccact tctgccaact tgtaggggca cgtcgccctc 1620
tgagctgagt ggccagccag tgccattcca ctccactcag ggctctctgg gccagtcctc 1680
ctgggagccc ccaccacaac acttcccagg catggaattc c 1721

```

<210> 156

<211> 515

<212> PRT

<213> Homo sapiens

<400> 156

```

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
 1          5          10          15
Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20          25          30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35          40          45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50          55          60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65          70          75          80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85          90          95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100          105          110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
115          120          125
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
130          135          140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145          150          155          160
Ala Pro Asp Thr Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His
165          170          175
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
180          185          190
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
195          200          205
Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser
210          215          220
Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
225          230          235          240
Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
245          250          255
His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
260          265          270
Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
275          280          285
Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
290          295          300
Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
305          310          315          320
Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
325          330          335
Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
340          345          350
Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
355          360          365
Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr

```

370		375		380
Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser				
385		390		395
Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val				400
	405		410	415
Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala				
	420		425	430
Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg				
	435		440	445
Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His				
	450		455	460
Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro				
465		470		475
Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn				
	485		490	495
Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser				
	500		505	510
Ala Asn Leu				
515				

<210> 157
 <211> 4139
 <212> DNA
 <213> Homo sapiens

<400> 157
 ccgctccacc tctcaagcag ccagcgcctg cctgaatctg ttctgcccc tccccaccca 60
 tttcaccacc accatgacac cgggcaccca gtctcctttc ttctgctgc tgctcctcac 120
 agtgcttaca gttgttacag gttctgggtc tgcaagctct accccaggtg gagaaaagga 180
 gacttcggct acccagagaa gttcagtgcc cagctctact gagaagaatg ctgtgagtat 240
 gaccagcagc gtactctcca gccacagccc cggttcaggc tcctccacca ctcagggaca 300
 ggatgtcact ctggccccgg ccacggaacc agcttcaggt tcagctgcca cctggggaca 360
 ggatgtcacc tcgggtccag tcaccaggcc agccctgggc tccaccacc cgcagccca 420
 cgatgtcacc tcagccccgg acaacaagcc agccccgggc tccaccgcc cccagccca 480
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 540
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 600
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 660
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 720
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 780
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 840
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 900
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 960
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1020
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1080
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1140
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1200
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1260
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1320
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1380
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1440
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1500
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1560
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1620
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1680
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1740
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1800
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1860
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgcc cccagccca 1920

```

cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1980
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2040
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2100
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2160
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2220
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2280
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2340
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2400
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2460
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2520
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2580
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2640
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2700
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2760
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2820
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2880
tggtgtcacc tgggccccgg acaacaggcc cgccttgggc tccaccgccc ctccagtcca 2940
caatgtcacc tgggccccgg gctctgcatc aggtcagct tctactctgg tgcacaacgg 3000
cacctctgcc agggctacca caaccccagc cagcaagagc actccattct caattcccag 3060
ccaccactct gatactccta ccaccttgc cagccatagc accaagactg atgccagtag 3120
cactcactct agctcggtag ctctctcac ctctccaat cacagcactt ctcccagtt 3180
gtctactggg gtctctttct ttttctgtc ttttcacatt tcaaacctoc agtttaattc 3240
ctctctggaa gatccagca ccgactacta ccaagagctg cagagagaca tttctgaaat 3300
gtttttgcag atttataaac aagggggttt tctgggcctc tccaatatta agttcaggcc 3360
aggatctgtg gtggtacaat tgactctggc cttccgagaa ggtaccatca atgtccacga 3420
cgtggagaca cagttcaatc agtataaaac ggaagcagcc tctcgatata acctgacgat 3480
ctcagacgtc agcgtgagtg atgtgccatt tcctttctct gccagttctg gggctgggg 3540
gccaggctgg ggcacgcgc tgctggtgct ggtctgtgtt ctggttgccg tggccattgt 3600
ctatctcatt gccttggctg tctgtcagtg ccgccgaaag aactacgggc agctggacat 3660
ctttccagcc cgggatacct accatcctat gagcgagtac ccacctacc acacccatgg 3720
gcgctatgtg cccoctagca gtaccgatcg tagccctat gagaagggtt ctgcaggtaa 3780
cgggtggcagc agcctctctt acacaaaccc agcagtgcca gccgttctg ccaacttgta 3840
gggcacgtcg ccgctgagct gaggggccag ccagtgccat tccactccac tcaggttctt 3900
caggccagag cccctgcacc ctgtttgggc tgggtgagct ggagttcagg tgggctgctc 3960
acagcctcct tcagaggccc caccaatttc tcggacactt ctcagtggtg ggaagctcat 4020
gtgggccccct gaggtcatg cctgggaagt gttgtggggg ctcccaggag gactggccca 4080
gagagccctg agatagcggg gatcctgaac tggactgaat aaaacgtggt ctcccactg 4139

```

<210> 158

<211> 1255

<212> PRT

<213> Homo sapiens

<400> 158

```

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
 1          5          10          15
Val Leu Thr Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20          25          30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35          40          45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50          55          60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65          70          75          80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85          90          95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100          105          110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro

```

		115					120					125					
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	130					135					140						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		
145					150					155					160		
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His		
				165				170						175			
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala		
		180					185					190					
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro		
	195					200					205						
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	210					215					220						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		
225					230					235					240		
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His		
				245				250						255			
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala		
		260					265					270					
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro		
	275					280					285						
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	290					295					300						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		
305					310					315					320		
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His		
				325				330						335			
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala		
		340					345					350					
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro		
	355					360					365						
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	370					375					380						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		
385					390					395					400		
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His		
				405				410						415			
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala		
		420					425					430					
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro		
	435					440					445						
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	450					455					460						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		
465					470					475					480		
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His		
				485				490						495			
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala		
		500					505					510					
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro		
	515					520					525						
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr		
	530					535					540						
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser		
545					550					555					560		
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His		
				565				570						575			
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala		
		580					585					590					

Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		595					600					605			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
	610					615					620				
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
625					630					635					640
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				645					650					655	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			660					665					670		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
			675				680					685			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
	690					695					700				
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
705					710					715					720
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				725					730					735	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			740					745					750		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
			755				760					765			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
	770					775					780				
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
785					790					795					800
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				805					810					815	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			820					825					830		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
			835				840					845			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
	850					855					860				
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
865					870					875					880
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				885					890					895	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			900					905					910		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
			915				920					925			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn
	930					935					940				
Arg	Pro	Ala	Leu	Gly	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser
945					950					955					960
Ala	Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	Val	His	Asn	Gly
			965						970					975	
Thr	Ser	Ala	Arg	Ala	Thr	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe
			980					985					990		
Ser	Ile	Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His
		995					1000					1005			
Ser	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Ser	Val	Pro	Pro
	1010					1015					1020				
Leu	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val
1025					1030					1035					1040
Ser	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser
				1045					1050					1055	
Ser	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu	Leu	Gln	Arg	Asp

1060	1065	1070
Ile Ser Glu Met Phe Leu Gln	Ile Tyr Lys Gln Gly Gly	Phe Leu Gly
1075	1080	1085
Leu Ser Asn Ile Lys Phe Arg	Pro Gly Ser Val Val Val	Gln Leu Thr
1090	1095	1100
Leu Ala Phe Arg Glu Gly Thr	Ile Asn Val His Asp Val	Glu Thr Gln
1105	1110	1115
Phe Asn Gln Tyr Lys Thr	Glu Ala Ala Ser Arg Tyr	Asn Leu Thr Ile
1125	1130	1135
Ser Asp Val Ser Val Ser Asp	Val Pro Phe Pro Phe Ser	Ala Gln Ser
1140	1145	1150
Gly Ala Gly Val Pro Gly Trp	Gly Ile Ala Leu Leu Val	Leu Val Cys
1155	1160	1165
Val Leu Val Ala Leu Ala Ile	Val Tyr Leu Ile Ala Leu	Ala Val Cys
1170	1175	1180
Gln Cys Arg Arg Lys Asn Tyr	Gly Gln Leu Asp Ile Phe	Pro Ala Arg
1185	1190	1195
Asp Thr Tyr His Pro Met Ser	Glu Tyr Pro Thr Tyr His	Thr His Gly
1205	1210	1215
Arg Tyr Val Pro Pro Ser Ser	Thr Asp Arg Ser Pro Tyr	Glu Lys Val
1220	1225	1230
Ser Ala Gly Asn Gly Gly Ser	Ser Leu Ser Tyr Thr Asn	Pro Ala Val
1235	1240	1245
Ala Ala Ala Ser Ala Asn Leu		
1250	1255	

<210> 159

<211> 2627

<212> DNA

<213> Homo sapiens

<400> 159

```

gctgacgcct tccgagcgcgg cccggggggccc ggagcgggccg gagcagcccg ggtcctgacc 60
ccggcccggc tcccgtctccg ggctctgccg gcgggcgggc gagcgcggcg cggctccgggc 120
cggggggatg tctcggcgga cgcgctgcga ggatctggat gagctgcaact accaggacac 180
agattcagat gtgccggagc agaggggatag caagtgcagg gtcaaattgga cccatgagga 240
ggacgagcag ctgagggccc tggtagggca gtttgacag caggactgga agttcctggc 300
cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360
tccagacctt gtcaaggggc catggaccaa agaggaagac caaaaagtca tcgagctggg 420
taagaagtat ggcacaaagc agtggacact gattgccaag cacctgaagg gccggctggg 480
gaagcagtg cgtgaacgct ggcacaacca cctcaaccct gaggtgaaga agtcttgctg 540
gaccgaggag gaggaccgca tcatctgcga ggcccacaag gtgctgggca accgctgggc 600
cgagatcgcc aagatgttgc cagggaggac agacaatgct gtgaagaatc actggaactc 660
taccatcaaa aggaaggtgg acacaggagg cttcttgagc gagtccaaag actgcaagcc 720
cccagtgtac ttgctgctgg agctcgagga caaggacggc ctccagagtg cccagcccac 780
ggaaggccag ggaagtcttc tgaccaactg gccctccgtc cctcctacca taaaggagga 840
ggaaaacagt gaggaggaac ttgcagcagc caccacatcg aaggaacagg agcccatcgg 900
tacagatctg gacgcagtg gaacaccaga gcccttgag gaattcccga agcgtgagga 960
ccaggaaggc tccccaccag aaacgagcct gccttacaag tgggtgggtg aggcagctaa 1020
cctcctcctc cccgtgtgg gttctagcct ctctgaagcc ctggacttga tcgagtcgga 1080
ccctgatgct tgggtgtgacc tgagtaaatt tgacctccct gaggaaccat ctgcagagga 1140
cagtatcaac aacagcctag tgcagctgca agcgtcacat cagcagcaag tcctgccacc 1200
ccgccagcct tccgccttg tgcaccagtgt gaccgagtac cgcttgatg gccacaccat 1260
ctcagacctg agccggagca gccggggcg gctgatcccc atctcccca gcaactgaagt 1320
cgggggctct ggcattggca caccgcctc tgtgtctcaag cggcagagga agaggcgtgt 1380
ggctctgtcc cctgtcactg agaatagcac cagtctgtcc ttcctggatt cctgtaaacg 1440
cctcacgccc aagagcacac ctgttaagac cctgcccttc tcgccctccc agttttctgaa 1500
cttctggaac aaacaggaca cattggagct ggagagcccc tcgctgacat ccacccagct 1560

```

```

gtgcagccag aaggtggtgg tcaccacacc actgcaccgg gacaagacac ccctgcacca 1620
gaaacatgct gcgtttgtaa cccagatca gaagtactcc atggacaaca ctccccacac 1680
gccaaccccg ttcaagaacg ccctggagaa gtacggaccc ctgaagcccc tgccacagac 1740
cccgcacctg gaggaggact tgaaggaggt gctgcgttct gaggctggca tgaactcat 1800
catcgaggac gacatcaggc ccgagaagca gaagaggaag cctgggctgc ggcggagccc 1860
catcaagaaa gtccggaagt ctctggctct tgacattgtg gatgaggatg tgaagctgat 1920
gatgtccaca ctgcccaagt ctctatcctt gccgacaact gccccttcaa actcttccag 1980
cctcaccttg tcaggatatca aagaagacaa cagcttgctc aaccagggtt tcttgcaggc 2040
caagccccgag aaggcagcag tggcccagaa gccccgaagc cacttcacga cacctgcccc 2100
tatgtccagt gcctggaaga cgggtggcctg cggggggacc agggaccagc ttttcatgca 2160
ggagaaagcc cggcagctcc tgggcccgcct gaagcccagc cacacatctc ggacctcat 2220
cttgtcctga ggtgttgagg gtgtcacgag ccattctca tgtttacagg ggttgtgggg 2280
gcagaggggg tctgtgaatc tgagagtcac tcaggtgacc tcctgcaggg agccttctgc 2340
caccagcccc tccccagact ctcaggtgga ggcaacaggg ccatgtgctg ccctgttgcc 2400
gagcccagct gtgggcggct cctgggtgcta acaacaaagt tccacttcca ggtctgcctg 2460
gttccctccc caaggccaca gggagctccg tcagcttctc ccaagccac gtcaggcctg 2520
gcctcatctc agaccctgct taggatgggg gatgtggcca ggggtgctcc tgtgctcacc 2580
ctctcttggt gcattttttt ggaagaataa aattgcctct ctctttg 2627

```

<210> 160

<211> 700

<212> PRT

<213> Homo sapiens

<400> 160

```

Met Ser Arg Arg Thr Arg Cys Glu Asp Leu Asp Glu Leu His Tyr Gln
 1          5          10          15
Asp Thr Asp Ser Asp Val Pro Glu Gln Arg Asp Ser Lys Cys Lys Val
          20          25          30
Lys Trp Thr His Glu Glu Asp Glu Gln Leu Arg Ala Leu Val Arg Gln
          35          40          45
Phe Gly Gln Gln Asp Trp Lys Phe Leu Ala Ser His Phe Pro Asn Arg
          50          55          60
Thr Asp Gln Gln Cys Gln Tyr Arg Trp Leu Arg Val Leu Asn Pro Asp
65          70          75          80
Leu Val Lys Gly Pro Trp Thr Lys Glu Glu Asp Gln Lys Val Ile Glu
          85          90          95
Leu Val Lys Lys Tyr Gly Thr Lys Gln Trp Thr Leu Ile Ala Lys His
          100          105          110
Leu Lys Gly Arg Leu Gly Lys Gln Cys Arg Glu Arg Trp His Asn His
          115          120          125
Leu Asn Pro Glu Val Lys Lys Ser Cys Trp Thr Glu Glu Glu Asp Arg
          130          135          140
Ile Ile Cys Glu Ala His Lys Val Leu Gly Asn Arg Trp Ala Glu Ile
          145          150          155          160
Ala Lys Met Leu Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Trp
          165          170          175
Asn Ser Thr Ile Lys Arg Lys Val Asp Thr Gly Gly Phe Leu Ser Glu
          180          185          190
Ser Lys Asp Cys Lys Pro Pro Val Tyr Leu Leu Leu Glu Leu Glu Asp
          195          200          205
Lys Asp Gly Leu Gln Ser Ala Gln Pro Thr Glu Gly Gln Gly Ser Leu
          210          215          220
Leu Thr Asn Trp Pro Ser Val Pro Pro Thr Ile Lys Glu Glu Glu Asn
          225          230          235          240
Ser Glu Glu Glu Leu Ala Ala Ala Thr Thr Ser Lys Glu Gln Glu Pro
          245          250          255
Ile Gly Thr Asp Leu Asp Ala Val Arg Thr Pro Glu Pro Leu Glu Glu
          260          265          270

```


Phe Pro Lys Arg Glu Asp Gln Glu Gly Ser Pro Pro Glu Thr Ser Leu
 275 280 285
 Pro Tyr Lys Trp Val Val Glu Ala Ala Asn Leu Leu Ile Pro Ala Val
 290 295 300
 Gly Ser Ser Leu Ser Glu Ala Leu Asp Leu Ile Glu Ser Asp Pro Asp
 305 310 315 320
 Ala Trp Cys Asp Leu Ser Lys Phe Asp Leu Pro Glu Glu Pro Ser Ala
 325 330 335
 Glu Asp Ser Ile Asn Asn Ser Leu Val Gln Leu Gln Ala Ser His Gln
 340 345 350
 Gln Gln Val Leu Pro Pro Arg Gln Pro Ser Ala Leu Val Pro Ser Val
 355 360 365
 Thr Glu Tyr Arg Leu Asp Gly His Thr Ile Ser Asp Leu Ser Arg Ser
 370 375 380
 Ser Arg Gly Glu Leu Ile Pro Ile Ser Pro Ser Thr Glu Val Gly Gly
 385 390 395 400
 Ser Gly Ile Gly Thr Pro Pro Ser Val Leu Lys Arg Gln Arg Lys Arg
 405 410 415
 Arg Val Ala Leu Ser Pro Val Thr Glu Asn Ser Thr Ser Leu Ser Phe
 420 425 430
 Leu Asp Ser Cys Asn Ser Leu Thr Pro Lys Ser Thr Pro Val Lys Thr
 435 440 445
 Leu Pro Phe Ser Pro Ser Gln Phe Leu Asn Phe Trp Asn Lys Gln Asp
 450 455 460
 Thr Leu Glu Leu Glu Ser Pro Ser Leu Thr Ser Thr Pro Val Cys Ser
 465 470 475 480
 Gln Lys Val Val Val Thr Thr Pro Leu His Arg Asp Lys Thr Pro Leu
 485 490 495
 His Gln Lys His Ala Ala Phe Val Thr Pro Asp Gln Lys Tyr Ser Met
 500 505 510
 Asp Asn Thr Pro His Thr Pro Thr Pro Phe Lys Asn Ala Leu Glu Lys
 515 520 525
 Tyr Gly Pro Leu Lys Pro Leu Pro Gln Thr Pro His Leu Glu Glu Asp
 530 535 540
 Leu Lys Glu Val Leu Arg Ser Glu Ala Gly Ile Glu Leu Ile Ile Glu
 545 550 555 560
 Asp Asp Ile Arg Pro Glu Lys Gln Lys Arg Lys Pro Gly Leu Arg Arg
 565 570 575
 Ser Pro Ile Lys Lys Val Arg Lys Ser Leu Ala Leu Asp Ile Val Asp
 580 585 590
 Glu Asp Val Lys Leu Met Met Ser Thr Leu Pro Lys Ser Leu Ser Leu
 595 600 605
 Pro Thr Thr Ala Pro Ser Asn Ser Ser Ser Leu Thr Leu Ser Gly Ile
 610 615 620
 Lys Glu Asp Asn Ser Leu Leu Asn Gln Gly Phe Leu Gln Ala Lys Pro
 625 630 635 640
 Glu Lys Ala Ala Val Ala Gln Lys Pro Arg Ser His Phe Thr Thr Pro
 645 650 655
 Ala Pro Met Ser Ser Ala Trp Lys Thr Val Ala Cys Gly Gly Thr Arg
 660 665 670
 Asp Gln Leu Phe Met Gln Glu Lys Ala Arg Gln Leu Leu Gly Arg Leu
 675 680 685
 Lys Pro Ser His Thr Ser Arg Thr Leu Ile Leu Ser
 690 695 700

<210> 161

<211> 6861

<212> DNA

<213> Homo sapiens

<400> 161

```

gcctgggagg tgcgtcagat ccgagctcgc catccagttt cctctccact agtcccccca 60
gttggagatc tgggaccaac aaggcaccat ggcgcagaag ggccaactca gtgacgatga 120
gaagttcttc tttgtggaca aaaacttcat caacagccca gtggcccagg ctgactgggc 180
cgccaagaga ctcgctctggg tcccctcgga gaagcagggc ttcgaggcag ccagcattaa 240
ggaggagaag ggggatgagg tggttgtgga gctggtggag aatggcaaga aggtcacggt 300
tgggaaagat gacatccaga agatgaaccc acccaagttc tccaaggtgg aggacatggc 360
ggagctgacg tgcctcaacg aagcctccgt gctacacaac ctgagggagc ggtacttctc 420
agggctaata tatacgtaact ctggcctctt ctgctgggtg gtcaaccocct ataaacacct 480
gcccattctac tccggagaaga tctcgacat gtacaagggc aagaagaggc acgagatgcc 540
gcctcacatc tacgccatcg cagacacggc ctaccggagc atgcttcaag atcgggagga 600
ccagtccatt ctatgcacag gcgagtctgg agccgggaaa accgaaaaca ccaagaaggt 660
cattcagtac ctggccgtgg tggcctcctc ccacaagggc aagaaagaca caagtatcac 720
gggagagctg gaaaagcagc ttctacaagc aaacccgatt ctggaggctt tcggcaacgc 780
caaaacagtg aagaacgaca actcctcacg attcggcaaa ttcattccgc tcaacttcga 840
cgtcacgggt tacatcgtgg gagccaacat tgagacctat ctgctagaaa aatcacgggc 900
aattcgccaa gccagagacg agaggacatt ccacatcttt tactacatga ttgctggagc 960
caagggaag atgagaagt acttgctttt ggagggttc aacaactaca ccttctctc 1020
caatggcttt gtgcccattc cagcagccca ggatgatgag atgttccagg aaaccgtgga 1080
ggccatggca atcatgggtt tcagcgagga ggagcagcta tccatattga aggtggtatc 1140
atcggctctg cagcttgga atatcgtctt caagaaggaa agaaacacag accaggcgctc 1200
catgccagat aacacagctg ctcagaaagt ttgccacctc atgggaatta atgtgacaga 1260
tttcaccaga tccatcctca ctctcgtat caaggttggg cgagatgtgg tacagaaagc 1320
tcagacaaaa gaacaggctg actttgctgt agaggctttg gccaaaggcaa catatgagcg 1380
ccttttccgc tggatactca cccgcgtgaa caaagccctg gacaagacc atcggcaagg 1440
ggcttccctc ctggggatcc tggatatag tggatttgag atctttgagg tgaactcctt 1500
cgagcagctg tgcataact acaccaacga gaagctgcag cagctcttca accacacct 1560
gttcacctcg gagcaggagg agtaccagcg cgagggcata gagtggaaact tcatcgactt 1620
tgggctggac ctacagccct gcatcgagct catcgagcga ccgaacaacc ctccagggtgt 1680
gctggccctg ctggacgagg aatgctgggt ccccaaagcc acggacaagt ctttctgtga 1740
gaagctgtgc acggagcagg gcagccaccc caagttccag aagcccaagc agctcaagga 1800
caagactgag ttctccatca tccattatgc tgggaagggt gactataatg cgagtgcctg 1860
gctgaccaag aatatggacc cgtggaatga caacgtgact tccctgctca atgctcctc 1920
cgacaagttt gtggccgacc tgtggaagga cgtggaccgc atcgtgggcc tggaccagat 1980
ggccaagatg acggagagct cgctgccag cgctccaag accaagaagg gcatgttccg 2040
cacagtgggg cagctgtaca aggagcagct ggccaagctg atgaccacgc tacgcaacac 2100
cacgccaac ttctgtcgct gcatcatccc caaccacgag aagaggtcgg gcaagctgga 2160
tgcgttctcg gtgctggagc agctgcggtg caatggggtg ctggaaggca ttcgcatctg 2220
ccggcagggc ttccccaacc ggatcgtctt ccaggagttc cgccaacgct acgagatcct 2280
ggcggcgaat gccatcccca aaggcttcat ggacgggaag caggcctgca ttctcatgat 2340
caaagccctg gaacttgacc ccaacttata caggataggg cagagcaaaa tcttcttccg 2400
aactggcgct ctggcccacc tagaggagga gcgagatttg aagatcaccc atgtcatcat 2460
ggccttccag gcgatgtgtc gtggctactt ggccagaaag gcttttgcca agaggcagca 2520
gcagctgacc gccatgaagg tgattcagag gaactgcgcc gcctacctca agctgcggaa 2580
ctggcagtggt tggaggcttt tcaccaaaagt gaagccactg ctgcagggtg cacggcagga 2640
ggaggagatg caggccaagg aggatgaact gcagaagacc aaggagcggc agcagaaggc 2700
agagaatgag cttaaggagc tggaaacagaa gcaactgcag ctgaccgagg agaagaacct 2760
gctacaggaa cagctgcagg cagagacaga gctgtatgca gaggctgagg agatgcgggt 2820
gctgctggcg gccaaagaagc aggagctgga ggagatactg catgagatgg aggccgcct 2880
ggaggaggag gaagacaggg gccagcagct acaggctgaa aggaagaaga tggcccagca 2940
gatgctggac cttgaagaac agctggagga ggaggaagct gccaggcaga agctgcaact 3000
tgagaaggtc acggctgagg ccaagatcaa gaaactggag gatgagatcc tggatcatga 3060
tgatcagaac aataaactat caaaagaacg aaaactcctt gaggagagga ttagtgactt 3120
aacgacaaat cttgcagaag aggaagaaaa ggccaagaat cttaccaagc tgaaaaaaca 3180
gcatgaatct atgatttcag aactggaagt gctgctaaag aaggaagaga agagccgaca 3240
ggagctggag aagctgaaac ggaagctgga ggggtgatgcc agcgacttcc acgagcagat 3300
cgctgacctc caggcgcaga tcgcagagct caagatgcag ctggccaaga aggaggagga 3360

```

gctgcaggcg	gccctggcca	ggcttgacga	tgaatcgct	cagaagaaca	atgccctgaa	3420
gaagatccgg	gagctggagg	gccacatctc	agacctccag	gaggacctgg	actcagagcg	3480
ggccgccagg	aacaaggctg	aaaagcagaa	gcgagacctc	ggcgaggagc	tggaggccct	3540
aaagacagag	ctggaagaca	cactggacag	cacagccact	cagcaggagc	tcaggggccaa	3600
gagggagcag	gaggtgacgg	tgctgaagaa	ggccctggat	gaagagacgc	ggtcccatga	3660
ggctcaggtc	caggagatga	ggcagaaaca	cgcacaggcg	gtggaggagc	tcacagagca	3720
gcttgagcag	ttcaagaggg	ccaaggcgaa	cctagacaag	aataagcaga	cgctggagaa	3780
agagaacgca	gacctggccg	gggagctgcg	ggtcctgggc	caggccaagc	aggaggtgga	3840
acataagaag	aagaagctgg	aggcgcaggt	gcaggagctg	cagtccaagt	gcagcgatgg	3900
ggagcggggc	cgggcccagc	tcaatgacaa	agtccacaag	ctgcagaatg	aagttgagag	3960
cgtcacaggg	atgcttaacg	aggccgaggg	gaaggccatt	aagctggcca	aggacgtggc	4020
gtccctcagt	tcccagctcc	aggacaccca	ggagctgctt	caagaagaaa	cccggcagaa	4080
gctcaacgtg	tctacgaagc	tgcgccagct	ggaggaggag	cggaacagcc	tgcaagacca	4140
gctggacgag	gagatggagg	ccaagcagaa	cctggagcgc	cacatctcca	ctctcaacat	4200
ccagctctcc	gactcgaaga	agaagctgca	ggactttgcc	agcaccgtgg	aagctctgga	4260
agaggggaag	aagaggttcc	agaaggagat	cgagaacctc	accagcagt	acgaggagaa	4320
ggcggccgct	tatgataaac	tggaaaagac	caagaacagg	cttcagcagg	agctggacga	4380
cctggttggt	gatttggaca	accagcggca	actcgtgtcc	aacctggaaa	agaagcagag	4440
gaaatttgat	cagttgttag	ccgaggagaa	aaacatctct	tccaaatacg	cggatgagag	4500
ggacagagct	gagggcgaag	ccaggagaaa	ggaaccaag	gccctgtccc	tggctcgggc	4560
ccttgaagag	gccttggaa	ccaaagagga	actcgagcgg	accaacaaaa	tgctcaaagc	4620
cgaaatggaa	gacctggtca	gctccaagga	tgacgtgggc	aagaacgtcc	atgagctgga	4680
gaagtccaag	cgggccctgg	agaccagat	ggaggagatg	aagacgcagc	tggaaagagct	4740
ggaggacgag	ctgcaagcca	cggaggacgc	caaactgcgg	ctggaagtca	acatgcaggc	4800
gctcaagggc	cagttcgaaa	gggatctcca	agcccgggac	gagcagaatg	aggagaagag	4860
gaggcaactg	cagagacagc	ttcacgagta	tgagacggaa	ctggaagacg	agcgaaagca	4920
acgtgccctg	gcagctgcag	caaagaagaa	gctggaaggg	gacctgaaa	acctggagct	4980
tcaggccgac	tctgccatca	aggggaggga	ggaagccatc	aagcagctac	gcaaactgca	5040
ggtcagatg	aaggactttc	aaagagagct	ggaagatgcc	cgtgcctcca	gagatgagat	5100
ctttgccaca	gccaaagaga	atgagaagaa	agccaagagc	ttggaagcag	acctcatgca	5160
gctacaagag	gacctcgccg	ccgctgagag	ggctcgcaaa	caagcggacc	tcgagaagga	5220
ggaactggca	gaggagctgg	ccagtagcct	gtcggaagg	aacgcactcc	aggacgagaa	5280
gcgcccgcctg	gaggcccggg	tcgcccagct	ggaggaggag	ctggaggagg	agcagggcaa	5340
catggaggcc	atgagcgacc	gggtccgcaa	agccacacag	caggccgagc	agctcagcaa	5400
cgagctggcc	acagagcgca	gcacggccca	gaagaatgag	agtgcccggc	agcagctcga	5460
gcggcagaac	aaggagctcc	ggagcaagct	ccacgagatg	gagggggccg	tcaagtccaa	5520
gttcaagtc	acctcgcg	cgtcgagagc	caagattgca	cagctggagg	agcaggtcga	5580
gcaggaggcc	agagagaaac	aggcggccac	caagtcgctg	aagcagaaag	acaagaagct	5640
gaaggaaatc	ttgctgcagg	tggaggacga	gcgcaagatg	gccgagcagt	acaaggagca	5700
ggcagagaaa	ggcaatgcca	gggtcaagca	gctcaagagg	cagctggagg	aggcagagga	5760
ggagtcccag	cgcatcaacg	ccaaccgcag	gaagctgcag	cgggagctgg	atgaggccac	5820
ggagagcaac	gaggccatgg	gccgcgaggt	gaacgcactc	aagagcaagc	tcaggcgagg	5880
aaacgagacc	tctttcgttc	cttctagaag	gtctggagga	cgtagagtta	ttgaaaatgc	5940
agatggttct	gaggaggaaa	cggacactcg	agacgcagac	ttcaatggaa	ccaaggccag	6000
tgaataagca	actttctaca	gttttgcacc	acggcaagaa	aaccaaaaac	caaaaacaa	6060
aaacaaaaaa	aaccacaaca	caaccagaa	caaagcaaaa	cccagcagac	tgtacttagc	6120
attgtctaaa	tccattctca	aattccaaat	atcacagaca	cccctcacac	aaggaatata	6180
aaaaccacca	ccctccagcc	tgggcaacgt	agtaaaacct	catctataca	agaattttaa	6240
aataagctgg	gcgtggtggt	acacacctgt	ggtcccagct	actaggagg	ctgagccagg	6300
aagaacgctc	cagcccagga	cttcgaggct	gcaatgagct	ataattgcat	cattgcactc	6360
cagcctgggc	aacagagacc	ctgtctcaac	caccaccacc	accaccacc	ctactacccc	6420
tgtattcaag	gtaaaaattg	aagtttgtat	gatgtaagag	atgagaaaaa	cccaacagga	6480
aacacagaca	catcctccag	ttctatcaat	ggattgtgca	gacactgagt	ttttagaaaa	6540
acatatccac	ggtaacgggt	ccctggcaat	tctgtttaca	tgaaatgggg	agaaagtcc	6600
cgaaatgggt	gcgcgcggc	cccactccca	attcattccc	taacctgcaa	acctttccaa	6660
cttctcagct	caggcctttg	agaattcttt	ccccctctcc	tggtttccac	acctcagaca	6720
cgcacagttc	accaagtgcc	ttctgtagtc	acatgaattg	aaaaggagac	gctgctocca	6780
cggaggggag	caggaatgct	gcactgttta	cacctgact	gtgcttaaaa	acactttcac	6840
taataaatgg	ttataaatca	c				6861

<210> 162
 <211> 1972
 <212> PRT
 <213> Homo sapiens

<400> 162

Met	Ala	Gln	Lys	Gly	Gln	Leu	Ser	Asp	Asp	Glu	Lys	Phe	Leu	Phe	Val
1				5					10					15	
Asp	Lys	Asn	Phe	Ile	Asn	Ser	Pro	Val	Ala	Gln	Ala	Asp	Trp	Ala	Ala
		20						25					30		
Lys	Arg	Leu	Val	Trp	Val	Pro	Ser	Glu	Lys	Gln	Gly	Phe	Glu	Ala	Ala
	35						40					45			
Ser	Ile	Lys	Glu	Glu	Lys	Gly	Asp	Glu	Val	Val	Val	Glu	Leu	Val	Glu
	50					55					60				
Asn	Gly	Lys	Lys	Val	Thr	Val	Gly	Lys	Asp	Asp	Ile	Gln	Lys	Met	Asn
65				70					75					80	
Pro	Pro	Lys	Phe	Ser	Lys	Val	Glu	Asp	Met	Ala	Glu	Leu	Thr	Cys	Leu
			85						90					95	
Asn	Glu	Ala	Ser	Val	Leu	His	Asn	Leu	Arg	Glu	Arg	Tyr	Phe	Ser	Gly
		100						105					110		
Leu	Ile	Tyr	Thr	Tyr	Ser	Gly	Leu	Phe	Cys	Val	Val	Val	Asn	Pro	Tyr
	115						120					125			
Lys	His	Leu	Pro	Ile	Tyr	Ser	Glu	Lys	Ile	Val	Asp	Met	Tyr	Lys	Gly
	130					135					140				
Lys	Lys	Arg	His	Glu	Met	Pro	Pro	His	Ile	Tyr	Ala	Ile	Ala	Asp	Thr
145				150					155					160	
Ala	Tyr	Arg	Ser	Met	Leu	Gln	Asp	Arg	Glu	Asp	Gln	Ser	Ile	Leu	Cys
			165						170					175	
Thr	Gly	Glu	Ser	Gly	Ala	Gly	Lys	Thr	Glu	Asn	Thr	Lys	Lys	Val	Ile
		180						185					190		
Gln	Tyr	Leu	Ala	Val	Val	Ala	Ser	Ser	His	Lys	Gly	Lys	Lys	Asp	Thr
	195						200					205			
Ser	Ile	Thr	Gly	Glu	Leu	Glu	Lys	Gln	Leu	Leu	Gln	Ala	Asn	Pro	Ile
	210					215					220				
Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Val	Lys	Asn	Asp	Asn	Ser	Ser
225				230						235				240	
Arg	Phe	Gly	Lys	Phe	Ile	Arg	Ile	Asn	Phe	Asp	Val	Thr	Gly	Tyr	Ile
			245						250					255	
Val	Gly	Ala	Asn	Ile	Glu	Thr	Tyr	Leu	Leu	Glu	Lys	Ser	Arg	Ala	Ile
		260						265					270		
Arg	Gln	Ala	Arg	Asp	Glu	Arg	Thr	Phe	His	Ile	Phe	Tyr	Tyr	Met	Ile
	275						280					285			
Ala	Gly	Ala	Lys	Glu	Lys	Met	Arg	Ser	Asp	Leu	Leu	Leu	Glu	Gly	Phe
	290					295					300				
Asn	Asn	Tyr	Thr	Phe	Leu	Ser	Asn	Gly	Phe	Val	Pro	Ile	Pro	Ala	Ala
305				310						315				320	
Gln	Asp	Asp	Glu	Met	Phe	Gln	Glu	Thr	Val	Glu	Ala	Met	Ala	Ile	Met
			325						330					335	
Gly	Phe	Ser	Glu	Glu	Glu	Gln	Leu	Ser	Ile	Leu	Lys	Val	Val	Ser	Ser
		340						345					350		
Val	Leu	Gln	Leu	Gly	Asn	Ile	Val	Phe	Lys	Lys	Glu	Arg	Asn	Thr	Asp
	355					360						365			
Gln	Ala	Ser	Met	Pro	Asp	Asn	Thr	Ala	Ala	Gln	Lys	Val	Cys	His	Leu
	370					375					380				
Met	Gly	Ile	Asn	Val	Thr	Asp	Phe	Thr	Arg	Ser	Ile	Leu	Thr	Pro	Arg
385				390						395				400	
Ile	Lys	Val	Gly	Arg	Asp	Val	Val	Gln	Lys	Ala	Gln	Thr	Lys	Glu	Gln
			405						410					415	

Ala	Asp	Phe	Ala	Val	Glu	Ala	Leu	Ala	Lys	Ala	Thr	Tyr	Glu	Arg	Leu
			420					425					430		
Phe	Arg	Trp	Ile	Leu	Thr	Arg	Val	Asn	Lys	Ala	Leu	Asp	Lys	Thr	His
		435					440					445			
Arg	Gln	Gly	Ala	Ser	Phe	Leu	Gly	Ile	Leu	Asp	Ile	Ala	Gly	Phe	Glu
	450					455				460					
Ile	Phe	Glu	Val	Asn	Ser	Phe	Glu	Gln	Leu	Cys	Ile	Asn	Tyr	Thr	Asn
465					470					475					480
Glu	Lys	Leu	Gln	Gln	Leu	Phe	Asn	His	Thr	Met	Phe	Ile	Leu	Glu	Gln
			485						490					495	
Glu	Glu	Tyr	Gln	Arg	Glu	Gly	Ile	Glu	Trp	Asn	Phe	Ile	Asp	Phe	Gly
			500					505					510		
Leu	Asp	Leu	Gln	Pro	Cys	Ile	Glu	Leu	Ile	Glu	Arg	Pro	Asn	Asn	Pro
		515					520					525			
Pro	Gly	Val	Leu	Ala	Leu	Leu	Asp	Glu	Glu	Cys	Trp	Phe	Pro	Lys	Ala
	530					535				540					
Thr	Asp	Lys	Ser	Phe	Val	Glu	Lys	Leu	Cys	Thr	Glu	Gln	Gly	Ser	His
545					550					555					560
Pro	Lys	Phe	Gln	Lys	Pro	Lys	Gln	Leu	Lys	Asp	Lys	Thr	Glu	Phe	Ser
			565						570					575	
Ile	Ile	His	Tyr	Ala	Gly	Lys	Val	Asp	Tyr	Asn	Ala	Ser	Ala	Trp	Leu
			580					585					590		
Thr	Lys	Asn	Met	Asp	Pro	Leu	Asn	Asp	Asn	Val	Thr	Ser	Leu	Leu	Asn
		595					600					605			
Ala	Ser	Ser	Asp	Lys	Phe	Val	Ala	Asp	Leu	Trp	Lys	Asp	Val	Asp	Arg
	610					615					620				
Ile	Val	Gly	Leu	Asp	Gln	Met	Ala	Lys	Met	Thr	Glu	Ser	Ser	Leu	Pro
625					630					635					640
Ser	Ala	Ser	Lys	Thr	Lys	Lys	Gly	Met	Phe	Arg	Thr	Val	Gly	Gln	Leu
			645						650					655	
Tyr	Lys	Glu	Gln	Leu	Gly	Lys	Leu	Met	Thr	Thr	Leu	Arg	Asn	Thr	Thr
			660					665					670		
Pro	Asn	Phe	Val	Arg	Cys	Ile	Ile	Pro	Asn	His	Glu	Lys	Arg	Ser	Gly
		675					680					685			
Lys	Leu	Asp	Ala	Phe	Leu	Val	Leu	Glu	Gln	Leu	Arg	Cys	Asn	Gly	Val
	690					695					700				
Leu	Glu	Gly	Ile	Arg	Ile	Cys	Arg	Gln	Gly	Phe	Pro	Asn	Arg	Ile	Val
705					710					715					720
Phe	Gln	Glu	Phe	Arg	Gln	Arg	Tyr	Glu	Ile	Leu	Ala	Ala	Asn	Ala	Ile
			725					730					735		
Pro	Lys	Gly	Phe	Met	Asp	Gly	Lys	Gln	Ala	Cys	Ile	Leu	Met	Ile	Lys
			740					745					750		
Ala	Leu	Glu	Leu	Asp	Pro	Asn	Leu	Tyr	Arg	Ile	Gly	Gln	Ser	Lys	Ile
		755					760					765			
Phe	Phe	Arg	Thr	Gly	Val	Leu	Ala	His	Leu	Glu	Glu	Arg	Asp	Leu	
	770					775					780				
Lys	Ile	Thr	Asp	Val	Ile	Met	Ala	Phe	Gln	Ala	Met	Cys	Arg	Gly	Tyr
785					790					795					800
Leu	Ala	Arg	Lys	Ala	Phe	Ala	Lys	Arg	Gln	Gln	Gln	Leu	Thr	Ala	Met
			805						810					815	
Lys	Val	Ile	Gln	Arg	Asn	Cys	Ala	Ala	Tyr	Leu	Lys	Leu	Arg	Asn	Trp
			820					825					830		
Gln	Trp	Trp	Arg	Leu	Phe	Thr	Lys	Val	Lys	Pro	Leu	Leu	Gln	Val	Thr
	835						840					845			
Arg	Gln	Glu	Glu	Glu	Met	Gln	Ala	Lys	Glu	Asp	Glu	Leu	Gln	Lys	Thr
	850					855					860				
Lys	Glu	Arg	Gln	Gln	Lys	Ala	Glu	Asn	Glu	Leu	Lys	Glu	Leu	Glu	Gln
865					870					875					880
Lys	His	Ser	Gln	Leu	Thr	Glu	Glu	Lys	Asn	Leu	Leu	Gln	Glu	Gln	Leu

										885						890						895		
Gln	Ala	Glu	Thr	Glu	Leu	Tyr	Ala	Glu	Ala	Glu	Glu	Met	Arg	Val	Arg									
										900			905			910								
Leu	Ala	Ala	Lys	Lys	Gln	Glu	Leu	Glu	Glu	Ile	Leu	His	Glu	Met	Glu									
										915			920			925								
Ala	Arg	Leu	Glu	Glu	Glu	Glu	Asp	Arg	Gly	Gln	Gln	Leu	Gln	Ala	Glu									
										930			935			940								
Arg	Lys	Lys	Met	Ala	Gln	Gln	Met	Leu	Asp	Leu	Glu	Glu	Gln	Leu	Glu									
										945			950			955			960					
Glu	Glu	Glu	Ala	Ala	Arg	Gln	Lys	Leu	Gln	Leu	Glu	Lys	Val	Thr	Ala									
										965			970			975								
Glu	Ala	Lys	Ile	Lys	Lys	Leu	Glu	Asp	Glu	Ile	Leu	Val	Met	Asp	Asp									
										980			985			990								
Gln	Asn	Asn	Lys	Leu	Ser	Lys	Glu	Arg	Lys	Leu	Leu	Glu	Glu	Arg	Ile									
										995			1000			1005								
Ser	Asp	Leu	Thr	Thr	Asn	Leu	Ala	Glu	Glu	Glu	Glu	Lys	Ala	Lys	Asn									
										1010			1015			1020								
Leu	Thr	Lys	Leu	Lys	Asn	Lys	His	Glu	Ser	Met	Ile	Ser	Glu	Leu	Glu									
										1025			1030			1035			1040					
Val	Arg	Leu	Lys	Lys	Glu	Glu	Lys	Ser	Arg	Gln	Glu	Leu	Glu	Lys	Leu									
										1045			1050			1055								
Lys	Arg	Lys	Leu	Glu	Gly	Asp	Ala	Ser	Asp	Phe	His	Glu	Gln	Ile	Ala									
										1060			1065			1070								
Asp	Leu	Gln	Ala	Gln	Ile	Ala	Glu	Leu	Lys	Met	Gln	Leu	Ala	Lys	Lys									
										1075			1080			1085								
Glu	Glu	Glu	Leu	Gln	Ala	Ala	Leu	Ala	Arg	Leu	Asp	Asp	Glu	Ile	Ala									
										1090			1095			1100								
Gln	Lys	Asn	Asn	Ala	Leu	Lys	Lys	Ile	Arg	Glu	Leu	Glu	Gly	His	Ile									
										1105			1110			1115			1120					
Ser	Asp	Leu	Gln	Glu	Asp	Leu	Asp	Ser	Glu	Arg	Ala	Ala	Arg	Asn	Lys									
										1125			1130			1135								
Ala	Glu	Lys	Gln	Lys	Arg	Asp	Leu	Gly	Glu	Glu	Leu	Glu	Ala	Leu	Lys									
										1140			1145			1150								
Thr	Glu	Leu	Glu	Asp	Thr	Leu	Asp	Ser	Thr	Ala	Thr	Gln	Gln	Glu	Leu									
										1155			1160			1165								
Arg	Ala	Lys	Arg	Glu	Gln	Glu	Val	Thr	Val	Leu	Lys	Lys	Ala	Leu	Asp									
										1170			1175			1180								
Glu	Glu	Thr	Arg	Ser	His	Glu	Ala	Gln	Val	Gln	Glu	Met	Arg	Gln	Lys									
										1185			1190			1195			1200					
His	Ala	Gln	Ala	Val	Glu	Glu	Leu	Thr	Glu	Gln	Leu	Glu	Gln	Phe	Lys									
										1205			1210			1215								
Arg	Ala	Lys	Ala	Asn	Leu	Asp	Lys	Asn	Lys	Gln	Thr	Leu	Glu	Lys	Glu									
										1220			1225			1230								
Asn	Ala	Asp	Leu	Ala	Gly	Glu	Leu	Arg	Val	Leu	Gly	Gln	Ala	Lys	Gln									
										1235			1240			1245								
Glu	Val	Glu	His	Lys	Lys	Lys	Lys	Leu	Glu	Ala	Gln	Val	Gln	Glu	Leu									
										1250			1255			1260								
Gln	Ser	Lys	Cys	Ser	Asp	Gly	Glu	Arg	Ala	Arg	Ala	Glu	Leu	Asn	Asp									
										1265			1270			1275			1280					
Lys	Val	His	Lys	Leu	Gln	Asn	Glu	Val	Glu	Ser	Val	Thr	Gly	Met	Leu									
										1285			1290			1295								
Asn	Glu	Ala	Glu	Gly	Lys	Ala	Ile	Lys	Leu	Ala	Lys	Asp	Val	Ala	Ser									
										1300			1305			1310								
Leu	Ser	Ser	Gln	Leu	Gln	Asp	Thr	Gln	Glu	Leu	Leu	Gln	Glu	Glu	Thr									
										1315			1320			1325								
Arg	Gln	Lys	Leu	Asn	Val	Ser	Thr	Lys	Leu	Arg	Gln	Leu	Glu	Glu	Glu									
										1330			1335			1340								
Arg	Asn	Ser	Leu	Gln	Asp	Gln	Leu	Asp	Glu	Glu	Met	Glu	Ala	Lys	Gln									
										1345			1350			1355			1360					

Asn Leu Glu Arg His Ile Ser Thr Leu Asn Ile Gln Leu Ser Asp Ser
 1365 1370 1375
 Lys Lys Lys Leu Gln Asp Phe Ala Ser Thr Val Glu Ala Leu Glu Glu
 1380 1385 1390
 Gly Lys Lys Arg Phe Gln Lys Glu Ile Glu Asn Leu Thr Gln Gln Tyr
 1395 1400 1405
 Glu Glu Lys Ala Ala Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg
 1410 1415 1420
 Leu Gln Gln Glu Leu Asp Asp Leu Val Val Asp Leu Asp Asn Gln Arg
 1425 1430 1435 1440
 Gln Leu Val Ser Asn Leu Glu Lys Lys Gln Arg Lys Phe Asp Gln Leu
 1445 1450 1455
 Leu Ala Glu Glu Lys Asn Ile Ser Ser Lys Tyr Ala Asp Glu Arg Asp
 1460 1465 1470
 Arg Ala Glu Ala Glu Ala Arg Glu Lys Glu Thr Lys Ala Leu Ser Leu
 1475 1480 1485
 Ala Arg Ala Leu Glu Glu Ala Leu Glu Ala Lys Glu Glu Leu Glu Arg
 1490 1495 1500
 Thr Asn Lys Met Leu Lys Ala Glu Met Glu Asp Leu Val Ser Ser Lys
 1505 1510 1515 1520
 Asp Asp Val Gly Lys Asn Val His Glu Leu Glu Lys Ser Lys Arg Ala
 1525 1530 1535
 Leu Glu Thr Gln Met Glu Glu Met Lys Thr Gln Leu Glu Glu Leu Glu
 1540 1545 1550
 Asp Glu Leu Gln Ala Thr Glu Asp Ala Lys Leu Arg Leu Glu Val Asn
 1555 1560 1565
 Met Gln Ala Leu Lys Gly Gln Phe Glu Arg Asp Leu Gln Ala Arg Asp
 1570 1575 1580
 Glu Gln Asn Glu Glu Lys Arg Arg Gln Leu Gln Arg Gln Leu His Glu
 1585 1590 1595 1600
 Tyr Glu Thr Glu Leu Glu Asp Glu Arg Lys Gln Arg Ala Leu Ala Ala
 1605 1610 1615
 Ala Ala Lys Lys Lys Leu Glu Gly Asp Leu Lys Asp Leu Glu Leu Gln
 1620 1625 1630
 Ala Asp Ser Ala Ile Lys Gly Arg Glu Glu Ala Ile Lys Gln Leu Arg
 1635 1640 1645
 Lys Leu Gln Ala Gln Met Lys Asp Phe Gln Arg Glu Leu Glu Asp Ala
 1650 1655 1660
 Arg Ala Ser Arg Asp Glu Ile Phe Ala Thr Ala Lys Glu Asn Glu Lys
 1665 1670 1675 1680
 Lys Ala Lys Ser Leu Glu Ala Asp Leu Met Gln Leu Gln Glu Asp Leu
 1685 1690 1695
 Ala Ala Ala Glu Arg Ala Arg Lys Gln Ala Asp Leu Glu Lys Glu Glu
 1700 1705 1710
 Leu Ala Glu Glu Leu Ala Ser Ser Leu Ser Gly Arg Asn Ala Leu Gln
 1715 1720 1725
 Asp Glu Lys Arg Arg Leu Glu Ala Arg Ile Ala Gln Leu Glu Glu Glu
 1730 1735 1740
 Leu Glu Glu Glu Gln Gly Asn Met Glu Ala Met Ser Asp Arg Val Arg
 1745 1750 1755 1760
 Lys Ala Thr Gln Gln Ala Glu Gln Leu Ser Asn Glu Leu Ala Thr Glu
 1765 1770 1775
 Arg Ser Thr Ala Gln Lys Asn Glu Ser Ala Arg Gln Gln Leu Glu Arg
 1780 1785 1790
 Gln Asn Lys Glu Leu Arg Ser Lys Leu His Glu Met Glu Gly Ala Val
 1795 1800 1805
 Lys Ser Lys Phe Lys Ser Thr Ile Ala Ala Leu Glu Ala Lys Ile Ala
 1810 1815 1820
 Gln Leu Glu Glu Gln Val Glu Gln Glu Ala Arg Glu Lys Gln Ala Ala

1825 1830 1835 1840
 Thr Lys Ser Leu Lys Lys Asp Lys Lys Leu Lys Glu Ile Leu Leu
 1845 1850 1855
 Gln Val Glu Asp Glu Arg Lys Met Ala Glu Gln Tyr Lys Glu Gln Ala
 1860 1865 1870
 Glu Lys Gly Asn Ala Arg Val Lys Gln Leu Lys Arg Gln Leu Glu Glu
 1875 1880 1885
 Ala Glu Glu Glu Ser Gln Arg Ile Asn Ala Asn Arg Arg Lys Leu Gln
 1890 1895 1900
 Arg Glu Leu Asp Glu Ala Thr Glu Ser Asn Glu Ala Met Gly Arg Glu
 1905 1910 1915 1920
 Val Asn Ala Leu Lys Ser Lys Leu Arg Arg Gly Asn Glu Thr Ser Phe
 1925 1930 1935
 Val Pro Ser Arg Arg Ser Gly Gly Arg Arg Val Ile Glu Asn Ala Asp
 1940 1945 1950
 Gly Ser Glu Glu Glu Thr Asp Thr Arg Asp Ala Asp Phe Asn Gly Thr
 1955 1960 1965
 Lys Ala Ser Glu
 1970

<210> 163
 <211> 6900
 <212> DNA
 <213> Homo sapiens

<400> 163
 gcctgggagg tgcgtcagat ccgagctcgc catccagttt cctctccact agtcccccca 60
 gttggagatc tgggaaccaac aaggcaccat ggcgcagaag ggccaactca gtgacgatga 120
 gaagttcctc tttgtggaca aaaacttcat caacagccca gtggcccagg ctgactgggc 180
 cgccaagaga ctcgtctggg tcccctcgga gaagcagggc ttcgaggcag ccagcattaa 240
 ggaggagaag ggggatgagg tggttgtgga gctgggtggag aatggcaaga aggtcacggt 300
 tgggaaagat gacatccaga agatgaaccc acccaagttc tccaaggtgg aggacatggc 360
 ggagctgacg tgccctcaacg aagcctccgt gctacacaac ctgagggagc ggtacttctc 420
 agggctaata tatacgtact ctggcctctt ctgctgtgtg gtcaaccctt ataaacacct 480
 gccatctac tcggagaaga tcgtcgacat gtacaagggc aagaagaggc acgagatgcc 540
 gcctcacatc tacgccatcg cagacacggc ctaccggagc atgcttcaag atcgggagga 600
 ccagtccatt ctatgcacag gcgagttctg agccgggaaa accgaaaaca ccaagaagggt 660
 cattcagtac ctggccgtgg tggcctcctc ccacaagggc aagaaagaca caagtatcac 720
 gggagagctg gaaaagcagc ttctacaagc aaacccgatt ctggaggctt tcggcaacgc 780
 caaaacagtg aagaacgaca actcctcact attcggcaaa ttcattccgc tcaacttoga 840
 cgtcacgggt tacatcgtgg gagccaacat tgagacctat ctgctagaaa aatcacgggc 900
 aattcgccaa gccagagacg agaggacatt ccacatcttt tactacatga ttgctggagc 960
 caaggagaag atgagaagtg acttgctttt ggagggtctc aacaactaca ccttccctctc 1020
 caatggcttt gtgcccctcc cagcagccca ggatgatgag atgttccagg aaaccgtgga 1080
 ggccatggca atcatgggtt tcagcgagga ggagcagcta tccatattga aggtggtatc 1140
 atcggctctg cagcttggaa atatcgtctt caagaaggaa agaaacacag accaggcgtc 1200
 catgccagat aacacagctg ctcagaaagt ttgccacctc atgggaatta atgtgacaga 1260
 tttcaccaga tccatctca ctctcgtat caaggttggg cgagatgtgg tacagaaagc 1320
 tcagacaaaa gaacaggctg actttgctgt agaggctttg gccaaaggca catatgagcg 1380
 ccttttccgc tggatactca ccgcgtgaa caaagccctg gacaagacct atcggcaagg 1440
 ggcttccttc ctggggatcc tggatatagc tggatttgag atctttgagg tgaactcctt 1500
 cgagcagctg tgcactcaact acaccaacga gaagctgcag cagctcttca accacacctt 1560
 gttcatcctg gagcaggagg agtaccagcg cgagggcac gagtggaact tcatcgactt 1620
 tgggctggac ctacagccct gcatcgagct catcgagcga ccgaacaacc ctccaggtgt 1680
 gctggccctg ctggacgagg aatgctggtt ccccaaagcc acggacaagt ctttcgtgga 1740
 gaagctgtgc acggagcagg gcagccaccc caagttccag aagcccaagc agctcaagga 1800
 caagactgag ttctccatca tccattatgc tgggaagggt gactataatg cgagtgcctg 1860
 gctgaccaag aatatggacc cgctgaatga caacgtgact tccctgctca atgcctcctc 1920

cgacaagttt	gtggccgacc	tgtggaagga	cgtggaccgc	atcgtggggc	tggaccagat	1980
ggccaagatg	acggagagct	cgctgccag	cgctccaag	accaagaagg	gcatgttccg	2040
cacagtggg	cagctgtaca	aggagcagct	gggcaagctg	atgaccacgc	tacgcaacac	2100
cacgcccAAC	ttcgtgcgct	gcatcatccc	caaccacgag	aagagggtccg	gcaagctgga	2160
tgcgttccctg	gtgctggagc	agctgcgggtg	caatgggggtg	ctggaaggca	ttcgcattctg	2220
ccggcagggc	ttccccaacc	ggatcgtctt	ccaggagttc	cgccaacgct	acgagatcct	2280
ggcggcgaat	gccatcccca	aaggcttcat	ggacgggaag	caggcctgca	ttctcatgat	2340
caaagccctg	gaacttgacc	ccaacttata	caggataggg	cagagcaaaa	tcttcttccg	2400
aactggcgctc	ctggcccacc	tagaggagga	gcgagatttg	aagatcaccg	atgtcatcat	2460
ggccttccag	gcgatgtgtc	gtggctactt	ggccagaaaag	gcttttgcca	agaggcagca	2520
gcagctgacc	gccatgaagg	tgattcagag	gaactgcgcc	gcctacctca	agctgcggaa	2580
ctggcagtg	tggaggcttt	tcaccaaagt	gaagccactg	ctgcagggtga	cacggcagga	2640
ggaggagatg	caggccaagg	aggatgaact	gcagaagacc	aaggagcggc	agcagaaggc	2700
agagaatgag	cttaaggagc	tggaacagaa	gcactcgcag	ctgaccgagg	agaagaacct	2760
gctacaggaa	cagctgcagg	cagagacaga	gctgtatgca	gaggctgagg	agatgcgggt	2820
gcggtggcg	gccaagaagc	aggagctgga	ggagatactg	catgagatgg	aggcccgcct	2880
ggaggaggag	gaagacagg	gccagcagct	acaggctgaa	aggaagaaga	tggcccagca	2940
gatgctggac	cttgaagaac	agctggagga	ggaggaagct	gccaggcaga	agctgcaaact	3000
tgagaaggctc	acggctgagg	ccaagatcaa	gaaactggag	gatgagatcc	tggatcatgga	3060
tgatcagaac	aataaactat	caaaagaacg	aaaactcctt	gaggagagga	ttagtgaactt	3120
aacgacaaat	cttgcaag	aggaagaaaa	ggccaagaat	cttaccgaagc	tgaacaaacaa	3180
gcatgaatct	atgatttcag	aactggaagt	gcggctaag	aaggaagaga	agagccgaca	3240
ggagctggag	aagctgaaac	ggaagctgga	gggtgatgcc	agcgacttcc	acgagcagat	3300
cgctgacctc	caggcgcaga	tcgcagagct	caagatgcag	ctggccaaga	aggaggagga	3360
gctgcaggcg	gccttgcca	ggcttgacga	tgaaatcgct	cagaagaaca	atgccctgaa	3420
gaagatccgg	gagctggagg	gccacatctc	agacctccag	gaggacctgg	actcagagcg	3480
ggccgccagg	aacaaggctg	aaaagcagaa	gcgagacctc	ggcgaggagc	tggaggccct	3540
aaagacagag	ctggaagaca	cactggacag	cacagccact	cagcaggagc	tcaggggccaa	3600
gagggagcag	gaggtgacgg	tgctgaagaa	ggccttgat	gaagagacgc	ggtcccatga	3660
ggctcaggtc	caggagatga	ggcagaaaca	cgcacaggcg	gtggaggagc	tcacagagca	3720
gcttgagcag	ttcaagagg	ccaaggcgaa	cctagacaag	aataagcaga	cgctggagaa	3780
agagaacgca	gacctggccg	gggagctgcg	ggtcctgggc	caggccaagc	aggagggtgga	3840
acataagaag	aagaagctgg	aggcgcaggt	gcaggagctg	cagtccaagt	gcagcgatgg	3900
ggagcggggc	cgggcggagc	tcaatgacaa	agtccacaag	ctgcagaatg	aagttgagag	3960
cgtcacagg	atgcttaacg	aggccgagg	gaaggccatt	aagctggcca	aggacgtggc	4020
gtccctcagt	tcccagctcc	aggacaccca	ggagctgctt	caagaagaaa	cccggcagaa	4080
gctcaacgtg	tctacgaagc	tgcgccagct	ggaggaggag	cggaacagcc	tgcaagacca	4140
gctggacgag	gagatggagg	ccaagcagaa	cctggagcgc	cacatctcca	ctctcaacct	4200
ccagctctcc	gactcgaaga	agaagctgca	ggactttgcc	agcaccgtgg	aagctctgga	4260
agaggggaag	aagaggttcc	agaaggagat	cgagaacctc	accagcagct	acgaggagaa	4320
ggcggccgct	tatgataaac	tggaaaagac	caagaacagg	cttcagcagg	agctggacga	4380
cctggttggt	gatttgagca	accagcggca	actcgtgtcc	aacctggaaa	agaagcagag	4440
gaaatttgat	cagttgttag	ccgaggagaa	aaacatctct	tccaaataacg	cggatgagag	4500
ggacagagct	gaggcagaag	ccaggagaa	ggaaaccaag	gccctgtccc	tggctcgggc	4560
ccttgaagag	gccttggaa	ccaaagagga	actcgagcgg	accaacaaaa	tgctcaaagc	4620
cgaaatggaa	gacctggtca	gctccaagga	tgacgtgggc	aagaacgtcc	atgagctgga	4680
gaagtccaag	cgggccctgg	agaccagat	ggaggagatg	aagacgcagc	tggaaagact	4740
ggaggacgag	ctgcaagcca	cggaggacgc	caaaactgcg	ctggaagtca	acatgacggc	4800
gctcaagggc	cagttcgaaa	gggatctcca	agcccgggac	gagcagaatg	aggagaagag	4860
gaggcaactg	cagagacagc	ttcacgagta	tgagacggaa	ctggaagacg	agcgaagca	4920
acgtgccctg	gcagctgcag	caaagaagaa	gctggaagg	gacctgaaag	acctggagct	4980
tcaggccgac	tctgccatca	aggggaggg	ggaagccatc	aagcagctac	gcaaactgca	5040
ggctcagatg	aaggactttc	aaagagagct	ggaagatgcc	cgtgcctcca	gagatgagat	5100
ctttgccaca	gccaaagaga	atgagaagaa	agccaagagc	ttggaagcag	acctcatgca	5160
gctacaagag	gacctcgccg	ccgctgagag	ggctcgcaaa	caagcggacc	tcgagaagga	5220
ggaactggca	gaggagctgg	ccagtgcct	gtcgggaagg	aacgcactcc	aggacgagaa	5280
gcgcgcctg	gaggcccgga	tcgcccagct	ggaggaggag	ctggaggagg	agcagggcaa	5340
catggaggcc	atgagcgacc	gggtccgcaa	agccacacag	caggccgagc	agctcggcaa	5400
cgagctggcc	acagagcgca	gcacggccca	gaagaatgag	agtgcctggc	agcagctcga	5460

```

gcggcagaac aaggagctcc ggagcaagct ccacgagatg gagggggccg tcaagtccaa 5520
gttcaagtcc accatcgcg cgctggaggc caagattgca cagctggagg agcaggtcga 5580
gcaggaggcc agagagaaac aggcggccac caagtgcgtg aagcagaaag acaagaagct 5640
gaaggaaatc ttgctgcagg tggaggacga ggcgaagatg gccgagcagt acaaggagca 5700
ggcagagaaa ggcaatgcca gggtaagca gctcaagagg cagctggagg aggcagagga 5760
ggagtcccag cgcatacaac ccaaccgcag gaagctgcag cgggagctgg atgaggccac 5820
ggagagcaac gaggccatgg gccgcgaggt gaacgcactc aagagcaagc tcagagggcc 5880
ccccccacag gaaacttcgc agtgatgcac caggcgagga aacgagacct ctttcgttcc 5940
ttctagaagg tctggaggac gtagagttat tgaaaatgca gatggttctg aggaggaaac 6000
ggacactoga gacgcagact tcaatggaac caaggccagt gaataagcaa ctttctacag 6060
ttttgcacca cggcaagaaa accaaaaacc aaaacaaaca aacaaaaaaa acccaacaac 6120
aaccagaac aaagcaaaac ccagcagact gtacttagca ttgtctaaat ccattctcaa 6180
attccaaata tcacagacac ccctcacaca aggaatataa aaaccaccac cctccagcct 6240
gggcaacgta gtaaaacctc atctatacaa gaatttaaaa ataagctggg cgtgggtgga 6300
cacacctgtg gtcccagcta ctagggaggc tgagccagga agaacgctcc agcccaggac 6360
ttcgaggctg caatgagcta taattgcatc attgcactcc agcctgggca acagagaccc 6420
tgtctcaacc accaccacca ccaccacccc tactaccocct gtattcaagg taaaaattga 6480
agtttgtatg atgtaagaga tgagaaaaac ccaacaggaa acacagacac atcctccagt 6540
tctatcaatg gattgtgcag acactgagtt tttagaaaaa catatccacg gtaaccggtc 6600
cctggcaatt ctgtttacat gaaatgggga gaaagtcacc gaaatgggtg ccgcccggcc 6660
ccactcccaa ttcattccct aacctgcaaa cctttccaac ttctcacgtc aggcctttga 6720
gaattctttc cccctctcct ggtttccaca cctcagacac gcacagttca ccaagtgcct 6780
tctgtagtca catgaattga aaaggagacg ctgctcccac ggaggggagc aggaatgctg 6840
cactgtttac accctgactg tgcttaaaaa cactttcact aataaatggt tataaatcac 6900

```

<210> 164

<211> 1938

<212> PRT

<213> Homo sapiens

<400> 164

```

Met Ala Gln Lys Gly Gln Leu Ser Asp Asp Glu Lys Phe Leu Phe Val
 1           5           10           15
Asp Lys Asn Phe Ile Asn Ser Pro Val Ala Gln Ala Asp Trp Ala Ala
      20           25           30
Lys Arg Leu Val Trp Val Pro Ser Glu Lys Gln Gly Phe Glu Ala Ala
      35           40           45
Ser Ile Lys Glu Glu Lys Gly Asp Glu Val Val Val Glu Leu Val Glu
      50           55           60
Asn Gly Lys Lys Val Thr Val Gly Lys Asp Asp Ile Gln Lys Met Asn
      65           70           75           80
Pro Pro Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu
      85           90           95
Asn Glu Ala Ser Val Leu His Asn Leu Arg Glu Arg Tyr Phe Ser Gly
      100          105          110
Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val Val Asn Pro Tyr
      115          120          125
Lys His Leu Pro Ile Tyr Ser Glu Lys Ile Val Asp Met Tyr Lys Gly
      130          135          140
Lys Lys Arg His Glu Met Pro Pro His Ile Tyr Ala Ile Ala Asp Thr
      145          150          155          160
Ala Tyr Arg Ser Met Leu Gln Asp Arg Glu Asp Gln Ser Ile Leu Cys
      165          170          175
Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr Lys Lys Val Ile
      180          185          190
Gln Tyr Leu Ala Val Val Ala Ser Ser His Lys Gly Lys Lys Asp Thr
      195          200          205
Ser Ile Thr Gly Glu Leu Glu Lys Gln Leu Leu Gln Ala Asn Pro Ile

```

210	215	220
Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Lys Asn Asp Asn Ser Ser		
225	230	235
Arg Phe Gly Lys Phe Ile Arg Ile Asn Phe Asp Val Thr Gly Tyr Ile		240
	245	250
Val Gly Ala Asn Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg Ala Ile		255
	260	265
Arg Gln Ala Arg Asp Glu Arg Thr Phe His Ile Phe Tyr Tyr Met Ile		270
	275	280
Ala Gly Ala Lys Glu Lys Met Arg Ser Asp Leu Leu Glu Gly Phe		285
	290	295
Asn Asn Tyr Thr Phe Leu Ser Asn Gly Phe Val Pro Ile Pro Ala Ala		300
305	310	315
Gln Asp Asp Glu Met Phe Gln Glu Thr Val Glu Ala Met Ala Ile Met		320
	325	330
Gly Phe Ser Glu Glu Glu Gln Leu Ser Ile Leu Lys Val Val Ser Ser		335
	340	345
Val Leu Gln Leu Gly Asn Ile Val Phe Lys Lys Glu Arg Asn Thr Asp		350
	355	360
Gln Ala Ser Met Pro Asp Asn Thr Ala Ala Gln Lys Val Cys His Leu		365
	370	375
Met Gly Ile Asn Val Thr Asp Phe Thr Arg Ser Ile Leu Thr Pro Arg		380
385	390	395
Ile Lys Val Gly Arg Asp Val Val Gln Lys Ala Gln Thr Lys Glu Gln		400
	405	410
Ala Asp Phe Ala Val Glu Ala Leu Ala Lys Ala Thr Tyr Glu Arg Leu		415
	420	425
Phe Arg Trp Ile Leu Thr Arg Val Asn Lys Ala Leu Asp Lys Thr His		430
	435	440
Arg Gln Gly Ala Ser Phe Leu Gly Ile Leu Asp Ile Ala Gly Phe Glu		445
	450	455
Ile Phe Glu Val Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn		460
465	470	475
Glu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Ile Leu Glu Gln		480
	485	490
Glu Glu Tyr Gln Arg Glu Gly Ile Glu Trp Asn Phe Ile Asp Phe Gly		495
	500	505
Leu Asp Leu Gln Pro Cys Ile Glu Leu Ile Glu Arg Pro Asn Asn Pro		510
	515	520
Pro Gly Val Leu Ala Leu Leu Asp Glu Glu Cys Trp Phe Pro Lys Ala		525
	530	535
Thr Asp Lys Ser Phe Val Glu Lys Leu Cys Thr Glu Gln Gly Ser His		540
545	550	555
Pro Lys Phe Gln Lys Pro Lys Gln Leu Lys Asp Lys Thr Glu Phe Ser		560
	565	570
Ile Ile His Tyr Ala Gly Lys Val Asp Tyr Asn Ala Ser Ala Trp Leu		575
	580	585
Thr Lys Asn Met Asp Pro Leu Asn Asp Asn Val Thr Ser Leu Leu Asn		590
	595	600
Ala Ser Ser Asp Lys Phe Val Ala Asp Leu Trp Lys Asp Val Asp Arg		605
	610	615
Ile Val Gly Leu Asp Gln Met Ala Lys Met Thr Glu Ser Ser Leu Pro		620
625	630	635
Ser Ala Ser Lys Thr Lys Lys Gly Met Phe Arg Thr Val Gly Gln Leu		640
	645	650
Tyr Lys Glu Gln Leu Gly Lys Leu Met Thr Thr Leu Arg Asn Thr Thr		655
	660	665
Pro Asn Phe Val Arg Cys Ile Ile Pro Asn His Glu Lys Arg Ser Gly		670
	675	680
		685

Lys	Leu	Asp	Ala	Phe	Leu	Val	Leu	Glu	Gln	Leu	Arg	Cys	Asn	Gly	Val
690						695					700				
Leu	Glu	Gly	Ile	Arg	Ile	Cys	Arg	Gln	Gly	Phe	Pro	Asn	Arg	Ile	Val
705					710					715					720
Phe	Gln	Glu	Phe	Arg	Gln	Arg	Tyr	Glu	Ile	Leu	Ala	Ala	Asn	Ala	Ile
				725				730						735	
Pro	Lys	Gly	Phe	Met	Asp	Gly	Lys	Gln	Ala	Cys	Ile	Leu	Met	Ile	Lys
			740					745					750		
Ala	Leu	Glu	Leu	Asp	Pro	Asn	Leu	Tyr	Arg	Ile	Gly	Gln	Ser	Lys	Ile
		755					760					765			
Phe	Phe	Arg	Thr	Gly	Val	Leu	Ala	His	Leu	Glu	Glu	Glu	Arg	Asp	Leu
	770					775					780				
Lys	Ile	Thr	Asp	Val	Ile	Met	Ala	Phe	Gln	Ala	Met	Cys	Arg	Gly	Tyr
785					790				795						800
Leu	Ala	Arg	Lys	Ala	Phe	Ala	Lys	Arg	Gln	Gln	Gln	Leu	Thr	Ala	Met
				805					810					815	
Lys	Val	Ile	Gln	Arg	Asn	Cys	Ala	Ala	Tyr	Leu	Lys	Leu	Arg	Asn	Trp
			820					825						830	
Gln	Trp	Trp	Arg	Leu	Phe	Thr	Lys	Val	Lys	Pro	Leu	Leu	Gln	Val	Thr
	835						840					845			
Arg	Gln	Glu	Glu	Glu	Met	Gln	Ala	Lys	Glu	Asp	Glu	Leu	Gln	Lys	Thr
	850					855					860				
Lys	Glu	Arg	Gln	Gln	Lys	Ala	Glu	Asn	Glu	Leu	Lys	Glu	Leu	Glu	Gln
865					870				875						880
Lys	His	Ser	Gln	Leu	Thr	Glu	Glu	Lys	Asn	Leu	Leu	Gln	Glu	Gln	Leu
				885					890					895	
Gln	Ala	Glu	Thr	Glu	Leu	Tyr	Ala	Glu	Ala	Glu	Glu	Met	Arg	Val	Arg
			900					905					910		
Leu	Ala	Ala	Lys	Lys	Gln	Glu	Leu	Glu	Glu	Ile	Leu	His	Glu	Met	Glu
	915						920					925			
Ala	Arg	Leu	Glu	Glu	Glu	Glu	Asp	Arg	Gly	Gln	Gln	Leu	Gln	Ala	Glu
	930					935					940				
Arg	Lys	Lys	Met	Ala	Gln	Gln	Met	Leu	Asp	Leu	Glu	Glu	Gln	Leu	Glu
945					950				955						960
Glu	Glu	Glu	Ala	Ala	Arg	Gln	Lys	Leu	Gln	Leu	Glu	Lys	Val	Thr	Ala
				965					970					975	
Glu	Ala	Lys	Ile	Lys	Lys	Leu	Glu	Asp	Glu	Ile	Leu	Val	Met	Asp	Asp
			980					985					990		
Gln	Asn	Asn	Lys	Leu	Ser	Lys	Glu	Arg	Lys	Leu	Leu	Glu	Glu	Arg	Ile
	995						1000					1005			
Ser	Asp	Leu	Thr	Thr	Asn	Leu	Ala	Glu	Glu	Glu	Glu	Lys	Ala	Lys	Asn
	1010					1015					1020				
Leu	Thr	Lys	Leu	Lys	Asn	Lys	His	Glu	Ser	Met	Ile	Ser	Glu	Leu	Glu
1025					1030					1035					1040
Val	Arg	Leu	Lys	Lys	Glu	Glu	Lys	Ser	Arg	Gln	Glu	Leu	Glu	Lys	Leu
				1045					1050					1055	
Lys	Arg	Lys	Leu	Glu	Gly	Asp	Ala	Ser	Asp	Phe	His	Glu	Gln	Ile	Ala
			1060					1065					1070		
Asp	Leu	Gln	Ala	Gln	Ile	Ala	Glu	Leu	Lys	Met	Gln	Leu	Ala	Lys	Lys
	1075						1080					1085			
Glu	Glu	Glu	Leu	Gln	Ala	Ala	Leu	Ala	Arg	Leu	Asp	Asp	Glu	Ile	Ala
	1090					1095					1100				
Gln	Lys	Asn	Asn	Ala	Leu	Lys	Lys	Ile	Arg	Glu	Leu	Glu	Gly	His	Ile
1105					1110					1115					1120
Ser	Asp	Leu	Gln	Glu	Asp	Leu	Asp	Ser	Glu	Arg	Ala	Ala	Arg	Asn	Lys
			1125						1130					1135	
Ala	Glu	Lys	Gln	Lys	Arg	Asp	Leu	Gly	Glu	Glu	Leu	Glu	Ala	Leu	Lys
			1140					1145					1150		
Thr	Glu	Leu	Glu	Asp	Thr	Leu	Asp	Ser	Thr	Ala	Thr	Gln	Gln	Glu	Leu

1155	1160	1165
Arg Ala Lys Arg Glu Gln Glu Val Thr Val Leu Lys Lys Ala Leu Asp		
1170	1175	1180
Glu Glu Thr Arg Ser His Glu Ala Gln Val Gln Glu Met Arg Gln Lys		
1185	1190	1195
His Ala Gln Ala Val Glu Glu Leu Thr Glu Gln Leu Glu Gln Phe Lys		1200
1205	1210	1215
Arg Ala Lys Ala Asn Leu Asp Lys Asn Lys Gln Thr Leu Glu Lys Glu		
1220	1225	1230
Asn Ala Asp Leu Ala Gly Glu Leu Arg Val Leu Gly Gln Ala Lys Gln		
1235	1240	1245
Glu Val Glu His Lys Lys Lys Lys Leu Glu Ala Gln Val Gln Glu Leu		
1250	1255	1260
Gln Ser Lys Cys Ser Asp Gly Glu Arg Ala Arg Ala Glu Leu Asn Asp		
1265	1270	1275
Lys Val His Lys Leu Gln Asn Glu Val Glu Ser Val Thr Gly Met Leu		
1285	1290	1295
Asn Glu Ala Glu Gly Lys Ala Ile Lys Leu Ala Lys Asp Val Ala Ser		
1300	1305	1310
Leu Ser Ser Gln Leu Gln Asp Thr Gln Glu Leu Leu Gln Glu Glu Thr		
1315	1320	1325
Arg Gln Lys Leu Asn Val Ser Thr Lys Leu Arg Gln Leu Glu Glu Glu		
1330	1335	1340
Arg Asn Ser Leu Gln Asp Gln Leu Asp Glu Glu Met Glu Ala Lys Gln		
1345	1350	1355
Asn Leu Glu Arg His Ile Ser Thr Leu Asn Ile Gln Leu Ser Asp Ser		
1365	1370	1375
Lys Lys Lys Leu Gln Asp Phe Ala Ser Thr Val Glu Ala Leu Glu Glu		
1380	1385	1390
Gly Lys Lys Arg Phe Gln Lys Glu Ile Glu Asn Leu Thr Gln Gln Tyr		
1395	1400	1405
Glu Glu Lys Ala Ala Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg		
1410	1415	1420
Leu Gln Gln Glu Leu Asp Asp Leu Val Val Asp Leu Asp Asn Gln Arg		
1425	1430	1435
Gln Leu Val Ser Asn Leu Glu Lys Lys Gln Arg Lys Phe Asp Gln Leu		
1445	1450	1455
Leu Ala Glu Glu Lys Asn Ile Ser Ser Lys Tyr Ala Asp Glu Arg Asp		
1460	1465	1470
Arg Ala Glu Ala Glu Ala Arg Glu Lys Glu Thr Lys Ala Leu Ser Leu		
1475	1480	1485
Ala Arg Ala Leu Glu Glu Ala Leu Glu Ala Lys Glu Glu Leu Glu Arg		
1490	1495	1500
Thr Asn Lys Met Leu Lys Ala Glu Met Glu Asp Leu Val Ser Ser Lys		
1505	1510	1515
Asp Asp Val Gly Lys Asn Val His Glu Leu Glu Lys Ser Lys Arg Ala		
1525	1530	1535
Leu Glu Thr Gln Met Glu Glu Met Lys Thr Gln Leu Glu Glu Leu Glu		
1540	1545	1550
Asp Glu Leu Gln Ala Thr Glu Asp Ala Lys Leu Arg Leu Glu Val Asn		
1555	1560	1565
Met Gln Ala Leu Lys Gly Gln Phe Glu Arg Asp Leu Gln Ala Arg Asp		
1570	1575	1580
Glu Gln Asn Glu Glu Lys Arg Arg Gln Leu Gln Arg Gln Leu His Glu		
1585	1590	1595
Tyr Glu Thr Glu Leu Glu Asp Glu Arg Lys Gln Arg Ala Leu Ala Ala		
1605	1610	1615
Ala Ala Lys Lys Lys Leu Glu Gly Asp Leu Lys Asp Leu Glu Leu Gln		
1620	1625	1630

Ala Asp Ser Ala Ile Lys Gly Arg Glu Glu Ala Ile Lys Gln Leu Arg
 1635 1640 1645
 Lys Leu Gln Ala Gln Met Lys Asp Phe Gln Arg Glu Leu Glu Asp Ala
 1650 1655 1660
 Arg Ala Ser Arg Asp Glu Ile Phe Ala Thr Ala Lys Glu Asn Glu Lys
 1665 1670 1675 1680
 Lys Ala Lys Ser Leu Glu Ala Asp Leu Met Gln Leu Gln Glu Asp Leu
 1685 1690 1695
 Ala Ala Ala Glu Arg Ala Arg Lys Gln Ala Asp Leu Glu Lys Glu Glu
 1700 1705 1710
 Leu Ala Glu Glu Leu Ala Ser Ser Leu Ser Gly Arg Asn Ala Leu Gln
 1715 1720 1725
 Asp Glu Lys Arg Arg Leu Glu Ala Arg Ile Ala Gln Leu Glu Glu Glu
 1730 1735 1740
 Leu Glu Glu Glu Gln Gly Asn Met Glu Ala Met Ser Asp Arg Val Arg
 1745 1750 1755 1760
 Lys Ala Thr Gln Gln Ala Glu Gln Leu Ser Asn Glu Leu Ala Thr Glu
 1765 1770 1775
 Arg Ser Thr Ala Gln Lys Asn Glu Ser Ala Arg Gln Gln Leu Glu Arg
 1780 1785 1790
 Gln Asn Lys Glu Leu Arg Ser Lys Leu His Glu Met Glu Gly Ala Val
 1795 1800 1805
 Lys Ser Lys Phe Lys Ser Thr Ile Ala Ala Leu Glu Ala Lys Ile Ala
 1810 1815 1820
 Gln Leu Glu Glu Gln Val Glu Gln Glu Ala Arg Glu Lys Gln Ala Ala
 1825 1830 1835 1840
 Thr Lys Ser Leu Lys Gln Lys Asp Lys Lys Leu Lys Glu Ile Leu Leu
 1845 1850 1855
 Gln Val Glu Asp Glu Arg Lys Met Ala Glu Gln Tyr Lys Glu Gln Ala
 1860 1865 1870
 Glu Lys Gly Asn Ala Arg Val Lys Gln Leu Lys Arg Gln Leu Glu Glu
 1875 1880 1885
 Ala Glu Glu Glu Ser Gln Arg Ile Asn Ala Asn Arg Arg Lys Leu Gln
 1890 1895 1900
 Arg Glu Leu Asp Glu Ala Thr Glu Ser Asn Glu Ala Met Gly Arg Glu
 1905 1910 1915 1920
 Val Asn Ala Leu Lys Ser Lys Leu Arg Gly Pro Pro Pro Gln Glu Thr
 1925 1930 1935
 Ser Gln

<210> 165

<211> 958

<212> DNA

<213> Homo sapiens

<400> 165

```

tctaaagctc agtggagctg ggtcatctca ggccttggct ccttgaactt ttggccgccca 60
tgtgcttccc gaaggtcctc tctgatgaca tgaagaagct gaaggcccca atggtaatgc 120
tcctccctac ttctgctcag gggttggggg cctgggtctc agcgtgtgac actgaggaca 180
ctgtgggaca cctgggaccc tggagggaca aggatccggc cctttgggtgc caactctgcc 240
tctcttcaca gcaccaggcc atagaaagat tttatgataa aatgcaaaat gcagaatcag 300
gacgtggaca ggtgatgtcg agcctggcag agctggagga cgacttcaaa gagggctacc 360
tgagacagt ggcggttat tatgaggagc agcaccaga gctcactcct ctacttgaaa 420
aagaaagaga tggattacgg tgccgaggca acagatcccc tgtcccggat gttgaggatc 480
ccgcaaccga ggagcctggg gagagctttt gtracaaggt catgagatgg ttccaggcca 540
tgctgcagcg gctgcagacc tgggtggcacg gggttctggc ctgggtgaag gagaaggtgg 600
tggccctggg ccatgcagtg caggccctct ggaaacagtt ccagagtttc tgctgctctc 660

```

239

tgtcagagct cttcatgtcc tctttccagt cctacggagc cccacggggg gacaaggagg 720
 agctgacacc ccagaagtgc tctgaacccc aatcctcaaa atgaagatac tgacaccacc 780
 tttgccctcc ccgtcacgc gcaccacccc tgacctctcc ctcagctgtc ctgtgccccg 840
 ccctctcccg cacactcagt cccctgcct ggcgcttcctg ccgcagctct gacctggtgc 900
 tgtcgccctg gcatcttaat aaaacctgct tatacttccc tggcagggag ataccatg 958

<210> 166

<211> 234

<212> PRT

<213> Homo sapiens

<400> 166

Met	Cys	Phe	Pro	Lys	Val	Leu	Ser	Asp	Asp	Met	Lys	Lys	Leu	Lys	Ala
1				5					10					15	
Arg	Met	Val	Met	Leu	Leu	Pro	Thr	Ser	Ala	Gln	Gly	Leu	Gly	Ala	Trp
			20					25					30		
Val	Ser	Ala	Cys	Asp	Thr	Glu	Asp	Thr	Val	Gly	His	Leu	Gly	Pro	Trp
		35					40					45			
Arg	Asp	Lys	Asp	Pro	Ala	Leu	Trp	Cys	Gln	Leu	Cys	Leu	Ser	Ser	Gln
	50					55					60				
His	Gln	Ala	Ile	Glu	Arg	Phe	Tyr	Asp	Lys	Met	Gln	Asn	Ala	Glu	Ser
65					70				75					80	
Gly	Arg	Gly	Gln	Val	Met	Ser	Ser	Leu	Ala	Glu	Leu	Glu	Asp	Asp	Phe
			85						90					95	
Lys	Glu	Gly	Tyr	Leu	Glu	Thr	Val	Ala	Ala	Tyr	Tyr	Glu	Glu	Gln	His
			100						105					110	
Pro	Glu	Leu	Thr	Pro	Leu	Leu	Glu	Lys	Glu	Arg	Asp	Gly	Leu	Arg	Cys
		115					120					125			
Arg	Gly	Asn	Arg	Ser	Pro	Val	Pro	Asp	Val	Glu	Asp	Pro	Ala	Thr	Glu
		130					135					140			
Glu	Pro	Gly	Glu	Ser	Phe	Cys	Asx	Lys	Val	Met	Arg	Trp	Phe	Gln	Ala
145					150				155						160
Met	Leu	Gln	Arg	Leu	Gln	Thr	Trp	Trp	His	Gly	Val	Leu	Ala	Trp	Val
			165						170					175	
Lys	Glu	Lys	Val	Val	Ala	Leu	Val	His	Ala	Val	Gln	Ala	Leu	Trp	Lys
			180					185					190		
Gln	Phe	Gln	Ser	Phe	Cys	Cys	Ser	Leu	Ser	Glu	Leu	Phe	Met	Ser	Ser
		195					200					205			
Phe	Gln	Ser	Tyr	Gly	Ala	Pro	Arg	Gly	Asp	Lys	Glu	Glu	Leu	Thr	Pro
	210					215					220				
Gln	Lys	Cys	Ser	Glu	Pro	Gln	Ser	Ser	Lys						
225						230									

<210> 167

<211> 958

<212> DNA

<213> Homo sapiens

<400> 167

tctaaagctc agtggagctg ggtcatctca ggccttggct ccttgaactt ttggccgcca 60
 tgtgcttccc gaaggctcctc tctgatgaca tgaagaagct gaaggcccca atggtaatgc 120
 tcctccctac ttctgctcag gggttggggg cctgggtctc agcgtgtgac actgaggaca 180
 ctgtgggaca cctgggaccc tggagggaca aggatccggc cctttggtgc caactctgcc 240
 tctcttcaca gcaccaggcc atagaaagat tttatgataa aatgcaaaat gcagaatcag 300
 gacgtggaca ggtgatgtcg agcctggcag agctggagga cgacttcaaa gagggctacc 360
 tggagacagt ggcggcttat tatgaggagc agcaccaga gctcactcct ctacttgaaa 420
 aagaaagaga tggattacgg tgccgaggca acagatcccc tgtcccggat gttgaggatc 480
 ccgcaaccga ggagcctggg gagagctttt gtgacaaggt catgagatgg ttccaggcca 540

```

tgctgcagcg gctgcagacc tgggtggcacg gggtttctggc ctgggtgaag gagaaggtgg 600
tggccctggg ccatgcagtg caggccctct ggaaacagtt ccagagtttc tgctgctctc 660
tgtcagagct cttcatgtcc tctttccagt cctacggagc ccacacgggg gacaaggagg 720
agctgacacc ccagaagtgc tctgaacccc aatcctcaaa atgaagatac tgacaccacc 780
tttgccctcc ccgtcaccgc gcacccaccc tgacccctcc ctcagctgtc ctgtgccccg 840
ccctctcccg cacactcagt ccccctgcct ggcgttcctg ccgcagctct gacctggtgc 900
tgtcgccctg gcattctaat aaaacctgct tatacttccc tggcagggag ataccatg 958

```

<210> 168

<211> 234

<212> PRT

<213> Homo sapiens

<400> 168

```

Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
 1          5          10          15
Arg Met Val Met Leu Leu Pro Thr Ser Ala Gln Gly Leu Gly Ala Trp
      20          25          30
Val Ser Ala Cys Asp Thr Glu Asp Thr Val Gly His Leu Gly Pro Trp
      35          40          45
Arg Asp Lys Asp Pro Ala Leu Trp Cys Gln Leu Cys Leu Ser Ser Gln
      50          55          60
His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala Glu Ser
      65          70          75          80
Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp Asp Phe
      85          90          95
Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu Gln His
      100          105          110
Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu Arg Cys
      115          120          125
Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala Thr Glu
      130          135          140
Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe Gln Ala
      145          150          155          160
Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala Trp Val
      165          170          175
Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu Trp Lys
      180          185          190
Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser
      195          200          205
Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu Thr Pro
      210          215          220
Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
      225          230

```

<210> 169

<211> 1005

<212> DNA

<213> Homo sapiens

<400> 169

```

tgtgtgtgta ttgtgtggat gccgcgcgtg tcttctcttc tttccagaga tggctaacag 60
gggcccggag tatggcttaa gccgagaggt gcaggagaag atcgagcaga agtatgatgc 120
ggacctggag aacaagctgg tggactggat catcctgcag tgcgccgagg acatagagca 180
cccgcctccc ggcaggggccc attttcagaa atggttaatg gacgggacgg tcctgtgcaa 240
gctgataaat agttttatacc caccaggaca agagcccata cccaagatct cagagtcaaa 300
gatggctttt aagcagatgg agcaaattct ccagttccta aaagctgcgg agacctatgg 360
tgtcagaacc accgacatct ttcagacggt ggatctatgg gaagggaagg acatggcagc 420

```



```

tgtgcagagg accctgatgg ctttaggcag cgttgcagtc accaaggatg atggctgcta 480
tcggggagag ccacccctggg ttccacaggaa agcccagcag aatcggagag gcttttccga 540
ggagcagcctt cgccaggggac agaacgtaat aggcctgcag atggggcagca acaagggagc 600
ctcccaggcgg ggcacgacag ggtacgggat gccaggcag atcatgttag gacgcggcat 660
cctgcccctg gtagagagga cgaatgttcc acaccatggg ctctacgaaa aagaaatagt 720
tagtcacctt ctgaccttct cctctttctc aaagccttct gtccctgggt tttgcaagtg 780
ctgcatttcc gccgagaatc cgcgttgctt actgctgcca cctcctgttc atttagaact 840
atgcaaagac tccgcttccg ttttcctgag ctccctcgggc cccagagtct ctgtttgatt 900
atttatttat ttatttattt atttgccaaa aattctcctc ttcaacttat agaatgcacc 960
taataaagta attaagtctt gtggaaaaaa aaaaaaaaaa aaaaaa 1005

```

<210> 170

<211> 282

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Ala Asn Arg Gly Pro Ser Tyr Gly Leu Ser Arg Glu Val Gln Glu
 1          5          10          15
Lys Ile Glu Gln Lys Tyr Asp Ala Asp Leu Glu Asn Lys Leu Val Asp
          20          25          30
Trp Ile Ile Leu Gln Cys Ala Glu Asp Ile Glu His Pro Pro Pro Gly
          35          40          45
Arg Ala His Phe Gln Lys Trp Leu Met Asp Gly Thr Val Leu Cys Lys
          50          55          60
Leu Ile Asn Ser Leu Tyr Pro Pro Gly Gln Glu Pro Ile Pro Lys Ile
65          70          75          80
Ser Glu Ser Lys Met Ala Phe Lys Gln Met Glu Gln Ile Ser Gln Phe
          85          90          95
Leu Lys Ala Ala Glu Thr Tyr Gly Val Arg Thr Thr Asp Ile Phe Gln
          100          105          110
Thr Val Asp Leu Trp Glu Gly Lys Asp Met Ala Ala Val Gln Arg Thr
          115          120          125
Leu Met Ala Leu Gly Ser Val Ala Val Thr Lys Asp Asp Gly Cys Tyr
          130          135          140
Arg Gly Glu Pro Ser Trp Phe His Arg Lys Ala Gln Gln Asn Arg Arg
145          150          155          160
Gly Phe Ser Glu Glu Gln Leu Arg Gln Gly Gln Asn Val Ile Gly Leu
          165          170          175
Gln Met Gly Ser Asn Lys Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr
          180          185          190
Gly Met Pro Arg Gln Ile Met Leu Gly Arg Gly Ile Leu Pro Leu Val
          195          200          205
Glu Arg Thr Asn Val Pro His His Gly Leu Tyr Glu Lys Glu Ile Val
210          215          220
Ser His Leu Leu Thr Phe Ser Ser Phe Ser Lys Pro Ser Val Pro Gly
225          230          235          240
Phe Cys Lys Cys Cys Ile Ser Ala Glu Asn Pro Arg Cys Leu Leu Leu
          245          250          255
Pro Pro Pro Val His Leu Glu Leu Cys Lys Asp Ser Ala Ser Val Phe
          260          265          270
Leu Ser Ser Ser Gly Pro Arg Val Ser Val
          275          280

```

<210> 171

<211> 942

<212> DNA

<213> Homo sapiens

<400> 171

```

atgagaattg cagtgatttg cttttgcctc ctaggcatca cctgtgccat accagttaaa 60
caggctgatt ctggaagtgc tgaggaaaag cagctttaca acaaataccc agatgctgtg 120
gccacatggc taaaccctga cccatctcag aagcagaatc tcctagcccc acagaatgct 180
gtgtcctctg aagaaaccaa tgacttttaa caagagaccc ttccaagtaa gtccaacgaa 240
agccatgacc acatggatga tatggatgat gaagatgatg atgaccatgt ggacagccag 300
gactccattg actcgaacga ctctgatgat gtagatgaca ctgatgattc tcaccagtct 360
gatgagtctc accattctga tgaatctgat gaactgggtc ctgattttcc caccggacctg 420
ccagcaaccg aagttttcac tccagttgtc cccacagtag acacatatga tggccgaggt 480
gatagtgtgg tttatggact gaggtcaaaa tctaagaagt ttgcagacc tgacatccag 540
tacctgatg ctacagacga gcacatcacc tcacacatgg aaagcgagga gttgaatggt 600
gcatacaagg ccatccccgt tgcccaggac ctgaacgcgc cttctgattg ggacagccgt 660
gggaaggaca gttatgaaac gagtcagctg gatgaccaga gtgctgaagc ccacagccac 720
aagcagtcca gattatataa gcggaaagct aatgatgaga gcaatgagca ttccgatgtg 780
attgatagtc aggaactttc caaagtcagc cgtgaattcc acagccatga atttcacagc 840
catgaagata tgctggttgt agaccccaaa agtaagggaag aagataaaca cctgaaattt 900
cgtattttctc atgaattaga tagtgcattc tctgagggtc at 942

```

<210> 172

<211> 314

<212> PRT

<213> Homo sapiens

<400> 172

```

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
 1           5           10           15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
 20           25           30
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
 35           40           45
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu
 50           55           60
Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu
 65           70           75           80
Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His
 85           90           95
Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp
100           105           110
Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu
115           120           125
Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu
130           135           140
Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly
145           150           155           160
Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg
165           170           175
Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu His Ile Thr Ser His
180           185           190
Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala
195           200           205
Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser
210           215           220
Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Ala His Ser His
225           230           235           240
Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu
245           250           255
His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu
260           265           270

```

Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp
 275 280 285
 Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His
 290 295 300
 Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
 305 310

<210> 173
 <211> 1524
 <212> DNA
 <213> Homo sapiens

<400> 173
 gcagagcaca gcatcgctcgg gaccagactc gtctcaggcc agttgcagcc ttctcagcca 60
 aacgccgacc aaggaaaact cactaccatg agaattgcag tgatttgctt ttgcctocta 120
 ggcacacact gtgccatacc agttaaacag gctgattctg gaagttctga ggaaaagcag 180
 ctttacaaca aatacccaga tgctgtggcc acatggctaa accctgaccc atctcagaag 240
 cagaatctcc tagccccaca gacccttcca agtaagtcca acgaaagcca tgaccacatg 300
 gatgatattg atgatgaaga tgatgatgac catgtggaca gccaggactc cattgactcg 360
 aacgactctg atgatgtaga tgacactgat gattctcacc agtctgatga gtctcaccat 420
 tctgatgaat ctgatgaact ggtcactgat tttcccacgg acctgccagc aaccgaagtt 480
 ttcactccag ttgtccccac agtagacaca tatgatggcc gaggtgatag tgtgggtttr 540
 ggactgaggt caaaatctaa gaagtttctg agacctgaca tccagtaccc tgatgctaca 600
 gacgaggaca tcacctcaca catggaaagc gaggagtga atggtgcata caaggccatc 660
 cccgttgccc aggacctgaa cgcgccttct gattgggaca gccgtgggaa ggacagttat 720
 gaaacgagtc agctggatga ccagagtgtc gaaaccaca gccacaagca gtccagatta 780
 tataagcggg aagccaatga tgagagcaat gagcattccg atgtgattga tagtcaggaa 840
 ctttccaaag tcagccgtga attccacagc catgaatttc acagccatga agatatgctg 900
 gttgtagacc ccaaaagtaa ggaagaagat aaacacctga aatttcgtat ttctcatgaa 960
 ttagatagtg catcttctga ggtcaattaa aaggagaaaa aatacaattt ctcacttttc 1020
 atttagtcaa aagaaaaaat gctttatagc aaaatgaaag agaacatgaa atgcttcttt 1080
 ctcaagttat tgggtgaatg tgtatctatt tgagtctgga aataactaat gtgtttgata 1140
 attagtttag tttgtggctt catggaaact ccctgtaaac taaaagcttc agggttatgt 1200
 ctatgttcat tctatagaag aaatgcaaac tatcactgta ttttaatat ttgtattctc 1260
 tcatgaatag aaatttatgt agaagcaaac aaaatacttt taccacttta aaaagagaat 1320
 ataacatttt atgtcactat aatcttttgt tttttaagtt agtgtatat ttgttgtgat 1380
 tatctttttg tgggtggaat aaatctttta tcttgaatgt aataagaatt tgggtggtgc 1440
 aattgcttat ttgttttccc acggttgtcc agcaattaat aaaacataac cttttttact 1500
 gcctaaaaaa aaaaaaaaaa aaaa 1524

<210> 174
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 174
 Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
 1 5 10 15
 Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
 20 25 30
 Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
 35 40 45
 Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
 50 55 60
 Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
 65 70 75 80
 Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp
 85 90 95

```

Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser
      100      105      110
Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala
      115      120      125
Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly
      130      135      140
Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
      145      150      155      160
Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr
      165      170      175
Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro
      180      185      190
Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys
      195      200      205
Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His
      210      215      220
Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser
      225      230      235      240
Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
      245      250      255
Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
      260      265      270
Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile
      275      280      285
Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
      290      295      300

```

<210> 175
 <211> 861
 <212> DNA
 <213> Homo sapiens

```

<400> 175
atgagaattg cagtgatttg cttttgcctc ctaggcacat cctgtgccat accagttaaa 60
caggctgatt ctggaagttc tgaggaaaag cagaatgctg tgtcctctga agaaaccaat 120
gacttttaaac aagagaccct tccaagtaag tccaacgaaa gccatgacca catggatgat 180
atggatgatg aagatgatga tgaccatgtg gacagccagg actccattga ctogaacgac 240
tctgatgatg tagatgacac tgatgattct caccagtctg atgagtctca ccattctgat 300
gaatctgatg aactggtcac tgattttccc acggacctgc cagcaaccga agttttcact 360
ccagttgtcc ccacagtaga cacatatgat ggccgagggt atagtgtggt ttatggactg 420
aggtcaaaat ctaagaagtt tcgcagacct gacatccagt accctgatgc tacagacgag 480
cacatcacct cacacatgga aagcgaggag ttgaatggtg catacaaggc catccccgtt 540
gcccgaggacc tgaacgcgcc ttctgattgg gacagccgtg ggaaggacag ttatgaaacg 600
agtcagctgg atgaccagag tgctgaagcc cacagccaca agcagtcacg attatataag 660
cgaaagcta atgatgagag caatgagcat tccgatgtga ttgatagtca ggaactttcc 720
aaagtcagcc gtgaattcca cagccatgaa tttcacagcc atgaagatat gctggttgta 780
gaccccaaaa gtaaggaaga agataaacac ctgaaatttc gtattttctca tgaattagat 840
agtgcattct ctgaggtcaa t
      861

```

<210> 176
 <211> 287
 <212> PRT
 <213> Homo sapiens

```

<400> 176
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
  1           5           10          15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Asn

```

<400>	177					
agagactcaa	gatgattccc	tttttaccca	tgttttctct	actattgctg	cttattgtta	60
accctataaa	cgccaacaat	cattatgaca	agatcttggc	tcatagtcgt	atcaggggtc	120
gggaccaagg	cccaaatgtc	tgtgcccttc	aacagatttt	gggcaccaa	aagaaatact	180
tcagcacttg	taagaactgg	tataaaaagt	ccatctgtgg	acagaaaacg	actgttttat	240
atgaatgttg	cctctggttat	atgagaatgg	aaggaatgaa	aggctgccca	gcagttttgc	300
ccattgacca	tgtttatggc	actctgggca	ctgtgggagc	caccacaacg	cagcgcattt	360
ctgagcctc	aaaactgagg	gaggagatcg	agggaaaggg	atccttcact	tactttgcac	420
cgagtaaatga	ggcttgggac	aacttggatt	ctgatatccg	tagaggtttg	gagagcaacg	480
tgaatgttga	attactgaat	gotttacata	gtcacatgat	taataagaga	atgttgacca	540
aggacttaaa	aaatggcatg	attattcctt	caatgtataa	caatttgggg	cttttcatta	600
accattatcc	taatgggggt	gtcactgtta	atttgtgctcg	aatcatccat	gggaaccaga	660
ttgcaacaaa	tgggtgttgc	catgtcattg	acogtgtgct	tacacaaatt	ggtacctcaa	720
ttcaagactt	cattgaagca	gaagatgacc	tttcatcttt	tagagcagct	gccatcacat	780
cggacataat	ggaggccctt	ggaagagacg	gtcacttcac	actctttgct	cccaccaatg	840
aggcttttga	gaaacttcca	cgaggtgtcc	tagaaagggt	catggggagc	aaagtggctt	900
cgaagctct	tatgaagtac	cacatcttaa	atactctoca	gtgttctgag	tctattatgg	960
gaggagcagt	ctttgagacg	ctggaaggaa	atacaattga	gataggatgt	gacggtgaca	1020
gtataaacgt	aaatggaatc	aaaatggtga	acaaaaagga	tattgtgaca	aataatggtg	1080

```

tgatccattt gattgatcag gtcctaattc ctgattctgc caaacaagtt attgagctgg 1140
ctggaaaaca gcaaaccacc ttcacggatc ttgtggccca attaggcttg gcatctgctc 1200
tgaggccaga tggagaatac actttgctgg cacctgtgaa taatgcattt tctgatgata 1260
ctctcagcat ggttcagcgc ctctttaaatt taattctgca gaatcacata ttgaaagtaa 1320
aagttggcct taatgagctt tacaacgggc aaatactgga aaccatcgga ggcaaacagc 1380
tcagagtctt cgtatatcgt acagctgtct gcattgaaaa ttcatgcatg gagaaagggg 1440
gtaagcaagg gagaaacggg gcgattcaca tattccgcga gatcatcaag ccagcagaga 1500
aatcctcca tgaaaagtta aaacaagata agcgctttag caccttcctc agcctacttg 1560
aagctgcaga cttgaaagag ctcttgacac aacctggaga ctggacatta tttgtgccaa 1620
ccaatgatgc ttttaaggga atgactagtg aagaaaaaga aattctgata cgggacaaaa 1680
atgctcttca aaacatcatt ctttatcacc tgacaccagg agttttcatt ggaaaaggat 1740
ttgaacctgg tgttactaac attttaaaga ccacacaagg aagcaaaatc tttctgaaag 1800
aagtaaataa tacacttctg gtgaatgaat tgaaatcaaa agaattctgac atcatgacaa 1860
caaattggtg aattcatggt gtagataaac tcctctatcc agcagacaca cctgttgga 1920
atgatcaact gctggaaata cttaataaat taatcaata catccaaatt aagtttgttc 1980
gtggttagcac cttcaaagaa atccccgtga ctgtctatac aactaaaatt ataaccaaag 2040
ttgtggaacc aaaaattaaa gtgattgaag gcagtcttca gcctattatc aaaactgaag 2100
gaccacact aacaaaagtc aaaattgaag gtgaacctga attcagactg attaaagaag 2160
gtgaaacaat aactgaagtg atccatggag agccaattat taaaaaatac accaaaatca 2220
ttgatggagt gcctgtggaa ataactgaaa aagagacacg agaagaacga atcattacag 2280
gtcctgaaat aaaatacact aggatttcta ctggagggtg agaaacagaa gaaactctga 2340
agaaattggt acaagaagag gtcaccaagg tcaccaaatt cattgaagggt ggtgatggtc 2400
atttatttga agatgaagaa attaaaagac tgcttcaggg agacacaccc gtgaggaagt 2460
tgcaagccaa caaaaaagtt caaggttcta gaagacgatt aagggaagggt cgttctcagt 2520
gaaaatccaa aaaccagaaa aaaatgttta tacaacccta agtcaataac ctgaccttag 2580
aaaattgtga gagccaagtt gacttcagga actgaaacat cagcacaaag aagcaatcat 2640
caaataattc tgaacacaaa tttaatatat ttttttctga atgagaaaaca tgagggaaat 2700
tgtggagtta gcctcctgtg gtaaaggaat tgaagaaaat ataacacctt acaccttttt 2760
tcatcttgac attaaaagtt ctggctaact ttggaatcca ttagagaaaa atccttgtca 2820
ccagattcat tacaattcaa atcgaagagt tgtgaactgt tatcccattg aaaagaccga 2880
gccttgtatg tatgttatgg atacataaaa tgcacgcaag ccattatctc tccatgggaa 2940
gctaagttat aaaaatagggt gcttgggtgta caaaactttt tatatcaaaa ggctttgcac 3000
atttctatat gagtgggttt actggtaaata tatgttatat tttacaacta attttgtact 3060
ctcagaatgt ttgtcatatg cttcttgcaa tgcataattt ttaatctcaa acgtttcaat 3120
aaaaccattt ttcagatata aagagaatta cttcaaattg agtaattcag aaaaactcaa 3180
gatttaagtt aaaaagtggt ttggacttgg gaa 3213

```

<210> 178

<211> 836

<212> PRT

<213> Homo sapiens

<400> 178

```

Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Ile Val
1           5           10           15
Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
20          25          30
Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
35          40          45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
50          55          60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
65          70          75          80
Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85          90          95
Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100         105         110
Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
115         120         125

```

Lys	Gly	Ser	Phe	Thr	Tyr	Phe	Ala	Pro	Ser	Asn	Glu	Ala	Trp	Asp	Asn
	130					135					140				
Leu	Asp	Ser	Asp	Ile	Arg	Arg	Gly	Leu	Glu	Ser	Asn	Val	Asn	Val	Glu
145					150					155					160
Leu	Leu	Asn	Ala	Leu	His	Ser	His	Met	Ile	Asn	Lys	Arg	Met	Leu	Thr
				165					170					175	
Lys	Asp	Leu	Lys	Asn	Gly	Met	Ile	Ile	Pro	Ser	Met	Tyr	Asn	Asn	Leu
			180					185					190		
Gly	Leu	Phe	Ile	Asn	His	Tyr	Pro	Asn	Gly	Val	Val	Thr	Val	Asn	Cys
		195					200					205			
Ala	Arg	Ile	Ile	His	Gly	Asn	Gln	Ile	Ala	Thr	Asn	Gly	Val	Val	His
	210					215					220				
Val	Ile	Asp	Arg	Val	Leu	Thr	Gln	Ile	Gly	Thr	Ser	Ile	Gln	Asp	Phe
225					230					235					240
Ile	Glu	Ala	Glu	Asp	Asp	Leu	Ser	Ser	Phe	Arg	Ala	Ala	Ala	Ile	Thr
				245					250					255	
Ser	Asp	Ile	Leu	Glu	Ala	Leu	Gly	Arg	Asp	Gly	His	Phe	Thr	Leu	Phe
			260					265					270		
Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Leu	Pro	Arg	Gly	Val	Leu	Glu
		275					280					285			
Arg	Phe	Met	Gly	Asp	Lys	Val	Ala	Ser	Glu	Ala	Leu	Met	Lys	Tyr	His
	290					295					300				
Ile	Leu	Asn	Thr	Leu	Gln	Cys	Ser	Glu	Ser	Ile	Met	Gly	Gly	Ala	Val
305					310					315					320
Phe	Glu	Thr	Leu	Glu	Gly	Asn	Thr	Ile	Glu	Ile	Gly	Cys	Asp	Gly	Asp
			325						330					335	
Ser	Ile	Thr	Val	Asn	Gly	Ile	Lys	Met	Val	Asn	Lys	Lys	Asp	Ile	Val
			340					345					350		
Thr	Asn	Asn	Gly	Val	Ile	His	Leu	Ile	Asp	Gln	Val	Leu	Ile	Pro	Asp
		355					360					365			
Ser	Ala	Lys	Gln	Val	Ile	Glu	Leu	Ala	Gly	Lys	Gln	Gln	Thr	Thr	Phe
	370					375					380				
Thr	Asp	Leu	Val	Ala	Gln	Leu	Gly	Leu	Ala	Ser	Ala	Leu	Arg	Pro	Asp
385					390					395					400
Gly	Glu	Tyr	Thr	Leu	Leu	Ala	Pro	Val	Asn	Asn	Ala	Phe	Ser	Asp	Asp
			405						410					415	
Thr	Leu	Ser	Met	Val	Gln	Arg	Leu	Leu	Lys	Leu	Ile	Leu	Gln	Asn	His
			420					425					430		
Ile	Leu	Lys	Val	Lys	Val	Gly	Leu	Asn	Glu	Leu	Tyr	Asn	Gly	Gln	Ile
		435					440					445			
Leu	Glu	Thr	Ile	Gly	Gly	Lys	Gln	Leu	Arg	Val	Phe	Val	Tyr	Arg	Thr
	450					455					460				
Ala	Val	Cys	Ile	Glu	Asn	Ser	Cys	Met	Glu	Lys	Gly	Ser	Lys	Gln	Gly
465					470					475					480
Arg	Asn	Gly	Ala	Ile	His	Ile	Phe	Arg	Glu	Ile	Ile	Lys	Pro	Ala	Glu
			485						490					495	
Lys	Ser	Leu	His	Glu	Lys	Leu	Lys	Gln	Asp	Lys	Arg	Phe	Ser	Thr	Phe
			500					505					510		
Leu	Ser	Leu	Leu	Glu	Ala	Ala	Asp	Leu	Lys	Glu	Leu	Leu	Thr	Gln	Pro
		515					520					525			
Gly	Asp	Trp	Thr	Leu	Phe	Val	Pro	Thr	Asn	Asp	Ala	Phe	Lys	Gly	Met
	530					535					540				
Thr	Ser	Glu	Glu	Lys	Glu	Ile	Leu	Ile	Arg	Asp	Lys	Asn	Ala	Leu	Gln
545					550					555					560
Asn	Ile	Ile	Leu	Tyr	His	Leu	Thr	Pro	Gly	Val	Phe	Ile	Gly	Lys	Gly
			565						570					575	
Phe	Glu	Pro	Gly	Val	Thr	Asn	Ile	Leu	Lys	Thr	Thr	Gln	Gly	Ser	Lys
			580					585					590		
Ile	Phe	Leu	Lys	Glu	Val	Asn	Asp	Thr	Leu	Leu	Val	Asn	Glu	Leu	Lys

<400>	179					
aacagaactg	caacggagag	actcaagatg	attccctttt	tacccatggt	ttctctacta	60
ttgctgctta	ttgttaaccc	tataaacgcc	aacaatcatt	atgacaagat	cttgggtcat	120
agtcgtatca	ggggtcggga	ccaaggcccc	aatgtctgtg	cccttcaaca	gattttgggc	180
aaaaaaaaa	aataacttcag	cacttgaag	aactggtata	aaaagtccat	ctgtggagcg	240
aaaacgactg	ttttatatga	atggtgcctt	ggttatatga	gaatggaagg	aatgaaagcg	300
tgcccagcag	ttttgcccat	tgacctgttt	tatggcactc	tgggcactcg	gggagccacc	360
acaacgcagc	gctattctga	cgcccaaaaa	ctgaggggagg	agatcgaggg	aaagggatcc	420
ttcacttact	ttgcaccgag	taatgaggct	tgggacaact	tggattctga	tatccgtaga	480
ggtttgagag	gcaacgtgaa	tgttgaaatta	ctgaatgctt	tacatagtca	catgattaat	540
aagagaatgt	tgaccaagga	cttaaaaaat	ggcatgatca	ttccttcaat	gtataacaat	600
ttggggcttt	tcattaacca	ttatcctaatt	ggggttgtta	ctgttaattg	tgctcgaatc	660
atccatggga	accagattgc	aacaaatggt	gtgtgccatg	tcattgaccg	tgtctttaca	720
caaattggta	cctcaattca	agacttcatt	gaagcagaag	atgacctttc	atctttttaga	780
gcagctgcc	tcacatcgga	catattggag	gcccttgga	gagacggtca	cttcacactc	840
tttgctccca	ccaatgaggc	ttttgagaaa	cttccacgag	gtgtcctaga	aaggttcatg	900
ggagacaaag	tggcttcgga	agctcttatg	aagtaccaca	tcttaaatat	tctccagtgt	960
tctgagtcta	ttatgggag	agcagtcctt	gagacgtctg	aaggaaatat	aattgagata	1020
ggatgtgacg	gtgacagtat	aacagtaaat	ggaatcaaaa	tgtgtgaaca	aaaggataatt	1080
gtgacaaata	atggtgtgat	ccatttgatt	gatcaggctc	taattcctga	ttctgccaaa	1140
caagttattg	agctggctgg	aaaacagcaa	accaccttca	cggatcttgt	ggcccaatta	1200


```

ggcttggcat ctgctctgag gccagatgga gaatacactt tgctggcacc tgtgaataat 1260
gcattttctg atgataactct cagcatgggt cagcgccctcc tttaaattaat tctgcagaat 1320
cacatattga aagtaaaagt tggccttaaat gagctttaca acggggcaaat actggaaacc 1380
atcgaggga aacagctcag agtccttcgt tatcgtacag ctgtctgcat tgaaaattca 1440
tgcattggaga aaggagtaga gcaagggaga aacgggtgca ttcacatatt cgcgagatc 1500
atcaagccag cagagaaatc cctccatgaa aagttaaaac aagataagcg ctttagcacc 1560
ttcctcagcc tacttgaagc tgcagacttg aaagagctcc tgacacaacc tggagactgg 1620
acattatttg tgccaaccaa tgatgctttt aagggaatga ctagtgaaga aaaagaaatt 1680
ctgatacggg acaaaaatgc tcttcaaaac atcattcttt atcacctgac accaggagtt 1740
ttcattggaa aaggatttga acctggtgtt actaacattt taaagaccac acaaggaagc 1800
aaaatctttc tgaaagaagt aaatgataca cttctggtga atgaattgaa atcaaaagaa 1860
tctgacatca tgacaacaaa tgggtgaatt catgtttag ataaactcct ctatccagca 1920
gacacacctg ttggaatga tcaactgctg gaaatactta ataaattaat caaatatc 1980
caaatgaagt ttgttcgttg tagcaccttc aaagaaatcc ccgtgactgt ctataagcca 2040
attattaaaa aatacaccaa aatcattgat ggagtgcctg tggaaataac tgaaaaagag 2100
acacgagaag aacgaatcat tacaggtcct gaaataaaat acactaggat ttctactgga 2160
ggtggagaaa cagaagaaac tctgaagaaa ttgttacaag aagaggtcac caaggtcacc 2220
aaattcattg aagggtggtga tggtcattta tttgaagatg aagaaattaa aagactgctt 2280
caggagagaca caccgctgag gaagttgcaa gccacaacaaa aagttcaagg ttctagaaga 2340
cgattaaggg aaggctggtc tcagtgaaaa tccaaaaacc agaaaaaaat gtttatacaa 2400
ccctaagtc ataacctgac cttagaaaaat tgtgagagcc aagttgactt caggaactga 2460
aacatcagca caaagaagca atcatcaaat aattctgaac acaaatttaa tatttttttt 2520
tctgaatgag aaacatgagg gaaattgttg agttagcctc ctgtggagtt agcctcctgt 2580
ggtaaaggaa ttgaagaaaa tataacacct tacacccttt ttcatcttga cattaaaagt 2640
tctggctaac tttggaatcc attagagaaa aatccttgtc accagattca ttacaattca 2700
aatcgaagag ttgtgaactg ttatcccatt gaaaagaccg agccttgtat gtatgttatg 2760
gatacataaa atgcacgcaa gccattatct ctccatggga agctaagtta taaaaatagg 2820
tgcttgggtg acaaaaacttt ttatatcaaa aggctttgca catttctata tgagtgggtt 2880
tactggtaaa ttatgttatt ttttacaact aattttgtac tctcagaatg tttgtcatat 2940
gcttcttgca atgcataatt tttaatctca aacgtttcaa taaaaccatt tttcagatat 3000
aaagagaatt acttcaaatt gagtaattca gaaaaactca agattttaagt taaaaagtgg 3060
tttggacttg ggaacag 3077

```

<210> 180

<211> 779

<212> PRT

<213> Homo sapiens

<400> 180

```

Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Ile Val
1           5           10           15
Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
20           25           30
Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
35           40           45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
50           55           60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
65           70           75           80
Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85           90           95
Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100          105          110
Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
115          120          125
Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
130          135          140
Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
145          150          155          160

```

Leu	Leu	Asn	Ala	Leu	His	Ser	His	Met	Ile	Asn	Lys	Arg	Met	Leu	Thr
				165					170					175	
Lys	Asp	Leu	Lys	Asn	Gly	Met	Ile	Ile	Pro	Ser	Met	Tyr	Asn	Asn	Leu
			180					185					190		
Gly	Leu	Phe	Ile	Asn	His	Tyr	Pro	Asn	Gly	Val	Val	Thr	Val	Asn	Cys
		195					200					205			
Ala	Arg	Ile	Ile	His	Gly	Asn	Gln	Ile	Ala	Thr	Asn	Gly	Val	Val	His
		210				215					220				
Val	Ile	Asp	Arg	Val	Leu	Thr	Gln	Ile	Gly	Thr	Ser	Ile	Gln	Asp	Phe
225						230				235					240
Ile	Glu	Ala	Glu	Asp	Leu	Ser	Ser	Phe	Arg	Ala	Ala	Ala	Ile	Thr	
				245				250					255		
Ser	Asp	Ile	Leu	Glu	Ala	Leu	Gly	Arg	Asp	Gly	His	Phe	Thr	Leu	Phe
			260					265					270		
Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Leu	Pro	Arg	Gly	Val	Leu	Glu
			275				280					285			
Arg	Phe	Met	Gly	Asp	Lys	Val	Ala	Ser	Glu	Ala	Leu	Met	Lys	Tyr	His
		290				295					300				
Ile	Leu	Asn	Thr	Leu	Gln	Cys	Ser	Glu	Ser	Ile	Met	Gly	Gly	Ala	Val
305					310					315					320
Phe	Glu	Thr	Leu	Glu	Gly	Asn	Thr	Ile	Glu	Ile	Gly	Cys	Asp	Gly	Asp
				325					330					335	
Ser	Ile	Thr	Val	Asn	Gly	Ile	Lys	Met	Val	Asn	Lys	Lys	Asp	Ile	Val
			340					345					350		
Thr	Asn	Asn	Gly	Val	Ile	His	Leu	Ile	Asp	Gln	Val	Leu	Ile	Pro	Asp
		355					360					365			
Ser	Ala	Lys	Gln	Val	Ile	Glu	Leu	Ala	Gly	Lys	Gln	Gln	Thr	Thr	Phe
		370				375					380				
Thr	Asp	Leu	Val	Ala	Gln	Leu	Gly	Leu	Ala	Ser	Ala	Leu	Arg	Pro	Asp
385					390					395					400
Gly	Glu	Tyr	Thr	Leu	Leu	Ala	Pro	Val	Asn	Asn	Ala	Phe	Ser	Asp	Asp
				405					410					415	
Thr	Leu	Ser	Met	Val	Gln	Arg	Leu	Leu	Lys	Leu	Ile	Leu	Gln	Asn	His
			420					425					430		
Ile	Leu	Lys	Val	Lys	Val	Gly	Leu	Asn	Glu	Leu	Tyr	Asn	Gly	Gln	Ile
		435					440					445			
Leu	Glu	Thr	Ile	Gly	Gly	Lys	Gln	Leu	Arg	Val	Phe	Val	Tyr	Arg	Thr
		450				455					460				
Ala	Val	Cys	Ile	Glu	Asn	Ser	Cys	Met	Glu	Lys	Gly	Ser	Lys	Gln	Gly
465					470					475					480
Arg	Asn	Gly	Ala	Ile	His	Ile	Phe	Arg	Glu	Ile	Ile	Lys	Pro	Ala	Glu
				485					490					495	
Lys	Ser	Leu	His	Glu	Lys	Leu	Lys	Gln	Asp	Lys	Arg	Phe	Ser	Thr	Phe
			500					505					510		
Leu	Ser	Leu	Glu	Ala	Ala	Asp	Leu	Lys	Glu	Leu	Leu	Thr	Gln	Pro	
			515				520					525			
Gly	Asp	Trp	Thr	Leu	Phe	Val	Pro	Thr	Asn	Asp	Ala	Phe	Lys	Gly	Met
		530				535					540				
Thr	Ser	Glu	Glu	Lys	Glu	Ile	Leu	Ile	Arg	Asp	Lys	Asn	Ala	Leu	Gln
545					550					555					560
Asn	Ile	Ile	Leu	Tyr	His	Leu	Thr	Pro	Gly	Val	Phe	Ile	Gly	Lys	Gly
				565					570					575	
Phe	Glu	Pro	Gly	Val	Thr	Asn	Ile	Leu	Lys	Thr	Thr	Gln	Gly	Ser	Lys
			580					585					590		
Ile	Phe	Leu	Lys	Glu	Val	Asn	Asp	Thr	Leu	Leu	Val	Asn	Glu	Leu	Lys
			595				600					605			
Ser	Lys	Glu	Ser	Asp	Ile	Met	Thr	Thr	Asn	Gly	Val	Ile	His	Val	Val
						615					620				
Asp	Lys	Leu	Leu	Tyr	Pro	Ala	Asp	Thr	Pro	Val	Gly	Asn	Asp	Gln	Leu

625		630		635		640
Leu Glu Ile Leu	Asn Lys Leu Ile Lys Tyr Ile	Gln Ile Lys Phe Val				
	645	650		655		
Arg Gly Ser Thr	Phe Lys Glu Ile Pro Val Thr	Val Tyr Lys Pro Ile				
	660	665		670		
Ile Lys Lys Tyr	Thr Lys Ile Ile Asp Gly Val	Pro Val Glu Ile Thr				
	675	680		685		
Glu Lys Glu Thr	Arg Glu Glu Arg Ile Ile Thr	Gly Pro Glu Ile Lys				
	690	695		700		
Tyr Thr Arg Ile	Ser Thr Gly Gly Gly Glu Thr	Glu Glu Thr Leu Lys				
705	710	715		720		
Lys Leu Leu Gln	Glu Glu Val Thr Lys Val Thr	Lys Phe Ile Glu Gly				
	725	730		735		
Gly Asp Gly His	Leu Phe Glu Asp Glu Glu Ile	Lys Arg Leu Leu Gln				
	740	745		750		
Gly Asp Thr Pro	Val Arg Lys Leu Gln Ala Asn	Lys Lys Val Gln Gly				
	755	760		765		
Ser Arg Arg Arg	Leu Arg Glu Gly Arg Ser Gln					
770	775					

<210> 181
 <211> 2088
 <212> DNA
 <213> Homo sapiens

<400> 181
 gaattcggca cgagcgcgcg gogaatctca acgctgcgcc gtctgcgggc gcttcgggc 60
 caccagtttc tctgctttcc accctggcgc cccccagccc tggctcccca gctgegtgc 120
 cccgggcgtc cacgccctgc gggcttagcg ggttcagtgg gctcaatctg cgcagcgcca 180
 cctccatgtt gaccaagcct ctacaggggc ctcccgcgcc ccccgggacc cccacgcgcg 240
 cgccaggagg caaggatcgg gaagcgttcg aggccgagta tcgactcggc cccctcctgg 300
 gtaagggggg ctttgccacc gtcttcgcag gacaccgcct cacagatcga ctccaggtgg 360
 ccatcaaagt gattccccgg aatcgtgtgc tgggctggtc ccccttgta gactcagtca 420
 catgcccact cgaagtgcga ctgctatgga aagtgggtgc aggtgggtgg caccctggcg 480
 tgatccgcct gcttgactgg tttagacacac aggaaggctt catgctggtc ctcgagcggc 540
 ctttgcccgc ccaggatctc tttagactata tcacagagaa gggcccactg ggtgaaggcc 600
 caagccgctg cttctttggc caagtagtgg cagccatcca gcactgccat tcccggtggg 660
 ttgtccatcg tgacatcaag gatgagaaca tcctgataga cctacgccgt ggtgtgtgca 720
 aactcattga ttttggttct ggtgccctgc ttcatgatga accctacact gactttgatg 780
 ggacaagggt gtacagcccc ccagagtggg tctctcgaca ccagtaccat gactcccg 840
 ccactgtctg gtcactgggc atcctcctct atgacatggt gtgtggggac attccctttg 900
 agagggacca ggagattctg gaagctgagc tccacttccc agcccatgtc tcccagact 960
 gctgtgccct aatccgcgcg tgccctggccc ccaaaccctc ttcccgaacc tccctggaag 1020
 agatcctgct ggacccttgg atgcaaacac cagccgagga tgttaccct caaccctcc 1080
 aaaggaggcc ctgccccttt ggccctggtc ttgctaccct aagcctggcc tggcctggcc 1140
 tggcccccga tggtcagaag agccatccca tggccatgtc acagggatag atggacattt 1200
 gttgacttgg ttttacaggc cattaccagt cattaaagtc cagtattact aaggtaaggg 1260
 attgaggatc aggggttaga agacataaac caagtttgcc cagttccctt cccaatccta 1320
 caaaggagcc ttccctccag aacctgtggt cctgattttt ggagggggaa cttcttgctt 1380
 ctcattttgc taaggaagtt ttttttggtg aagttgttcc cattttgagc cccgggactc 1440
 ttattttgat gatgtgtcac cccacattgg caccctctac taccaccaca caaacttagt 1500
 tcatatgctt ttacttgggc aagggtgctt tccttccaat accccagtag cttttatttt 1560
 agtaaaggga ccccttcccc tagcctaggg tcccatattg ggtcaagctg cttacctgcc 1620
 tcagcccagg attttttatt ttgggggagg taatggcctg ttgttaccac aaggttcttt 1680
 tttttttttt tttttttttg ggtgagggga ccctactttg ttatcccaag tgctcttatt 1740
 ctggtgagaa gaaccttaat tccataattt gggaagggaat ggaagatgga caccacgga 1800
 caccaccaga caataggatg ggatggatgg ttttttgggg gatgggctag gggaaataag 1860
 gcttgctgtt tgttttccct gggcgctccc tccaattttg cagatttttt caacctctc 1920

<400>	182														
Met	Leu	Thr	Lys	Pro	Leu	Gln	Gly	Pro	Pro	Ala	Pro	Pro	Gly	Thr	Pro
1				5				10						15	
Thr	Pro	Pro	Pro	Gly	Gly	Lys	Asp	Arg	Glu	Ala	Phe	Glu	Ala	Glu	Tyr
			20					25				30			
Arg	Leu	Gly	Pro	Leu	Leu	Gly	Lys	Gly	Gly	Phe	Gly	Thr	Val	Phe	Ala
		35					40					45			
Gly	His	Arg	Leu	Thr	Asp	Arg	Leu	Gln	Val	Ala	Ile	Lys	Val	Ile	Pro
	50					55					60				
Arg	Asn	Arg	Val	Leu	Gly	Trp	Ser	Pro	Leu	Ser	Asp	Ser	Val	Thr	Cys
65					70					75				80	
Pro	Leu	Glu	Val	Ala	Leu	Leu	Trp	Lys	Val	Gly	Ala	Gly	Gly	Gly	His
				85					90					95	
Pro	Gly	Val	Ile	Arg	Leu	Leu	Asp	Trp	Phe	Glu	Thr	Gln	Glu	Gly	Phe
			100					105					110		
Met	Leu	Val	Leu	Glu	Arg	Pro	Leu	Pro	Ala	Gln	Asp	Leu	Phe	Asp	Tyr
		115					120					125			
Ile	Thr	Glu	Lys	Gly	Pro	Leu	Gly	Glu	Gly	Pro	Ser	Arg	Cys	Phe	Phe
	130					135					140				
Gly	Gln	Val	Val	Ala	Ala	Ile	Gln	His	Cys	His	Ser	Arg	Gly	Val	Val
145				150						155					160
His	Arg	Asp	Ile	Lys	Asp	Glu	Asn	Ile	Leu	Ile	Asp	Leu	Arg	Arg	Gly
				165					170					175	
Cys	Ala	Lys	Leu	Ile	Asp	Phe	Gly	Ser	Gly	Ala	Leu	Leu	His	Asp	Glu
			180					185					190		
Pro	Tyr	Thr	Asp	Phe	Asp	Gly	Thr	Arg	Val	Tyr	Ser	Pro	Pro	Glu	Trp
		195					200					205			
Ile	Ser	Arg	His	Gln	Tyr	His	Ala	Leu	Pro	Ala	Thr	Val	Trp	Ser	Leu
	210					215					220				
Gly	Ile	Leu	Leu	Tyr	Asp	Met	Val	Cys	Gly	Asp	Ile	Pro	Phe	Glu	Arg
225				230						235				240	
Asp	Gln	Glu	Ile	Leu	Glu	Ala	Glu	Leu	His	Phe	Pro	Ala	His	Val	Ser
				245					250					255	
Pro	Asp	Cys	Cys	Ala	Leu	Ile	Arg	Arg	Cys	Leu	Ala	Pro	Lys	Pro	Ser
			260					265					270		
Ser	Arg	Pro	Ser	Leu	Glu	Glu	Ile	Leu	Leu	Asp	Pro	Trp	Met	Gln	Thr
			275				280					285			
Pro	Ala	Glu	Asp	Val	Thr	Pro	Gln	Pro	Leu	Gln	Arg	Arg	Pro	Cys	Pro
	290					295					300				
Phe	Gly	Leu	Val	Leu	Ala	Thr	Leu	Ser	Leu	Ala	Trp	Pro	Gly	Leu	Ala
305				310						315					320
Pro	Asn	Gly	Gln	Lys	Ser	His	Pro	Met	Ala	Met	Ser	Gln	Gly		
				325					330						

```
<210> 183
<211> 2304
<212> DNA
<213> Homo sapiens
```

<400> 183

```

gtccccgcag cgccgtcgcg cccctcctgcc gcaggccacc gaggcgcgcg ccgtctagcg 60
ccccgacctc gccaccatga gagccctgct ggcgcgcctg cttctctgcg tcctgggtcgt 120
gagcgactcc aaaggcagca atgaacttca tcaagttcca tcgaactgtg actgtctaaa 180
tgagggaaca tgtgtgtcca acaagtactt ctccaacatt cactgggtgca actgccccaa 240
gaaattcgga gggcagcact gtgaaataga taagtcaaaa acctgctatg aggggaatgg 300
tcactttttac cgaggaaagg ccagcactga caccatgggc cgccctgcc tgccctggaa 360
ctctgccact gtccctcagc aaacgtacca tgcccacaga tctgatgtct ttcagctggg 420
cctggggaaa cataattact gcaggaaccc agacaaccgg aggcgacctt ggtgctatgt 480
gcaggtgggc ctaaagccgc ttgtccaaga gtgcatgggt catgactgcg cagatggaaa 540
aaagccctcc tctcctccag aagaattaaa atttcagtgt ggccaaaaga ctctgaggcc 600
ccgctttaag attattgggg gagaattcac caccatcgag aaccagccct ggtttgccgc 660
catctacagg aggcaccggg ggggctctgt cacctacgtg tgtggaggca gcctcatcag 720
cccttgctgg gtgatcagcg ccacacactg cttcattgat tacccaaaga aggaggacta 780
catcgtctac ctgggtcgtc caaggcttaa ctccaacacg caaggggaga tgaagtttga 840
ggtggaaaac ctcatcctac acaaggacta cagcgtgac acgcttgctc accacaacga 900
cattgccttg ctgaagatcc gttccaagga gggcaggtgt ggcagccat cccggactat 960
acagaccatc tgccctgccct cgatgtataa cgatcccag tttggcacia gctgtgagat 1020
cactggcttt ggaaaagaga attctaccga ctatctctat ccggagcagc tgaataagac 1080
tgtttggaag ctgatttccc accgggagtg tgcagcccc cactactacg gctctgaagt 1140
caccacaaaa atgctatgtg ctgctgaccc ccaatggaaa acagattcct gccagggaga 1200
ctcaggggga cccctcgtct gttccctcca aggcgcgatg actttgactg gaattgtgag 1260
ctggggccgt ggatgtgccc tgaaggacaa gccaggcgtc tacacgagag tctcacactt 1320
cttaccctgg atccgcagtc acaccaagga agagaatggc ctggccctct gaggggtccc 1380
aggaggaaaa cgggcaccac ccgctttctt gctggttgtc atttttgcag tagagtcata 1440
tccatcagct gtaagaagag actgggaaga taggctctgc acagatggat ttgcctgtgg 1500
caccaccagg gtgaacgaca atagctttac cctcacggat aggcctgggt gctggctgcc 1560
cagaccctct ggcaggatg gaggggtggt cctgactcaa catgttactg accagcaact 1620
tgtctttttc tggactgaag cctgcaggag ttaaaaaggg cagggcattct cctgtgcatg 1680
ggctcgaagg gagagccagc tcccccgacc ggtgggcatt tgtgaggccc atggttgaga 1740
aatgaataat ttcccaatta ggaagtgtaa gcagctgagg tctcttgagg gagcttagcc 1800
aatgtgggag cagcggtttg gggagcagag acactaacga cttcagggca gggctctgat 1860
attccatgaa tgtatcagga aatatatatg tgtgtgtatg tttgcacact tggtgtgtgg 1920
gctgtgagtg taagtgtgag taagagctgg tgtctgattg ttaagtctaa atatttcctt 1980
aaactgtgtg gactgtgatg ccacacagag tggctcttct ggagagggtta taggtcactc 2040
ctggggccctc ttgggtcccc cagctgacag tgcctgggaa tgtacttatt ctgcagcatg 2100
acctgtgacc agcactgtct cagtttcact ttcacataga tgtcccttct ttggccagtt 2160
atcccttctt tttagcctag ttcattccaat cctcactggg tggggtgagg accactcctt 2220
aactgaata tttatatctt actatcttct tttatatctt tgtaatttta aataaaagtg 2280
atcaataaaa tgtgattttt ctga 2304

```

<210> 184

<211> 431

<212> PRT

<213> Homo sapiens

<400> 184

```

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1      5      10      15
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20      25      30
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35      40      45
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50      55      60
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65      70      75      80
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85      90      95

```

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Ile Glu Asn Gln Pro Trp
 180 185 190
 Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
 195 200 205
 Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
 210 215 220
 Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
 225 230 235 240
 Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
 245 250 255
 Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
 260 265 270
 His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
 275 280 285
 Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
 290 295 300
 Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
 305 310 315 320
 Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
 325 330 335
 Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
 340 345 350
 Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
 355 360 365
 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
 370 375 380
 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
 385 390 395 400
 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
 405 410 415
 Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
 420 425 430

<210> 185

<211> 2123

<212> DNA

<213> Homo sapiens

<400> 185

gggaggagcg gagcgggtgcg gaggctctgc tcggatcgag gtctgcagcg cagcttcggg 60
 agcatgagtg ctgcagtgac tgcagggaag ctggcacggg caccggccga ccctgggaaa 120
 gccgggggtcc ccggagttgc agctcccggg gctccggcgg cggctccacc ggcgaaagag 180
 atcccggagg tcctagtga cccacgcagc cggcggcgct atgtgcgggg ccgctttttg 240
 ggcaagggcg gctttgcaa gtgcttcgag atctcggacg cggacaccaa ggagggtgtc 300
 gggggaaga ttgtgcctaa gtctctgctg ctcaagccgc accagaggga gaagatgtcc 360
 atggaaatat ccattcaccg cagcctcgcc caccagcacg tcgtaggatt ccacggcttt 420
 ttcgaggaca acgacttcgt gttcgtggtg ttggagctct gccgccggag gtctctcctg 480
 gagccgcaca agaggaggaa agccctgact gagcctgagg cccgatacta cctacggcaa 540

```

atttgtcttg gctgccagta cctgcaccga aaccgagtta ttcatcgaga cctcaagctg 600
ggcaaccttt tcctgaatga agatctggag gtgaaaatag gggatttttg actggcaacc 660
aaagtcgaaat atgacgggga gaggaagaag accctgtgtg ggactcctaa ttacatagct 720
cccgaggtgc tgagcaagaa agagcacagt ttcgaggtgg atgtgtggtc cattgggtgt 780
atcatgtata ccttgtttagt gggcaaacca ctttttgaga cttcttgctt aaaagagacc 840
tacctccgga tcaagaagaa tgaatacagt attcccaagc acatcaaccc cgtggccgcc 900
tccctcatcc agaagatgct tcagacagat cccactgccc gcccaaccat taacgagctg 960
cttaatgaag agttctttac ttctggctat atccctgccc gtctcccat cactgcctg 1020
accattccac caagggttttc gattgctccc agcagcctgg accccagcaa ccggaagccc 1080
ctcacagtcc tcaataaagg cttggagaac cccctgcctg agcgtccccc ggaaaaagaa 1140
gaaccagtgg ttcgagagac aggtgaggtg gtcgactgcc acctcagtga catgctgcag 1200
cagctgcaca gtgtcaatgc ctccaagccc tcggagcgtg ggctggtcag gcaagaggag 1260
gctgaggatc ctgcctgcac ccccatcttc tgggtcagca agtgggtgga ctattcggac 1320
aagtacggcc ttgggtatca gctctgtgat aacagcgtgg ggggtgctctt caatgactca 1380
acacgcctca tcctctacaa tgatggtgac agcctgcagt acatagagcg tgacggcact 1440
gagtcctacc tcaccgtgag ttcccatccc aactccttga tgaagaagat caccctcctt 1500
aaatattttc gcaattacat gagcgagcac ttgctgaagg caggtgccaa catcacgccg 1560
cgcgaaaggtg atgagctcgc ccggtgccc tacctacgga cctgggtccg caccgcagc 1620
gccatcatcc tgcacctcag caacggcagc gtgcagatca acttcttcca ggatcacacc 1680
aagctcatct tgtgccact gatggcagcc gtgacctaca tcgacgagaa gcgggacttc 1740
cgcacatacc ccctgagctc cctggaggag tacggctgct gcaaggagct gccagcccg 1800
ctcgcctacg ccgcactat ggtggacaag ctgctgagct cacgctcggc cagcaaccgt 1860
ctcaaggcct cctaatagct gccctccct cgggactggg gccctcctca ctcccacctg 1920
catctggggc ccatactggt tggctccgc ggtgccatgt ctgcagtgtg ccccccagcc 1980
ccggtggctg ggcagagctg catcatcctt gcaggtgggg gttgctgtat aagttatttt 2040
tgtacatgtt cgggtgtggg ttctacagac ttgtccctt cccctcaac cccaccatat 2100
gaattgtaca gaatttttct att

```

<210> 186

<211> 603

<212> PRT

<213> Homo sapiens

<400> 186

```

Met Ser Ala Ala Val Thr Ala Gly Lys Leu Ala Arg Ala Pro Ala Asp
 1          5          10          15
Pro Gly Lys Ala Gly Val Pro Gly Val Ala Ala Pro Gly Ala Pro Ala
 20          25          30
Ala Ala Pro Pro Ala Lys Glu Ile Pro Glu Val Leu Val Asp Pro Arg
 35          40          45
Ser Arg Arg Arg Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe
 50          55          60
Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr Lys Glu Val Phe Ala
 65          70          75          80
Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Arg Glu
 85          90          95
Lys Met Ser Met Glu Ile Ser Ile His Arg Ser Leu Ala His Gln His
100          105          110
Val Val Gly Phe His Gly Phe Phe Glu Asp Asn Asp Phe Val Phe Val
115          120          125
Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Pro His Lys Arg
130          135          140
Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile
145          150          155          160
Val Leu Gly Cys Gln Tyr Leu His Arg Asn Arg Val Ile His Arg Asp
165          170          175
Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile
180          185          190
Gly Asp Phe Gly Leu Ala Thr Lys Val Glu Tyr Asp Gly Glu Arg Lys

```

	195					200				205					
Lys	Thr	Leu	Cys	Gly	Thr	Pro	Asn	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Ser
	210					215					220				
Lys	Lys	Glu	His	Ser	Phe	Glu	Val	Asp	Val	Trp	Ser	Ile	Gly	Cys	Ile
225					230					235					240
Met	Tyr	Thr	Leu	Leu	Val	Gly	Lys	Pro	Pro	Phe	Glu	Thr	Ser	Cys	Leu
				245						250					255
Lys	Glu	Thr	Tyr	Leu	Arg	Ile	Lys	Lys	Asn	Glu	Tyr	Ser	Ile	Pro	Lys
			260					265					270		
His	Ile	Asn	Pro	Val	Ala	Ala	Ser	Leu	Ile	Gln	Lys	Met	Leu	Gln	Thr
		275						280				285			
Asp	Pro	Thr	Ala	Arg	Pro	Thr	Ile	Asn	Glu	Leu	Leu	Asn	Asp	Glu	Phe
	290					295					300				
Phe	Thr	Ser	Gly	Tyr	Ile	Pro	Ala	Arg	Leu	Pro	Ile	Thr	Cys	Leu	Thr
305					310					315					320
Ile	Pro	Pro	Arg	Phe	Ser	Ile	Ala	Pro	Ser	Ser	Leu	Asp	Pro	Ser	Asn
				325					330						335
Arg	Lys	Pro	Leu	Thr	Val	Leu	Asn	Lys	Gly	Leu	Glu	Asn	Pro	Leu	Pro
			340					345					350		
Glu	Arg	Pro	Arg	Glu	Lys	Glu	Glu	Pro	Val	Val	Arg	Glu	Thr	Gly	Glu
		355					360					365			
Val	Val	Asp	Cys	His	Leu	Ser	Asp	Met	Leu	Gln	Gln	Leu	His	Ser	Val
	370					375				380					
Asn	Ala	Ser	Lys	Pro	Ser	Glu	Arg	Gly	Leu	Val	Arg	Gln	Glu	Glu	Ala
385					390					395					400
Glu	Asp	Pro	Ala	Cys	Ile	Pro	Ile	Phe	Trp	Val	Ser	Lys	Trp	Val	Asp
				405					410						415
Tyr	Ser	Asp	Lys	Tyr	Gly	Leu	Gly	Tyr	Gln	Leu	Cys	Asp	Asn	Ser	Val
			420					425					430		
Gly	Val	Leu	Phe	Asn	Asp	Ser	Thr	Arg	Leu	Ile	Leu	Tyr	Asn	Asp	Gly
		435					440					445			
Asp	Ser	Leu	Gln	Tyr	Ile	Glu	Arg	Asp	Gly	Thr	Glu	Ser	Tyr	Leu	Thr
	450					455					460				
Val	Ser	Ser	His	Pro	Asn	Ser	Leu	Met	Lys	Lys	Ile	Thr	Leu	Leu	Lys
465					470					475					480
Tyr	Phe	Arg	Asn	Tyr	Met	Ser	Glu	His	Leu	Leu	Lys	Ala	Gly	Ala	Asn
				485					490						495
Ile	Thr	Pro	Arg	Glu	Gly	Asp	Glu	Leu	Ala	Arg	Leu	Pro	Tyr	Leu	Arg
			500					505					510		
Thr	Trp	Phe	Arg	Thr	Arg	Ser	Ala	Ile	Ile	Leu	His	Leu	Ser	Asn	Gly
		515					520					525			
Ser	Val	Gln	Ile	Asn	Phe	Phe	Gln	Asp	His	Thr	Lys	Leu	Ile	Leu	Cys
	530					535					540				
Pro	Leu	Met	Ala	Ala	Val	Thr	Tyr	Ile	Asp	Glu	Lys	Arg	Asp	Phe	Arg
545					550					555					560
Thr	Tyr	Arg	Leu	Ser	Leu	Leu	Glu	Glu	Tyr	Gly	Cys	Cys	Lys	Glu	Leu
				565				570						575	
Ala	Ser	Arg	Leu	Arg	Tyr	Ala	Arg	Thr	Met	Val	Asp	Lys	Leu	Leu	Ser
			580					585					590		
Ser	Arg	Ser	Ala	Ser	Asn	Arg	Leu	Lys	Ala	Ser					
	595						600								

<210> 187

<211> 2617

<212> DNA

<213> Homo sapiens

<400> 187


```

aagcagtctc aagcctgccg cagggagaag atggcggtcg ccgtgagaac tttgcaggaa 60
cagctggaaa aggccaaaag gagtcttaag aacgtggatg agaacattcg caagctcacc 120
gggcgggacc cgaatgatgt gaggcccatc caagccagat tgctggccct ttctggtcct 180
ggtggaggta gaggacgtgg tagttttattg ctgaggcgtg gattctcaga tagtggagga 240
ccccagcca aacagagaga ccttgaaggg gcagtcagta ggctgggcgg ggagcgtcgg 300
accagaagag aatcacgcca ggaaagcgac cgggaggatg atgatgttaa aaagccagca 360
ttgcagtctt cagttgtagc tacctccaaa gagcgcacac gtagagacct tatccaggat 420
caaaatatgg atgaaaaggg aaagcaaaag aaccgacgaa tatttggctt attgatgggc 480
actcttcaga aatttaaaca agaatccaact gttgctactg aaaggcaaaa caggcgccag 540
gaaattgaac aaaaacttga agtgaggcg gaagaagaaa gaaagcagggt tgaatatgaa 600
aggagagaac tgtttgaaga gaggcgtgct aaacagacag aactgcggct tttagaacag 660
aaggttgagc ttgcgcagct gcaagaagaa tggaatgaac ataatgcaa aataattaaa 720
tatataagaa ctaagacaaa gccccatttg ttttatattc ccggaagaat gtgtccagct 780
acccaaaaac taatagaaga gtcacagaga aaaatgaacg ctttatttga tggtagacgc 840
atcgaatttg cagaacaaat aaataaaatg gaggctaggc ctagaagaca atcaatgaag 900
gaaaaagagc atcaggtggt gcgtaatgaa gaacacaagg cggaacaaga agagggtaag 960
gtggctcagc gagaggaaga gttggtggag acaggtaacc agcacaatga tgttgaaata 1020
gaggaagcag gagaggaaga ggaaaaggaa atagggattg ttcatagtga tgcagagaaa 1080
gagcaggagg aggaggaaca aaaacaggaa atggaggtta agatggagga ggaaactgag 1140
gtaaaggaaa gtgagaagca gcaggatagt cagcctgaag aagttatgga tgtgctagag 1200
atggttgaga atgtcaaaca tgtaattgct gaccaggagg taatggaaac taatcgagtt 1260
gaaagtgtag aaccttcaga aaatgaagct agcaaagaat tggaaccaga aatggaattt 1320
gaaattgagc cagataaaga atgtaaatcc ctttctcctg ggaaagagaa tgtcagtgtc 1380
ttagacatgg aaaaggagtc tgacgaaaaa gaagaaaaag aatctgagcc ccaacctgag 1440
cctgtggctc aacctcaggc tcagtctcag cccagctcc agcttcaatc ccagtcgag 1500
ccacagcctc agctacaacc tgagcctgct caacctcagc ttcagtctca gccccagctt 1560
cagcttcaat cccagtgcc a tgcaagtctc cagtcctatc ctccctctca acctgaggat 1620
ttgtcattag ctgtttttaca gccaacacct caagttactc aggagcatgg gcattttcta 1680
cctgagagga aggattttcc tgtagagtct gtaaaactga ctgaggtacc agtagacca 1740
gtcttgacag tacatccaga gagcgagagc gaaaccaata ctaggagcag gtagtagagg 1800
cgaactagaa atagaaccac caagagtaga agtcgaagca gtagcagtag cagttctagt 1860
agcagttcaa ccagtagcag cagtggaaat agttccagca gtggaagtag tagcagtcgc 1920
agtagttcca gtagcagctc cagtacaagt ggcagcagca gcagagatag cagcagcagc 1980
actagtagta gtagtgagag tagaagtcgg agtaggggcc ggggacataa tagagataga 2040
aagcacagaa ggagcgtgga tcggaagaga agggatactt caggactaga aagaagtcac 2100
aaatcttcaa aaggtggtag tagtagagat acaaaaggat caaaggataa gaattcccg 2160
tccgacagaa agaggtctat atcagagagt agtcgatcag gcaaaagatc ttcaagaagt 2220
gaaagagacc gaaaatcaga caggaaagac aaaagcgctt aatggaagaa gccaggcttt 2280
cttagccatt ctttgcagca gaagatttct tgatgaaaaa ggattacctt tccttgtaaa 2340
gaggatgctg ccttaagaat tgcatgttgt aaaaaatctt tttggaagat acagactgtt 2400
tgtttaccag acattcttgt actttttgca taattttgta agagttattt atcaaaatta 2460
tgtgaggttc caaaatatgt aaaaatgata ataataaaaa aagattaaca tcccttgta 2520
tcttttttaa atatcctata ctcttcagta agaatctgta tattttaata ggcaaatctt 2580
taagtctgtt cccttcaatt ctgtatcata cattgct 2617

```

<210> 188

<211> 743

<212> PRT

<213> Homo sapiens

<400> 188

```

Met Ala Val Ala Val Arg Thr Leu Gln Glu Gln Leu Glu Lys Ala Lys
 1           5           10          15
Glu Ser Leu Lys Asn Val Asp Glu Asn Ile Arg Lys Leu Thr Gly Arg
 20          25          30
Asp Pro Asn Asp Val Arg Pro Ile Gln Ala Arg Leu Leu Ala Leu Ser
 35          40          45
Gly Pro Gly Gly Gly Arg Gly Arg Gly Ser Leu Leu Leu Arg Arg Gly
 50          55          60

```

Phe	Ser	Asp	Ser	Gly	Gly	Pro	Pro	Ala	Lys	Gln	Arg	Asp	Leu	Glu	Gly
65					70					75					80
Ala	Val	Ser	Arg	Leu	Gly	Gly	Glu	Arg	Arg	Thr	Arg	Arg	Glu	Ser	Arg
				85					90					95	
Gln	Glu	Ser	Asp	Pro	Glu	Asp	Asp	Asp	Val	Lys	Lys	Pro	Ala	Leu	Gln
			100					105					110		
Ser	Ser	Val	Val	Ala	Thr	Ser	Lys	Glu	Arg	Thr	Arg	Arg	Asp	Leu	Ile
		115					120					125			
Gln	Asp	Gln	Asn	Met	Asp	Glu	Lys	Gly	Lys	Gln	Arg	Asn	Arg	Arg	Ile
	130					135					140				
Phe	Gly	Leu	Leu	Met	Gly	Thr	Leu	Gln	Lys	Phe	Lys	Gln	Glu	Ser	Thr
145					150					155					160
Val	Ala	Thr	Glu	Arg	Gln	Asn	Arg	Arg	Gln	Glu	Ile	Glu	Gln	Lys	Leu
				165					170					175	
Glu	Val	Gln	Ala	Glu	Glu	Glu	Arg	Lys	Gln	Val	Glu	Asn	Glu	Arg	Arg
			180					185					190		
Glu	Leu	Phe	Glu	Glu	Arg	Arg	Ala	Lys	Gln	Thr	Glu	Leu	Arg	Leu	Leu
	195						200					205			
Glu	Gln	Lys	Val	Glu	Leu	Ala	Gln	Leu	Gln	Glu	Glu	Trp	Asn	Glu	His
	210					215					220				
Asn	Ala	Lys	Ile	Ile	Lys	Tyr	Ile	Arg	Thr	Lys	Thr	Lys	Pro	His	Leu
225					230					235					240
Phe	Tyr	Ile	Pro	Gly	Arg	Met	Cys	Pro	Ala	Thr	Gln	Lys	Leu	Ile	Glu
				245					250					255	
Glu	Ser	Gln	Arg	Lys	Met	Asn	Ala	Leu	Phe	Asp	Gly	Arg	Arg	Ile	Glu
			260				265						270		
Phe	Ala	Glu	Gln	Ile	Asn	Lys	Met	Glu	Ala	Arg	Pro	Arg	Arg	Gln	Ser
	275						280					285			
Met	Lys	Glu	Lys	Glu	His	Gln	Val	Val	Arg	Asn	Glu	Glu	His	Lys	Ala
	290					295					300				
Glu	Gln	Glu	Glu	Gly	Lys	Val	Ala	Gln	Arg	Glu	Glu	Glu	Leu	Val	Glu
305				310						315					320
Thr	Gly	Asn	Gln	His	Asn	Asp	Val	Glu	Ile	Glu	Glu	Ala	Gly	Glu	Glu
				325					330					335	
Glu	Glu	Lys	Glu	Ile	Gly	Ile	Val	His	Ser	Asp	Ala	Glu	Lys	Glu	Gln
		340					345						350		
Glu	Glu	Glu	Glu	Gln	Lys	Gln	Glu	Met	Glu	Val	Lys	Met	Glu	Glu	Glu
		355					360					365			
Thr	Glu	Val	Arg	Glu	Ser	Glu	Lys	Gln	Gln	Asp	Ser	Gln	Pro	Glu	Glu
	370					375					380				
Val	Met	Asp	Val	Leu	Glu	Met	Val	Glu	Asn	Val	Lys	His	Val	Ile	Ala
385					390					395					400
Asp	Gln	Glu	Val	Met	Glu	Thr	Asn	Arg	Val	Glu	Ser	Val	Glu	Pro	Ser
				405					410					415	
Glu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Glu	Pro	Glu	Met	Glu	Phe	Glu	Ile
		420					425						430		
Glu	Pro	Asp	Lys	Glu	Cys	Lys	Ser	Leu	Ser	Pro	Gly	Lys	Glu	Asn	Val
	435						440					445			
Ser	Ala	Leu	Asp	Met	Glu	Lys	Glu	Ser	Asp	Glu	Lys	Glu	Glu	Lys	Glu
	450					455					460				
Ser	Glu	Pro	Gln	Pro	Glu	Pro	Val	Ala	Gln	Pro	Gln	Ala	Gln	Ser	Gln
465					470					475					480
Pro	Gln	Leu	Gln	Leu	Gln	Ser	Gln	Ser	Glu	Pro	Gln	Pro	Gln	Leu	Gln
				485					490					495	
Pro	Glu	Pro	Ala	Gln	Pro	Gln	Leu	Gln	Ser	Gln	Pro	Gln	Leu	Gln	Leu
		500						505					510		
Gln	Ser	Gln	Cys	His	Ala	Val	Leu	Gln	Ser	His	Pro	Pro	Ser	Gln	Pro
		515					520				525				
Glu	Asp	Leu	Ser	Leu	Ala	Val	Leu	Gln	Pro	Thr	Pro	Gln	Val	Thr	Gln

530		535		540
Glu His Gly His Phe Leu	Pro Glu Arg Lys Asp	Phe Pro Val Glu Ser		
545	550	555	560	
Val Lys Leu Thr Glu Val	Pro Val Asp Pro Val	Leu Thr Val His Pro		
	565	570	575	
Glu Ser Glu Ser Glu Thr	Asn Thr Arg Ser Arg	Ser Arg Gly Arg Thr		
	580	585	590	
Arg Asn Arg Thr Thr Lys	Ser Arg Ser Arg Ser	Ser Ser Ser Ser		
	595	600	605	
Ser Ser Ser Ser Thr Ser	Ser Ser Ser Gly Ser	Ser Ser Ser Ser		
	610	615	620	
Gly Ser Ser Ser Ser Arg	Ser Ser Ser Ser Ser	Ser Ser Ser Thr Ser		
625	630	635	640	
Gly Ser Ser Ser Arg Asp	Ser Ser Ser Ser Thr	Ser Ser Ser Ser Glu		
	645	650	655	
Ser Arg Ser Arg Ser Arg	Gly Arg Gly His Asn	Arg Asp Arg Lys His		
	660	665	670	
Arg Arg Ser Val Asp Arg	Lys Arg Arg Asp Thr	Ser Gly Leu Glu Arg		
	675	680	685	
Ser His Lys Ser Ser Lys	Gly Gly Ser Ser Arg	Asp Thr Lys Gly Ser		
	690	695	700	
Lys Asp Lys Asn Ser Arg	Ser Asp Arg Lys Arg	Ser Ile Ser Glu Ser		
705	710	715	720	
Ser Arg Ser Gly Lys Arg	Ser Ser Arg Ser Glu	Arg Asp Arg Lys Ser		
	725	730	735	
Asp Arg Lys Asp Lys Arg	Arg			
	740			

<210> 189
 <211> 1182
 <212> DNA
 <213> Homo sapiens

<400> 189
 gaattccgct agactaagtt ggtcatgatg cagaagctac tcaaattgcag tcggcttgctc 60
 ctggctcttg cctcatcctt ggttctggaa tcctcagttc aaggttatcc tacgcagaga 120
 gccaggtaac aatgggtgcg ctgcaatcca gacagtaatt ctgcaaactg ccttgaagaa 180
 aaaggaccaaa tgttcgaact acttccagggt gaatccaaca agatcccccg tctgaggact 240
 gacctttttc caaagacgag aatccaggac ttgaatcgta tcttcccact ttctgaggac 300
 tactctggat caggcttcgg ctccggctcc ggctctggat caggatctgg gagtggcttc 360
 ctaacggaaa tggaaacagga ttaccaacta gtagacgaaa gtgatgcttt ccatgacaac 420
 cttagggtctc ttgacaggaa tctgcctca gacagccagg acttgggtca acatggatta 480
 gaagaggatt ttatgttata aaagaggatt ttcccacctt gacaccaggc aatgtagtta 540
 gcatatttta tgtaccatgg ttatatgatt aatcttggga caaagaattt tatagaaatt 600
 ttttaaacatc tgaaaaagaa gcttaagttt tatcatcctt ttttttctca tgaattctta 660
 aaggattatg ctttaatgct gttatctatc ttattgttct tgaaaatacc tgcatttttt 720
 ggtatcatgt tcaaccaaca tcattatgaa attaattaga ttcccatggc cataaaatgg 780
 ctttaaaagaa tatatatata ttttttaaagt agcttgagaa gcaaattggc aggtaatat 840
 tcatacctaa attaagactc tgacttggat tgtgaattat aatgatatgc cccttttctt 900
 ataaaaacaa aaaaaaata atgaaacaca gtgaatttgt agagtggggg tatttgacat 960
 atttttacagg gtggagtgtg ctatatacta ttacctttga atgtgtttgc agagctagt 1020
 gatgtgtttg tctacaagta tgattgctgt tacataacac cccaaattaa ctcccaaatt 1080
 aaaacacagt tgtgtgtgca atacctcata ctgctttacc tttttttcct ggatatctgt 1140
 gtattttcaa atgttactat atattaaagc agaaatataa cc 1182

<210> 190
 <211> 158
 <212> PRT

<213> Homo sapiens

<400> 190

```

Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu Ala
 1           5           10           15
Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg
           20           25           30
Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn
           35           40           45
Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser
           50           55           60
Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg Ile
65           70           75           80
Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser Gly Ser
           85           90           95
Gly Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Phe
           100          105          110
Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Glu Ser Asp Ala
           115          120          125
Phe His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser Asp Ser
           130          135          140
Gln Asp Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met Leu
145           150           155

```

<210> 191

<211> 1595

<212> DNA

<213> Homo sapiens

<400> 191

```

ccgggttcgca aagaagctga cttcagaggg ggaaactttc ttcttittagg aggcgggttag 60
ccctgttcca cgaacccagg agaactgctg gccagattaa ttagacattg ctatgggaga 120
cgtgtaaaca cactacttat cattgatgca tatataaaac cattttattht tgcgtattat 180
ttcagaggaa gcgcctctga tttgtttctt ttttcccttt ttgctctttc tggctgtgtg 240
gtttggagaa agcacagttg gagtagccgg ttgctaaata agtcccagagc gcgagcggag 300
acgatgcagc ggagactggg tcagcagtggt agcgtcgcgg tgttcctgct gagctacgcg 360
gtgccctcct gcgggcgcgc ggtggagggg ctcagccgcc gcctcaaaag agctgtgtct 420
gaacatcagc tcctccatga caaggggaag tccatccaag atttacggcg acgattcttc 480
cttcaccatc tgatcgcaga aatccacaca gctgaaatca gagctacctc ggaggtgtcc 540
cctaactcca agccctctcc caacacaaag aaccaccccg tccgatttgg gtctgatgat 600
gagggcagat acctaactca ggaaactaac aaggtggaga cgtacaaaga gcagccgctc 660
aagacacctg ggaagaaaaa gaaaggcaag cccgggaaac gcaaggagca ggaaaagaaa 720
aaacggcgaa ctgcgtctgc ctggttagac tctggagtga ctgggagtgg gctagaaggg 780
gaccacctgt ctgacacctc cacaacgtcg ctggagctcg attcacggta acaggcttct 840
ctggcccgtg gcctcagcgg ggtgctctca gctgggtttt ggagcctccc ttctgccttg 900
gcttgacaaa acctagaatt ttctcccttt atgtatctct atcgattgtg tagcaattga 960
cagagaataa ctcagaatat tgtctgcctt aaagcagtac cccctacca cacaccccc 1020
tgtctccag caccatagag aggcgctaga gccatttctt ctttctccac cgtcacccaa 1080
catcaatcct ttaccactct accaaataat ttcatattca agcttcagaa gctagtgacc 1140
atcttcataa tttgctggag aagtgtattht cttcccctta ctctcacacc tgggcaaact 1200
ttcttcagtg tttttcattt cttacgttct ttcacttcaa gggagaatat agaagcattt 1260
gatattatct acaaacactg cagaacagca tcatgtcata aacgattctg agccattcac 1320
actttttatt taattaaatg tatttaatta aatctcaaat ttattttaat gtaaagaact 1380
taaattatgt tttaaacaca tgccctaaat ttgtttaatt aaatttaact ctggtttcta 1440
ccagtcata caaaataaat ggtttctgaa aatgtttaag tattaactta caaggatata 1500
ggtttttctc atgtatcttht ttgttcattg gcaagatgaa ataatttttc tagggtaatg 1560
ccgtaggaaa aataaaaactt cacattttaa aaaaaa 1595

```

<210> 192
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 192
 Met Gln Arg Arg Leu Val Gln Gln Trp Ser Val Ala Val Phe Leu Leu
 1 5 10 15
 Ser Tyr Ala Val Pro Ser Cys Gly Arg Ser Val Glu Gly Leu Ser Arg
 20 25 30
 Arg Leu Lys Arg Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly
 35 40 45
 Lys Ser Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile
 50 55 60
 Ala Glu Ile His Thr Ala Glu Ile Arg Ala Thr Ser Glu Val Ser Pro
 65 70 75 80
 Asn Ser Lys Pro Ser Pro Asn Thr Lys Asn His Pro Val Arg Phe Gly
 85 90 95
 Ser Asp Asp Glu Gly Arg Tyr Leu Thr Gln Glu Thr Asn Lys Val Glu
 100 105 110
 Thr Tyr Lys Glu Gln Pro Leu Lys Thr Pro Gly Lys Lys Lys Lys Gly
 115 120 125
 Lys Pro Gly Lys Arg Lys Glu Gln Glu Lys Lys Lys Arg Arg Thr Arg
 130 135 140
 Ser Ala Trp Leu Asp Ser Gly Val Thr Gly Ser Gly Leu Glu Gly Asp
 145 150 155 160
 His Leu Ser Asp Thr Ser Thr Thr Ser Leu Glu Leu Asp Ser Arg
 165 170 175

<210> 193
 <211> 2657
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> 2623, 2624, 2625, 2626, 2627, 2628, 2629
 <223> n = A,T,C or G

<400> 193
 gaattcggca cgagctgcag ggtcaggagg agaatcgtgg ggccaggagg gcagaggcac 60
 actccatctt cgtgctcctc acaggccctg cctccctgcc tgctaaggac acagggaagg 120
 gggccccac ctcagtgcct gcctcccttc cctgtgcctg tgtacctggc agtcacagcc 180
 acctggcgtg tcccagaaac caaccggctg acctcatctc ctgcccgcc ccacctccat 240
 tggctttggc ttttggcggt tgtgctgccc gacctttct cctgtccgga tgcgcagggc 300
 agggcctgag ccgtcgagct gcacccacag caggctgcct ttggtgactc accgggtgaa 360
 cgggggcatt gcgaggcatc ccctccctgg gtttggtctc tgcccacggg gctgacagta 420
 gaaatcacag gctgtgagac agctggagcc cagctctgct tgaacctatt ttaggtctct 480
 gatccccgct tctcttttag actcccctag agctcagcca gtgctcaacc tgaggctggg 540
 ggtctctgag gaagagtgag ttggagctga ggggtctggg gctgtcccct gagagagggg 600
 ccagaggcag tgtcaagagc cgggcagctc gattgtggct caccctccat cactcccagg 660
 gcccttgcc cagcagccgc agctcccaac cacaatatcc tttggggttt ggcctacgga 720
 gctggggcgg atgaccccca aatagccctg cgagattccc cctagacccg ccgcacatt 780
 ggtcaggcat gccctcctc atcgctggca cagcccagag ggtataaaca gtgctggagg 840
 ctggcggggc aggccagctg agtcctgagc agcagcccag cggatcctga gaacttcagg 900
 gtgagtttgg ggacccttga ttgttctttc tttttcgcta ttgtaaaatt catgttatat 960
 ggagggggca aagttttcag ggtgttgttt agaattggaa gatgtccctt gtatcaccat 1020
 ggaccctcat gataattttg tttctttcac tttctactct gttgacaacc attgtctcct 1080

```

cttatttttct tttcattttc tgtaactttt tcgttaaact ttagcttgca tttgtaacga 1140
atTTTTTaaat tcacttttTgt ttatttTgtca gattTgtaagt acttttctcta atcactttttt 1200
tttcaaggca atcagggTat attatattgt acttcagcac agtttttagag aacaattgtt 1260
ataattaaat gataaggtag aatatttctg catataaatt ctggctggcg tggaaatatt 1320
cttattggta gaaacaacta catcctggTc atcatcctgc ctttctcttt atggttacaa 1380
tgatatacac Tgtttgagat gaggataaaa tactctgagt ccaaaccggg cccctctgct 1440
aaccatgtTc atgccttctt ctttttccta cagctcctgg gcaacgtgct ggtTgtTgtg 1500
ctgtctcatc attttTggcaa agaattaatt ccaactcaaa aatgcaggct caacagtacc 1560
agcagcagcg Tcgaaaattt gcagctgcct tctTggcatt catTTtcata ctggcagctg 1620
TggTactgc Tgaagcaggg aagaaagaga aaccagaaaa aaaagtgaag aagtctgact 1680
gtggagaatg gcagtggagt gtgtgtgtgc ccaccagtgg agactgtggg ctgggcacac 1740
gggagggcac Tcggactgga gctgagtTca agcaaaccat gaagaccag agatgtaaga 1800
tcccctgcaa ctggaagaag caattTggcg cggagtTcaa ataccagtTc caggcctggg 1860
gagaatgtga cctgaacaca gccctgaaga ccagaactgg aagtctgaag cgagccctgc 1920
acaatgccga atgccagaag actgtcacca tctccaagcc ctgtggcaaa ctgaccaagc 1980
ccaaacctca agcagaatct aagaagaaga aaaaggagag caagaaacag gagaagatgc 2040
Tggattaaaa gatgtcacct gtggaacata aaaaggacat cagcaaacag gatcaattca 2100
ctcctcaggt gcaggctgcc tatcagaagg TggTggctgg Tgtggccaat gccctggctc 2160
acaataacca ctgagatctt tttccctctg ccaaaaatta Tggggacatc atgaagcccc 2220
ttgagcatct gacttctggc taataaagga aatttatttt cattgcaata gtgtgttTga 2280
attttttgtg Tctctcactc ggaaggacat atgggagggc aaatcattta aaacatcaga 2340
atgagtattt ggttttagagt ttggcaacat atgccatag ctggctgcca Tgaacaaagg 2400
Tggctataaaa gaggtcatca gtatatgaaa cagccccctg ctgtccattc cttattccat 2460
agaaaagcct TgactTgagg ttagattttt tttatatattt gttttgtgtt atttttttct 2520
ttaacatccc Taaaattttc cttacatgtt ttactagcca gatTTttcct cctctcctga 2580
ctactcccag Tcatagetgt ccctcttctc ttatgaagat ctnnnnnnnnc Tcgacctgca 2640
ggcaggcatg caagctt
2657

```

<210> 194

<211> 168

<212> PRT

<213> Homo sapiens

<400> 194

```

Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala
1          5          10          15
Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala
20         25         30
Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly
35         40         45
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu
50         55         60
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met
65         70         75         80
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly
85         90         95
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
100        105        110
Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
115        120        125
Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
130        135        140
Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Glu Gly
145        150        155        160
Lys Lys Gln Glu Lys Met Leu Asp
165

```

<210> 195

<211> 2972

<212> DNA

<213> Homo sapiens

<400> 195

```
tcttcggacc taggctgccc tgccgtcatg tgcgaaggga tcctttctcc gccagcgggc 60
ttgctgtccg atgacgatgt cgtagtttct cccatgtttg agtccacagc tgcagatttg 120
gggtctgtgg tacgcaagaa cctgctatca gactgctctg tcgtctctac ctccctagag 180
gacaagcagc aggttccatc tgaggacagt atggagaagg tgaagatata cttgaggggt 240
aggcccttgt taccttcaga gttggaacga caggaagatc agggtttgtgt ccgtattgag 300
aatgtggaga ccttgtttct acaagcacc cacttttccc agatctttgg gccagaagt 420
cggggaattg gccaaagccac acacaggttc accttttccc agatctttgg gccagaagt 420
ggacaggcat ccttcttcaa cctaactgtg aaggagatgg taaaggatgt actcaaagg 480
cagaactggc tcatctatac atatggagtc actaactcag ggaaaaccca cagattcaa 540
ggtaccatca aggatggagg gattctcccc cggtccctgg cgctgatctt caatagcctc 600
caaggccaac ttcattccaa acctgatctg aagcccttgc tctccaatga ggtaatctgg 660
ctagacagca agcagatccg acaggaggaa atgaagaagc tgtccctgct aaatggaggc 720
ctccaagagg aggagctgtc cacttccctg aaggaggatg tctacatcga aagtcggata 780
ggtaccagca ccagcttcga cagtggcatt gctgggctct cttctatcag tcagtgtacc 840
agcagtggcc agctggatga acaagtcac cgtggggcac agccagacac tgccccacta 900
cctgtcccgg caaacattcg cttctccatc tggatctcat tctttgagat ctacaacga 960
ctgctttatg acctattaga accgcctagc caacagcgca agaggcagac tttgcggcta 1020
tgcgaggatc aaaatggcaa tccctatgtg aaagatctca actggattca tgtgcaagat 1080
gctgaggagg cctggaagct cctaaaagtg ggtcgtaaga accagagctt tgccagcacc 1140
cacctcaacc agaactccag ccgcagtcac agcatcttct caatcaggat cctacacctt 1200
cagggggaag gagatatagt ccccaagatc agcagagctg cactctgtga tctggctggc 1260
tcagagcgct gcaaagatca gaagagtggg gaacggttga aggaagcagg aaacattaac 1320
acctctctac acacctggg ccgctgtatt gctgcccttc gtcaaaaacca gcagaaccgg 1380
tcaaagcaga acctgggttc cttccgtgac agcaagtga ctcgagtgtt ccaaggtttc 1440
ttcacaggcc gaggcogttc ctgcatgatt gtcaatgtga atccctgtgc atctacctat 1500
gatgaaactc ttcattgtggc caagtcttca gccattgcta gccagcttgt gcatgcccc 1560
cctatgcaac tgggattccc atccctgcac tcgttcatca aggaacatag tcttcaggta 1620
tccccagct tagagaaagg ggctaaggca gacacaggcc ttgatgatga tattgaaaat 1680
gaagctgaca tctccatgta tggcaaagag gagctcctac aagtttgtga agccatgaag 1740
acactgcttt tgaaggaaag acaggaaaag ctacagctgg agatgcatct ccgagatgaa 1800
atgtgcaatg agatggtaga acagatgcaa cagcgggaac agtgggtgcag tgaacatttg 1860
gacacccaaa aggaactatt ggaggaaatg tatgaagaaa aactaaatat cctcaaggag 1920
tcaactgaca gtttttacc aagaagagat caggagcggg atgaaaagat tgaagagcta 1980
gaagctctct tgcaggaaagc cagacaacag tcagtggccc atcagcaatc aggtctgaa 2040
ttggccctac ggcggtcaca aaggttggca gcttctgct ccaccagca gcttcaggag 2100
gttaaagcta aattacagca gtgcaaagca gagctaaact ctaccactga agagtgtgat 2160
aagtatcaga aaatgttaga accaccacc tcagccaagc ccttcaccat tgatgtggac 2220
aagaagttag aagagggcca gaagaatata aggtgttgcc gacagagct tcagaaactt 2280
ggtgagtctc tccaatcagc agagagagct tgttgccaca gcactggggc aggaaaactt 2340
cgtcaagcct tgaccacttg tgatgacatc ttaatcaaac aggaccagac tctggctgaa 2400
ctgcagaaca acatgggtgt agtgaaactg gaccttcgga agaaggcagc atgtattgct 2460
gagcagtatc atactgtgtt gaaactccaa ggccaggttt ctgccccaaa gcgccttgg 2520
accaaccagg aaaatcagca accaaaacca caaccaccag ggaagaaacc attccttcga 2580
aatttacttc cccgaacacc aacctgccaa agctcaacag actgcagccc ttatgcccgg 2640
atcctacgct cagggcgttc ccttttactc aaatctgggc cttttggcaa aaagtactaa 2700
ggctgtgggg aaagagaaga gcagtcattg cctgaggtg ggtcagctac tctcctgaag 2760
aaataggtct cttttatgct ttaccatata tcaggaatta tatccaggat gcaataactca 2820
gacactagct tttttctcac ttttgtatta taaccaccta tgtaatctca tgttgttgtt 2880
tttttttatt tacttatatg atttctatgc acacaaaaac agttatatta aagatattat 2940
tggtcacatt ttttattgaa aaaaaaaaaa aa 2972
```

<210> 196

<211> 890

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gln	Gly	Ile	Leu	Ser	Pro	Pro	Ala	Gly	Leu	Leu	Ser	Asp	Asp	1	5	10	15
Asp	Val	Val	Val	Ser	Pro	Met	Phe	Glu	Ser	Thr	Ala	Ala	Asp	Leu	Gly	20	25	30	
Ser	Val	Val	Arg	Lys	Asn	Leu	Leu	Ser	Asp	Cys	Ser	Val	Val	Ser	Thr	35	40	45	
Ser	Leu	Glu	Asp	Lys	Gln	Gln	Val	Pro	Ser	Glu	Asp	Ser	Met	Glu	Lys	50	55	60	
Val	Lys	Val	Tyr	Leu	Arg	Val	Arg	Pro	Leu	Leu	Pro	Ser	Glu	Leu	Glu	65	70	75	80
Arg	Gln	Glu	Asp	Gln	Gly	Cys	Val	Arg	Ile	Glu	Asn	Val	Glu	Thr	Leu	85	90	95	
Val	Leu	Gln	Ala	Pro	Lys	Asp	Ser	Phe	Ala	Leu	Lys	Ser	Asn	Glu	Arg	100	105	110	
Gly	Ile	Gly	Gln	Ala	Thr	His	Arg	Phe	Thr	Phe	Ser	Gln	Ile	Phe	Gly	115	120	125	
Pro	Glu	Val	Gly	Gln	Ala	Ser	Phe	Phe	Asn	Leu	Thr	Val	Lys	Glu	Met	130	135	140	
Val	Lys	Asp	Val	Leu	Lys	Gly	Gln	Asn	Trp	Leu	Ile	Tyr	Thr	Tyr	Gly	145	150	155	160
Val	Thr	Asn	Ser	Gly	Lys	Thr	His	Thr	Ile	Gln	Gly	Thr	Ile	Lys	Asp	165	170	175	
Gly	Gly	Ile	Leu	Pro	Arg	Ser	Leu	Ala	Leu	Ile	Phe	Asn	Ser	Leu	Gln	180	185	190	
Gly	Gln	Leu	His	Pro	Thr	Pro	Asp	Leu	Lys	Pro	Leu	Leu	Ser	Asn	Glu	195	200	205	
Val	Ile	Trp	Leu	Asp	Ser	Lys	Gln	Ile	Arg	Gln	Glu	Glu	Met	Lys	Lys	210	215	220	
Leu	Ser	Leu	Leu	Asn	Gly	Gly	Leu	Gln	Glu	Glu	Glu	Leu	Ser	Thr	Ser	225	230	235	240
Leu	Lys	Arg	Ser	Val	Tyr	Ile	Glu	Ser	Arg	Ile	Gly	Thr	Ser	Thr	Ser	245	250	255	
Phe	Asp	Ser	Gly	Ile	Ala	Gly	Leu	Ser	Ser	Ile	Ser	Gln	Cys	Thr	Ser	260	265	270	
Ser	Ser	Gln	Leu	Asp	Glu	Thr	Ser	His	Arg	Trp	Ala	Gln	Pro	Asp	Thr	275	280	285	
Ala	Pro	Leu	Pro	Val	Pro	Ala	Asn	Ile	Arg	Phe	Ser	Ile	Trp	Ile	Ser	290	295	300	
Phe	Phe	Glu	Ile	Tyr	Asn	Glu	Leu	Leu	Tyr	Asp	Leu	Leu	Glu	Pro	Pro	305	310	315	320
Ser	Gln	Gln	Arg	Lys	Arg	Gln	Thr	Leu	Arg	Leu	Cys	Glu	Asp	Gln	Asn	325	330	335	
Gly	Asn	Pro	Tyr	Val	Lys	Asp	Leu	Asn	Trp	Ile	His	Val	Gln	Asp	Ala	340	345	350	
Glu	Glu	Ala	Trp	Lys	Leu	Leu	Lys	Val	Gly	Arg	Lys	Asn	Gln	Ser	Phe	355	360	365	
Ala	Ser	Thr	His	Leu	Asn	Gln	Asn	Ser	Ser	Arg	Ser	His	Ser	Ile	Phe	370	375	380	
Ser	Ile	Arg	Ile	Leu	His	Leu	Gln	Gly	Glu	Gly	Asp	Ile	Val	Pro	Lys	385	390	395	400
Ile	Ser	Glu	Leu	Ser	Leu	Cys	Asp	Leu	Ala	Gly	Ser	Glu	Arg	Cys	Lys	405	410	415	
Asp	Gln	Lys	Ser	Gly	Glu	Arg	Leu	Lys	Glu	Ala	Gly	Asn	Ile	Asn	Thr	420	425	430	
Ser	Leu	His	Thr	Leu	Gly	Arg	Cys	Ile	Ala	Ala	Leu	Arg	Gln	Asn	Gln	435	440	445	

Gln	Asn	Arg	Ser	Lys	Gln	Asn	Leu	Val	Pro	Phe	Arg	Asp	Ser	Lys	Leu
	450					455					460				
Thr	Arg	Val	Phe	Gln	Gly	Phe	Phe	Thr	Gly	Arg	Gly	Arg	Ser	Cys	Met
465					470					475					480
Ile	Val	Asn	Val	Asn	Pro	Cys	Ala	Ser	Thr	Tyr	Asp	Glu	Thr	Leu	His
				485					490					495	
Val	Ala	Lys	Phe	Ser	Ala	Ile	Ala	Ser	Gln	Leu	Val	His	Ala	Pro	Pro
			500					505					510		
Met	Gln	Leu	Gly	Phe	Pro	Ser	Leu	His	Ser	Phe	Ile	Lys	Glu	His	Ser
		515					520					525			
Leu	Gln	Val	Ser	Pro	Ser	Leu	Glu	Lys	Gly	Ala	Lys	Ala	Asp	Thr	Gly
	530					535					540				
Leu	Asp	Asp	Asp	Ile	Glu	Asn	Glu	Ala	Asp	Ile	Ser	Met	Tyr	Gly	Lys
545					550					555					560
Glu	Glu	Leu	Leu	Gln	Val	Val	Glu	Ala	Met	Lys	Thr	Leu	Leu	Leu	Lys
				565					570						575
Glu	Arg	Gln	Glu	Lys	Leu	Gln	Leu	Glu	Met	His	Leu	Arg	Asp	Glu	Ile
			580					585					590		
Cys	Asn	Glu	Met	Val	Glu	Gln	Met	Gln	Gln	Arg	Glu	Gln	Trp	Cys	Ser
		595					600					605			
Glu	His	Leu	Asp	Thr	Gln	Lys	Glu	Leu	Leu	Glu	Glu	Met	Tyr	Glu	Glu
	610					615					620				
Lys	Leu	Asn	Ile	Leu	Lys	Glu	Ser	Leu	Thr	Ser	Phe	Tyr	Gln	Glu	Glu
625					630					635					640
Ile	Gln	Glu	Arg	Asp	Glu	Lys	Ile	Glu	Glu	Leu	Glu	Ala	Leu	Leu	Gln
				645					650						655
Glu	Ala	Arg	Gln	Gln	Ser	Val	Ala	His	Gln	Gln	Ser	Gly	Ser	Glu	Leu
			660					665					670		
Ala	Leu	Arg	Arg	Ser	Gln	Arg	Leu	Ala	Ala	Ser	Ala	Ser	Thr	Gln	Gln
		675					680					685			
Leu	Gln	Glu	Val	Lys	Ala	Lys	Leu	Gln	Gln	Cys	Lys	Ala	Glu	Leu	Asn
	690					695					700				
Ser	Thr	Thr	Glu	Glu	Leu	His	Lys	Tyr	Gln	Lys	Met	Leu	Glu	Pro	Pro
705					710					715					720
Pro	Ser	Ala	Lys	Pro	Phe	Thr	Ile	Asp	Val	Asp	Lys	Lys	Leu	Glu	Glu
				725					730						735
Gly	Gln	Lys	Asn	Ile	Arg	Leu	Leu	Arg	Thr	Glu	Leu	Gln	Lys	Leu	Gly
			740					745					750		
Glu	Ser	Leu	Gln	Ser	Ala	Glu	Arg	Ala	Cys	Cys	His	Ser	Thr	Gly	Ala
		755					760					765			
Gly	Lys	Leu	Arg	Gln	Ala	Leu	Thr	Thr	Cys	Asp	Asp	Ile	Leu	Ile	Lys
	770					775					780				
Gln	Asp	Gln	Thr	Leu	Ala	Glu	Leu	Gln	Asn	Asn	Met	Val	Leu	Val	Lys
785					790					795					800
Leu	Asp	Leu	Arg	Lys	Lys	Ala	Ala	Cys	Ile	Ala	Glu	Gln	Tyr	His	Thr
				805					810					815	
Val	Leu	Lys	Leu	Gln	Gly	Gln	Val	Ser	Ala	Lys	Lys	Arg	Leu	Gly	Thr
			820					825					830		
Asn	Gln	Glu	Asn	Gln	Gln	Pro	Asn	Gln	Gln	Pro	Pro	Gly	Lys	Lys	Pro
		835					840					845			
Phe	Leu	Arg	Asn	Leu	Leu	Pro	Arg	Thr	Pro	Thr	Cys	Gln	Ser	Ser	Thr
	850					855					860				
Asp	Cys	Ser	Pro	Tyr	Ala	Arg	Ile	Leu	Arg	Ser	Arg	Arg	Ser	Pro	Leu
865					870					875					880
Leu	Lys	Ser	Gly	Pro	Phe	Gly	Lys	Lys	Tyr						
				885					890						

<211> 768
 <212> DNA
 <213> Homo sapiens

<400> 197
 ccttcagcat aaaagctgat ccacaaacaa gaggagcacc agacctcctc ttggcttcga 60
 gatggcttcg ccacaccaag agcccaaacc tggagacctg attgagattt tccgccttgg 120
 ctatgagcac tggggcctgt atataggaga tggctacgtg atccatctgg ctccctccaag 180
 tgagtacccc ggggctgggt cctccagtgt cttctcagtc ctgagcaaca gtgcagaggt 240
 gaaacggggg cgcctggaag atgtggtggg aggctgttgc tatcgggtca acaacagctt 300
 ggaccatgag taccaaccac ggcccgtgga ggtgatcatc agttctgcga aggagatgg 360
 tggtcagaag atgaagtaca gtattgtgag caggaactgt gagcactttg tcgcccagct 420
 gagatatggc aagtcccgtc gtaaacaggt ggaaaaggcc aagggtgaag tcggtgtggc 480
 cacggcgctt ggaatcctgg ttgttgctgg atgctctttt gcgattagga gataccaaaa 540
 aaaagcaaca gcctgaagca gccacaaaat cctgtgttag aagcagctgt ggggggtcca 600
 gtggagatga gcctccccc tgcctccagc agcctgaccc tcgtgccttg tctcaggcgt 660
 tctctagatc ctttcctctg ttccctctc tcgctggcaa aagtatgatc taattgaaac 720
 aagactgaag gatcaataaa cagccatctg ccccttcaaa aaaaaaaa 768

<210> 198
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 198
 Met Ala Ser Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
 1 5 10 15
 Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Gly Asp Gly Tyr
 20 25 30
 Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
 35 40 45
 Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Gly Arg
 50 55 60
 Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
 65 70 75 80
 Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
 85 90 95
 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
 100 105 110
 Cys Glu His Phe Val Ala Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
 115 120 125
 Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
 130 135 140
 Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys
 145 150 155 160
 Lys Ala Thr Ala

<210> 199
 <211> 720
 <212> DNA
 <213> Homo sapiens

<400> 199
 gggggggggc ggagggcgct ctttccggg cgcgccacca cccgcgtagc accggcagcc 60
 gctgtcccg cagtctccag ccgtcccgcc cgcttgtggc caaactggct ccagtcactc 120
 ccgaaatgcc agtcgacttc actgggtact ggaagatgtt ggtcaacgag aatttcgagg 180
 agtacctgcg cgccctcgac gtcaatgtgg ccttgcgcaa aatcgccaac ttgctgaagc 240

```

cagacaaaga gatcgtgcag gacggtgacc atatgatcat ccgcacgctg agcactttta 300
ggaactacat catggacttc caagttggga aggagtttga ggaggatctg acaggcatag 360
atgaccgcaa gtgcatgaca acagtgcgct gggacggaga caagctccag tgtgtgcaga 420
agggtgagaa ggaggggctg ggctggaccc agtggatcga ggggtgatgag ctgcaccctag 480
agatgagagt ggaaggtgtg gtctgcaagc aagtattcaa gaaggtgcag tgaggcccaa 540
gcagacaacc ttgtoccaa ccaatcagcag gatgtgtgag ccaggatccc tctttgcaca 600
gcatgaggca aaaatgtcca gccaccccta ggcattctgtt agcagagtct gtctcttggc 660
tttgtcactt ttctttttct taaaacaaag ccatgccaat aaagtgcact gtgttcaaaa 720

```

<210> 200
 <211> 135
 <212> PRT
 <213> Homo sapiens

```

<400> 200
Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn
 1           5           10           15
Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys
      20           25           30
Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp
      35           40           45
His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp
      50           55           60
Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp
      65           70           75           80
Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
      85           90           95
Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu
      100          105          110
Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys
      115          120          125
Gln Val Phe Lys Lys Val Gln
      130          135

```

<210> 201
 <211> 2383
 <212> DNA
 <213> Homo sapiens

```

<400> 201
ggggctaccg cgccttttgc tccctggcgca cgcggagcct cctggagcct gccaccatcc 60
tgcctactac gtgctgccct ggcggcgag ccatgtgccg caccctggcc gccttcccca 120
ccacctgcct ggagagagcc aaagagttca agacacgtct ggggatcttt cttcacaaat 180
cagagctggg ctgcgatact gggagtactg gcaagtccga gtggggcagt aaacacagca 240
aagagaatag aaactttctc gaagatgtgc tgggggtggag agagtcgttc gacctgctgc 300
tgagcagtaa aaatggagtg gctgccttcc acgctttcct gaagacagag ttcagtgagg 360
agaacctgga gttctggctg gcctgtgagg agttcaagaa gatccgatca gctaccaagc 420
tggcctccag ggcacaccag atctttgagg agttcatttg cagtgaggcc cctaaagagg 480
tcaacattga ccatgagacc cgcgagctga cgaggatgaa cctgcagact gccacagcca 540
catgctttga tgcggctcag gggaagacac gtaccctgat ggagaaggac tcctaccac 600
gcttcttgaa gtgcctgct taccgggacc tggctgccc agcctcagcc gcctctgcca 660
ctctgtccag ctgcagcctg gacgagccct cacacacctg agtctccaag gcagtgagga 720
agccagccgg gaagagagg tgagtcacct atcccaggg tggctgcccc tgtgtgggag 780
gcaggttctg caaagcaagt gcaagaggac aaaaaaaaaa aaaaaaaaaa aaaaaaatgcg 840
ctccagcagc ctgtttggga agcagcagtc tctccttcag atactgtggg actcatgctg 900
gagaggagcc gcccacttcc aggacctgtg aataagggtc aatgatgagg gttgggtggg 960
ctctctgtgg ggcaaaaagg tggatatggg gttagcactg gctctcgttc tcaccggaga 1020

```

```

aggaagtgtt ctagtgtggt ttaggaaaca tgtggataaa gggaaccatg aaaatgagag 1080
gaggaaagac atccagatca gctgttttgc ctgttgctca gttgactctg attgcatcct 1140
gttttcctaa ttcccagact gttctgggca cggaaggac cctggatgtg gagtcttccc 1200
ctttggccct cctcaactggc ctctgggcta gccagagtc ccttagcttg tacctcgtaa 1260
cactcctgtg tgtctgtcca gccttgcaag catgtcaagg ccagcaagct gatgtgactc 1320
ttgccccatg cgagatatatt atacctcaaa cactggcctg tgagcccttt ccaagtcagt 1380
ggagagccct gaaaggaggc tcacttgaat ccagctcagt gctctgggtg gccccctgca 1440
ggtggccccct gacctgctg tgcagcaggg tccacctgtg agcaggcccg ccctggggcc 1500
tcttcctgga tgtgccccct ctgagttctg tgctgtctct tggaggcagg gccaggaga 1560
acaaagtgtg gaggcctcgg ggagtggctt ttccagctct catgccccgc agtgtggaac 1620
aaggcagaaa aggatcctag gaaataagtc tcttgccggt cctgagagt cctgctgaaa 1680
tccagccagt gttttttgtg gtatgagaac aggcataaag agatgccccg agatagaagg 1740
ggagccttgt gtttctttcc tgcagacgtg agatgaacac tggagtgggc agaggtggcm 1800
caggaccatg gcacccttag agtgcagaag ctggggggag aggctgcttc gaagggcagg 1860
actggggata cctgcctgtc acctcagggc atcactgaac aaacatttcc tgatggsaac 1920
tcctgcgcca gagcccaggc tggggaagtg aactaccag ggcagccctt ttgtggccca 1980
ggataatcaa cactgttctc tctgtacct gagctcctcc aggagattat ttaagtgtat 2040
tgtatcattg gttttctgtg attgtcataa cattgttttt gttattgttg gtgctgttgt 2100
tatttattat tgtaatttca gtttgcctct actggagaat ctcagcaggg gtttcagcct 2160
gactgtctcc ctttctctac cagactctac ctctgaatgt gctgggaacc tcttgagacc 2220
tgtcaggaac tcctcactgt ttaaataattt atttattgtg acaaattggag ctgggttctc 2280
agatatgaat gatgtttgca atccccattt tcctgtttca gcatgttata ttcttataaa 2340
ataaaagcaa aagtcaaata tgaaaaaaaa aaaaaaaaaa aaa 2383

```

<210> 202

<211> 202

<212> PRT

<213> Homo sapiens

<400> 202

```

Met Cys Arg Thr Leu Ala Ala Phe Pro Thr Thr Cys Leu Glu Arg Ala
 1          5          10          15
Lys Glu Phe Lys Thr Arg Leu Gly Ile Phe Leu His Lys Ser Glu Leu
 20          25          30
Gly Cys Asp Thr Gly Ser Thr Gly Lys Ser Glu Trp Gly Ser Lys His
 35          40          45
Ser Lys Glu Asn Arg Asn Phe Ser Glu Asp Val Leu Gly Trp Arg Glu
 50          55          60
Ser Phe Asp Leu Leu Leu Ser Ser Lys Asn Gly Val Ala Ala Phe His
 65          70          75          80
Ala Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Leu
 85          90          95
Ala Cys Glu Glu Phe Lys Lys Ile Arg Ser Ala Thr Lys Leu Ala Ser
100          105          110
Arg Ala His Gln Ile Phe Glu Glu Phe Ile Cys Ser Glu Ala Pro Lys
115          120          125
Glu Val Asn Ile Asp His Glu Thr Arg Glu Leu Thr Arg Met Asn Leu
130          135          140
Gln Thr Ala Thr Ala Thr Cys Phe Asp Ala Ala Gln Gly Lys Thr Arg
145          150          155          160
Thr Leu Met Glu Lys Asp Ser Tyr Pro Arg Phe Leu Lys Ser Pro Ala
165          170          175
Tyr Arg Asp Leu Ala Ala Gln Ala Ser Ala Ala Ser Ala Thr Leu Ser
180          185          190
Ser Cys Ser Leu Asp Glu Pro Ser His Thr
195          200

```

<210> 203

<211> 616
 <212> DNA
 <213> Homo sapiens

<400> 203
 ctcccctggg agcctggctg ccttgctctc cttcctgggt ctgtctctgc cacctgggtct 60
 gccacagatc catgatgtgc agttctctgg agcaggcgct ggctgtgctg gtcactacct 120
 tccacaagta ctctgccaag gagggcgaca agttcaagct gagtaagggg gaaatgaagg 180
 aacttctgca caaggagctg cccagctttg tggggcattc cagagaacca tgtgctgtga 240
 gggccttccg agtccatctg tttaatcctg tcattggaga cttgagaaac cagagcccag 300
 aagggaagag tgattgtccc aagatcacac agcactggag aaagtggatg aggaggggct 360
 gaagaagctg atgggcagcc tggatgagaa cagtgaccag caggtggact tccaggagta 420
 tgctgttttc ctggcactca tcaactgtcat gtgcaatgac ttcttccagg gctgcccaga 480
 ccgaccctga agcagaactc ttgacttcct gccatggatc tcttggggccc aggactgttg 540
 atgcctttga gttttgtatt caataaactt tttttgtctg ttgaaaaaaaa aaaaaaaaaa 600
 aaaaaaaaaa aaaaaa 616

<210> 204
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 204
 Met Met Cys Ser Ser Leu Glu Gln Ala Leu Ala Val Leu Val Thr Thr
 1 5 10 15
 Phe His Lys Tyr Ser Cys Gln Glu Gly Asp Lys Phe Lys Leu Ser Lys
 20 25 30
 Gly Glu Met Lys Glu Leu Leu His Lys Glu Leu Pro Ser Phe Val Gly
 35 40 45
 His Ser Arg Glu Pro Cys Ala Val Arg Ala Phe Arg Val His Leu Phe
 50 55 60
 Asn Pro Val Ile Gly Asp Leu Arg Asn Gln Ser Pro Glu Gly Lys Ser
 65 70 75 80
 Asp Cys Pro Lys Ile Thr Gln His Trp Arg Lys Trp Met Arg Arg Gly
 85 90 95

<210> 205
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 205
 ctgggtctgt ctctgccacc tggctctgcca cagatccatg atgtgcagtt ctctggagca 60
 ggcgctggct gtgctgggtc ctaccttcca caagtactcc tgccaagagg gcgacaagtt 120
 caagctgagt aagggggaaa tgaaggaaact tctgcacaag gagctgcca gctttgtggg 180
 ggagaaagtg gatgaggagg ggctgaagaa gctgatgggc agcctggatg agaacagtga 240
 ccagcaggtg gacttccagg agtatgtctg tttcctggca ctcatcactg tcatgtgcaa 300
 tgactttctc cagggctgcc cagaccgacc ctgaagcaga actcttgact tccctgccatg 360
 gatctcttgg gcccaggact gttgatgcct ttgagttttg tattcaataa actttttttg 420
 tctgttga 428

<210> 206
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Cys Ser Ser Leu Glu Gln Ala Leu Ala Val Leu Val Thr Thr Phe

270

1	5	10	15
His Lys Tyr Ser Cys Gln Glu Gly Asp Lys Phe Lys Leu Ser Lys Gly			
	20	25	30
Glu Met Lys Glu Leu Leu His Lys Glu Leu Pro Ser Phe Val Gly Glu			
	35	40	45
Lys Val Asp Glu Glu Gly Leu Lys Lys Leu Met Gly Ser Leu Asp Glu			
	50	55	60
Asn Ser Asp Gln Gln Val Asp Phe Gln Glu Tyr Ala Val Phe Leu Ala			
65	70	75	80
Leu Ile Thr Val Met Cys Asn Asp Phe Phe Gln Gly Cys Pro Asp Arg			
	85	90	95
Pro			

<210> 207

<211> 799

<212> DNA

<213> Homo sapiens

<400> 207

```

cactcccaaa gaactgggta ctcaacactg agcagatctg ttctttgagc taaaaaaccaat 60
gtgctgtacc aagagtttgc tcctggctgc tttgatgtca gtgctgtac tccacctctg 120
cggcgaatca gaagcagcaa gcaactttga ctgctgtcct ggatacacag accgtattct 180
tcatcctaaa tttattgtgg gcttcacacg gcagctggcc aatgaaggct gtgacatcaa 240
tgctatcatc tttcacacaa agaaaaagtt gtctgtgtgc gcaaatacaa aacagacttg 300
ggtgaaatat attgtgcgtc tcctcagtaa aaaagtcaag aacatgtaaa aactgtggct 360
tttctggaat ggaattggac atagcccaag aacagaaaga accttgctgg ggttggaggt 420
ttcacttgca catcatggag ggttttagtg ttatctaatt tgtgcctcac tggacttgtc 480
caattaatga agttgattca tattgcatca tagtttgctt tgtttaagca tcacattaaa 540
gttaaaactgt attttatgtt atttatagct gtaggttttc tgtgttttagc tatttaatac 600
taattttcca taagctattt tggtttagtg caaagtataa aattatatatt gggggggaat 660
aagattatat ggactttcct gcaagcaaca agctattttt taaaaaaaact atttaacatt 720
cttttgttta tattgttttg tctcctaaat tgttgtaatt gcattataaa ataagaaaaa 780
cattaataag acaaatatt
799

```

<210> 208

<211> 96

<212> PRT

<213> Homo sapiens

<400> 208

Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu	
1	5
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
	20
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
	35
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	
	50
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr	
65	70
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met	
	85
	90
	95

<210> 209

<211> 2133

<212> DNA

<213> Homo sapiens

<400> 209

```

cgggagagcg cgctctgcct gccgcctgcc tgcctgccac tgaggggtcc cagcaccatg 60
agggcctgga tcttctttct cctttgcctg gccgggaggg ccttggcagc ccctcagcaa 120
gaagccctgc ctgatgagac agaggtggtg gaagaaactg tggcagaggt gactgaggta 180
tctgtgggag ctaatcctgt ccaggtggaa gtaggagaat ttgatgatgg tgcagaggaa 240
accgaagagg aggtggtggc ggaaaatccc tgccagaacc aocactgcaa acacggcaag 300
gtgtgcgagc tggatgagaa caacaccccc atgtgogtgt gccaggaccc caccagctgc 360
ccagccccc a ttggcgagtt tgagaagggtg tgcagcaatg acaacaagac cttcgactct 420
tcctgocact tctttgccac aaagtgcacc ctggagggca ccaagaaggg ccacaagctc 480
cacctggact acatcgggcc ttgcaaatat atccccctt gcctggactc tgagctgacc 540
gaattccccc tgcgcctgct ggactggctc aagaacgtcc tggtcaccct gtatgagagg 600
gatgaggaca acaaccttct gactgagaag cagaagctgc ggggtaagaa gatccatgag 660
aatgagaagc gcctggaggc aggagaccac cccgtggagc tgctggcccc ggacttcgag 720
aagaactata acatgtacat cttccctgta cactggcagt tcggccagct ggaccagcac 780
cccattgacg ggtacctctc ccacaccgag ctggctccac tgcgtgctcc cctcatcccc 840
atggagcatt gcaccacccg ctttttcgag acctgtgacc tggacaatga caagtacatc 900
gccctggatg agtgggccgg ctgcttcggc atcaagcaga aggatatcga caaggatctt 960
gtgatctaaa tccactcctt ccacagtacc ggattctctc tttaaccctc cccttcgtgt 1020
ttcccccaat gtttaaaatg tttggatggt ttgttgttct gcctggagac aaggtgctaa 1080
catagattta agtgaataca ttaacggtgc taaaaatgaa aattctaacc caagacatga 1140
cattcttagc tgtaacttaa ctattaaggc cttttccaca cgcattaata gtcccatttt 1200
tctcttgcca tttgtagctt tgcccattgt cttattggca catgggtgga cacggatctg 1260
ctgggctctg ccttaaacac acattgcagc ttcaactttt ctcttttagt ttctgtttga 1320
aactaatact taccgagtcg gactttgtgt tcatttcatt tcaggggtctt ggctgcctgt 1380
gggcttcccc aggtggcctg gaggtgggca aagggaagta acagacacac gatgttgtca 1440
aggatggttt tgggactaga ggctcagtgg tgggagagat ccctgcagaa tccaccaacc 1500
agaacgtggt ttgctgagg ctgtaactga gagaagatt ctggggctgt cttatgaaaa 1560
tatagacatt ctcacataag ccagttcat caccatttcc tcocttaoct ttcagtgcag 1620
tttcttttca cattaggctg ttggttcaaa cttttgggag caccggactgt cagttctctg 1680
ggaagtggtc agcgcctcct gcagggtctc tcctcctctg tcttttggag aaccagggct 1740
cttctcaggg gctctagggg ctgccaggct gtttcagcca ggaaggccaa aatcaagagt 1800
gagatgtaga aagttgtaaa atagaaaaag tggagttggt gaatcgggtg ttctttcctc 1860
acatttggat gattgtcata aggttttttag catgttctct cttttcttca ccctccccct 1920
tgttcttcta ttaatcaaga gaaacttcaa agttaatggg atggctggat ctcacaggct 1980
gagaactcgt tcacctccaa gcatttcagt aaaaagctgc ttcttattaa tcatacaaac 2040
tctcaccatg atgtgaagag tttcacaat ctttcaaat aaaaagtaat gacttagaaa 2100
ctgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2133

```

<210> 210

<211> 303

<212> PRT

<213> Homo sapiens

<400> 210

```

Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1           5           10           15
Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
          20           25           30
Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
          35           40           45
Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
          50           55           60
Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
65           70           75           80
Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
          85           90           95
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys

```

100										105					110					
Ser	Asn	Asp	Asn	Lys	Thr	Phe	Asp	Ser	Ser	Cys	His	Phe	Phe	Ala	Thr					
115										120					125					
Lys	Cys	Thr	Leu	Glu	Gly	Thr	Lys	Lys	Gly	His	Lys	Leu	His	Leu	Asp					
130										135					140					
Tyr	Ile	Gly	Pro	Cys	Lys	Tyr	Ile	Pro	Pro	Cys	Leu	Asp	Ser	Glu	Leu					
145										150					155					
Thr	Glu	Phe	Pro	Leu	Arg	Met	Arg	Asp	Trp	Leu	Lys	Asn	Val	Leu	Val					
165										170					175					
Thr	Leu	Tyr	Glu	Arg	Asp	Glu	Asp	Asn	Asn	Leu	Leu	Thr	Glu	Lys	Gln					
180										185					190					
Lys	Leu	Arg	Val	Lys	Lys	Ile	His	Glu	Asn	Glu	Lys	Arg	Leu	Glu	Ala					
195										200					205					
Gly	Asp	His	Pro	Val	Glu	Leu	Leu	Ala	Arg	Asp	Phe	Glu	Lys	Asn	Tyr					
210										215					220					
Asn	Met	Tyr	Ile	Phe	Pro	Val	His	Trp	Gln	Phe	Gly	Gln	Leu	Asp	Gln					
225										230					235					
His	Pro	Ile	Asp	Gly	Tyr	Leu	Ser	His	Thr	Glu	Leu	Ala	Pro	Leu	Arg					
245										250					255					
Ala	Pro	Leu	Ile	Pro	Met	Glu	His	Cys	Thr	Thr	Arg	Phe	Phe	Glu	Thr					
260										265					270					
Cys	Asp	Leu	Asp	Asn	Asp	Lys	Tyr	Ile	Ala	Leu	Asp	Glu	Trp	Ala	Gly					
275										280					285					
Cys	Phe	Gly	Ile	Lys	Gln	Lys	Asp	Ile	Asp	Lys	Asp	Leu	Val	Ile						
290										295					300					

<210> 211

<211> 2228

<212> DNA

<213> Homo sapiens

<400> 211

```

ggtacagtca tcacaagcct gttcggcggg actgtgatgg ccagagagat gacgatctta 60
ggatcggtcg ttttgactct cctgttggcc ggctatttgg cacaacagta tttaccattg 120
cctactccta aagtgattgg tattgatctt ggcaccacct attgttctgt tgggggtgtt 180
tttcctggca caggaaaagt aaaggtgatt ccagatgaaa atgggcatat cagcataccc 240
agcatgggtg cttttactga caatgatgta tatgtgggat atgaaagcgt agagctggca 300
gattcaaatc ctcaaaacac aatatatgat gccaaaagat tcataggcaa gatttttacc 360
gcagaagagt tggaggctga aattggcaga taccatttta aggtttttaa caaaaatgga 420
atgggttgagt tttctgtgac aagtaatgag accatcacag tgtccccaga atatgttggc 480
tctcgactat tgttgaagtt aaaggaaatg gcagaggcat atcttggaat gccagttgcc 540
aatgctgtca tttctgtacc agcagaattt gatctaaaac agagaaattc aacaattgaa 600
gctgctaacc ttgcaggact gaagattttg aggttaataa atgaaccac agcagcagct 660
atggcctatg gtctccacaa ggctgacgtc ttccacgtct tggatgata cttgggcgga 720
ggaactctag atgtgtcttt actgaataaa caaggaggga tgtttctaac ccgagcaatg 780
tctggaaaca ataaacttgg aggacaggac ttcaatcaga gattgcttca gtacttatat 840
aaacagatct atcaaacata tggcttcgtg ccctctagga aagaggaaat ccacagattg 900
agacaagctg tggaaatggg caaattaaat ctgactcttc atcaatctgc tcagttgtca 960
gtattactaa cgggtggagg gcaggacagg aaggaacctc acagtagtga cactgaactg 1020
ccaaaagaca aactttcctc agcagatgac catcgcggtg acagtgggtt tggacgtggc 1080
ctttctgata agaaaagtgg agaaagtcag gttttatttg aaacagaaat atcacggaaa 1140
ctctttgata cccttaatga agacctcttt cagaaaatac tggtagccat tcagcaagta 1200
ttgaaagaag gccacctgga aaagactgag attgatgagg tggttttagt tgggggctcc 1260
actcgtattc ctcggtaccg tcaagtcatt caagagttct ttggaaaaga tcccaacaca 1320
tctgtagacc ctgacctagc agtagtaacg ggagtggcta tccaagcagg gattgatgga 1380
ggctcttggc ctctccaagt cagtgtctta gaaattccca ataagcattt acaaaaaacc 1440
aacttcaact gaattctgca gaaataatgg ttatttgtga acttgtctga tgatctcttc 1500
ccatttatca gattacctt tccacaaaag aaagtctcta aaatatcaca gattttacct 1560

```



```

gagggaaca tttagatata ggaaaatttt acatagtgtt ttgtcttagg attagacgtg 1620
accagattga tcctgtttga ttttggagag atcctattct aacaaatact ctaaaatgat 1680
aaaattgagg tacaactctc ttaaaagagt atggataact atattttctg gattctggag 1740
gttgataacc atatgcactt aacattatat tctataaaca ttaagtagtg ccagttatga 1800
gattcccagt tcttactaaa ttgtattagc aggagctggg aattacttgt attatcacat 1860
gtaactaata atttgaacta tacttgaagg accgtgttga tgtcagggtat ttacagtggg 1920
tggaagatag cagtattatt agcataagct gcatacgtaa tattcagtaa ctgccatatt 1980
atataacaaa tttacattca caaattcagt atcctgttaa gtgtcatatt cttgtaatct 2040
gcattctcca ggagttttat gtgtttaata gatgaattta ttttatttct aaagggtattc 2100
aaatgtttca gcaccatata atagaaatac ccaattatat tctagttcct ttatgtcctg 2160
tacatcatto tctgcttgga tttccattat tctgtttggg tagagaataa aattggtaat 2220
tgcatattg

```

<210> 212

<211> 471

<212> PRT

<213> Homo sapiens

<400> 212

```

Met Ala Arg Glu Met Thr Ile Leu Gly Ser Ala Val Leu Thr Leu Leu
 1           5           10           15
Leu Ala Gly Tyr Leu Ala Gln Gln Tyr Leu Pro Leu Pro Thr Pro Lys
          20          25          30
Val Ile Gly Ile Asp Leu Gly Thr Thr Tyr Cys Ser Val Gly Val Phe
          35          40          45
Phe Pro Gly Thr Gly Lys Val Lys Val Ile Pro Asp Glu Asn Gly His
          50          55          60
Ile Ser Ile Pro Ser Met Val Ser Phe Thr Asp Asn Asp Val Tyr Val
65          70          75          80
Gly Tyr Glu Ser Val Glu Leu Ala Asp Ser Asn Pro Gln Asn Thr Ile
          85          90          95
Tyr Asp Ala Lys Arg Phe Ile Gly Lys Ile Phe Thr Ala Glu Glu Leu
          100         105         110
Glu Ala Glu Ile Gly Arg Tyr Pro Phe Lys Val Leu Asn Lys Asn Gly
          115         120         125
Met Val Glu Phe Ser Val Thr Ser Asn Glu Thr Ile Thr Val Ser Pro
          130         135         140
Glu Tyr Val Gly Ser Arg Leu Leu Leu Lys Leu Lys Glu Met Ala Glu
145         150         155         160
Ala Tyr Leu Gly Met Pro Val Ala Asn Ala Val Ile Ser Val Pro Ala
          165         170         175
Glu Phe Asp Leu Lys Gln Arg Asn Ser Thr Ile Glu Ala Ala Asn Leu
          180         185         190
Ala Gly Leu Lys Ile Leu Arg Val Ile Asn Glu Pro Thr Ala Ala Ala
          195         200         205
Met Ala Tyr Gly Leu His Lys Ala Asp Val Phe His Val Leu Val Ile
          210         215         220
Asp Leu Gly Gly Gly Thr Leu Asp Val Ser Leu Leu Asn Lys Gln Gly
225         230         235         240
Gly Met Phe Leu Thr Arg Ala Met Ser Gly Asn Asn Lys Leu Gly Gly
          245         250         255
Gln Asp Phe Asn Gln Arg Leu Leu Gln Tyr Leu Tyr Lys Gln Ile Tyr
          260         265         270
Gln Thr Tyr Gly Phe Val Pro Ser Arg Lys Glu Glu Ile His Arg Leu
          275         280         285
Arg Gln Ala Val Glu Met Val Lys Leu Asn Leu Thr Leu His Gln Ser
          290         295         300
Ala Gln Leu Ser Val Leu Leu Thr Val Glu Glu Gln Asp Arg Lys Glu
305         310         315         320

```

<400>	213					
ggccggggaga	gtagcagtg	cttggacccc	agctctctc	cccccttctc	tctaaggatg	60
gcccagaagg	agaactccta	cccctggccc	tacggccgac	agacggctcc	atctggcctg	120
agcaccctgc	cccagcgagt	cctccggaaa	gagcctgtca	ccccatctgc	acttgctctc	180
atgagccgct	ccaatgtcca	gcccacagct	gccccctggc	agaaggtgat	ggagaatagc	240
agtgggacac	ccgacatctt	aacgcggcac	ttcacaattg	atgactttga	gattgggcgt	300
cctctgggca	aaggcaagtt	tggaaacgtg	tacttggtc	gggagaagaa	aagccatttc	360
atcgtggcgc	tcaaggtcct	cttcaagtc	cagatagaga	aggagggcgt	ggagcatcag	420
ctgcgcagag	agatcgaaat	ccaggcccac	ctgcaccatc	ccaacatcct	gcgtctctac	480
aactatTTTT	atgaccggag	gaggatctac	ttgattctag	agtatgcccc	ccgcggggag	540
ctctacaagg	agctgcagaa	gagctgcaca	tttgacgagc	agcgaacagc	cacgatcatg	600
gaggagttag	cagatgctct	aatgtactgc	catgggaaga	aggtgattca	cagagacata	660
aagccagaaa	atctgctctt	agggctcaag	ggagagctga	agattctgtg	cttcggctgg	720
tctgtgcatg	cgccctccct	gaggaggaag	acaatgtgtg	gcaccctgga	ctacctgcc	780
ccagagatga	ttgaggggcg	catgcacaat	gagaaggtgg	atctgtggtg	cattggagtg	840
ctttgctatg	agctgctgg	ggggaaccca	ccctttgaga	gtgcatcaca	caacgagacc	900
tatcgccgca	tcgtcaaggt	ggacctaaag	ttccccgctt	ctgtgcccac	gggagcccag	960
gacctcatct	ccaaactgct	caggcataac	ccctcggaac	ggctgcccc	ggcccagggtc	1020
tcagcccacc	cttgggtccg	ggccaactct	cggaggggtg	tgccctccctc	tgcccttcaa	1080
tctgtgcct	gattgctcct	gtcattcact	cgggtgcgtg	tgtttgtatg	tctgtgtatg	1140
tataggggaa	agaagggatc	cctaactgtt	cccttatctg	ttttctacct	cctcctttgt	1200
ttaataaaag	ctgaagcttt	ttgt				1224

```

<400> 214
Met Ala Gln Lys Glu Asn Ser Tyr Pro Trp Pro Tyr Gly Arg Gln Thr
 1             5             10             15
Ala Pro Ser Gly Leu Ser Thr Leu Pro Gln Arg Val Leu Arg Lys Glu

```

```
<210> 215
<211> 1421
<212> DNA
<213> Homo sapiens
```

<400> 215							
acttactgcg	ggacggcctt	ggagagtact	cggggttcgtg	aacttcccgg	aggcgcaatg	60	
agctgcatta	acctgccac	tgtgctgcc	ggctcccca	gcaagaccg	ggggcagatc	120	
caggtgatcc	tgggccgat	gttctcagga	aaaagcacag	agttgatgag	acgcgtccgt	180	
cgcttccaga	ttgctcagta	caagtgcctg	gtgatcaagt	atgccaaaga	cactcgctac	240	
agcagcagct	tctgcacaca	tgaccggaac	accatggagg	cgctgcccgc	ctgctgtctc	300	
cgagacgtgg	cccaggaggc	cctgggcgtg	gctgtcatag	gcatcgacga	ggggcagttt	360	
ttccctgaca	tcatggagtt	ctgcgaggcc	atggccaacg	ccggaagac	cgtaatttgt	420	
gctgcactgg	atgggacatt	ccagaggaag	ccattttggg	ccatcctgaa	cctggtgcgc	480	
ctggccgaga	gcgtggtgaa	gctgacggcg	gtgtgcattg	agtgttccg	ggaagcgccc	540	
tataccaaga	ggctcggcac	agagaaggag	gtcgagggtg	ttgggggagc	agacaagtac	600	

```

cactccgtgt gtcggctctg ctacttcaag aaggcctcag gccagcctgc cgggccggac 660
aactaaagaga actgcccagt gccaggaaaag ccaggggaag ccgtggctgc caggaagctc 720
tttgcacacac agcagattct gcaatgcagc cctgccaaact gagggacctg caagggccgc 780
ccgctccctt cctgcccactg ccgcctactg gacgctgccc tgcattgctgc ccagccactc 840
caggaggaag tcgggaggcg tggagggtga ccacaccttg gccttctggg aactctcctt 900
tgtgtggctg cccacacctg cgcattgctcc ctctctcct acccactggg ctgcttaaaag 960
cttccctctc agctgctggg acgatcgccc aggctggagc tggccccgct tgggtggcctg 1020
ggatctggca cactccctct ccttgggggtg agggacagag cccacagctg ttgacatcag 1080
cctgcttctt cccctctgcg gctttcactg ctgagtttct gttctccctg ggaagcctgt 1140
gccagcacct ttgagccttg gccacactg aggccttaggc ctctctgcct gggatgggct 1200
cccaccctcc cctgaggatg gcctggattc acgcctcctt gtttcccttt gggtcaaaag 1260
cccttccctac ctctgggtgat ggtttccaca ggaacaacag catctttcac caagatgggt 1320
ggcaccaacc ttgctgggac ttggatccca ggggcttatc tcttcaagtg tggagagggc 1380
agggtccacg cctctgctgt agcttatgaa attaactaat t 1421

```

<210> 216

<211> 234

<212> PRT

<213> Homo sapiens

<400> 216

```

Met Ser Cys Ile Asn Leu Pro Thr Val Leu Pro Gly Ser Pro Ser Lys
 1           5           10           15
Thr Arg Gly Gln Ile Gln Val Ile Leu Gly Pro Met Phe Ser Gly Lys
          20           25           30
Ser Thr Glu Leu Met Arg Arg Val Arg Arg Phe Gln Ile Ala Gln Tyr
      35           40           45
Lys Cys Leu Val Ile Lys Tyr Ala Lys Asp Thr Arg Tyr Ser Ser Ser
 50           55           60
Phe Cys Thr His Asp Arg Asn Thr Met Glu Ala Leu Pro Ala Cys Leu
65           70           75           80
Leu Arg Asp Val Ala Gln Glu Ala Leu Gly Val Ala Val Ile Gly Ile
          85           90           95
Asp Glu Gly Gln Phe Phe Pro Asp Ile Met Glu Phe Cys Glu Ala Met
      100          105          110
Ala Asn Ala Gly Lys Thr Val Ile Val Ala Ala Leu Asp Gly Thr Phe
      115          120          125
Gln Arg Lys Pro Phe Gly Ala Ile Leu Asn Leu Val Pro Leu Ala Glu
      130          135          140
Ser Val Val Lys Leu Thr Ala Val Cys Met Glu Cys Phe Arg Glu Ala
145          150          155          160
Ala Tyr Thr Lys Arg Leu Gly Thr Glu Lys Glu Val Glu Val Ile Gly
          165          170          175
Gly Ala Asp Lys Tyr His Ser Val Cys Arg Leu Cys Tyr Phe Lys Lys
      180          185          190
Ala Ser Gly Gln Pro Ala Gly Pro Asp Asn Lys Glu Asn Cys Pro Val
      195          200          205
Pro Gly Lys Pro Gly Glu Ala Val Ala Ala Arg Lys Leu Phe Ala Pro
      210          215          220
Gln Gln Ile Leu Gln Cys Ser Pro Ala Asn
225          230

```

<210> 217

<211> 2307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 1691, 1698, 1705, 1708, 1709, 1713, 1717, 1720, 1724, 1728,
1733, 1741, 1746, 1748, 1755, 1770, 1774, 1791, 1802, 1821,
1838, 1856, 1859, 1864, 1908, 1959, 1997, 2012, 2038, 2143

<223> n = A,T,C or G

<400> 217

```

agtcgaccccc gcgtccgggtt ttaatcaagc tgcccaaagt cccccaatca ctcttggaat 60
acacagagag aggcagcagc ttgctcagcg gacaaggatg ctggggcgtga gggaccaagg 120
cctgccctgc actcgggcct cctccagcca gtgctgacca gggacttctg acctgctggc 180
cagccaggac ctgtgtgggg aggccctcct gctgccttgg ggtgacaatc tcagctccag 240
gctacaggga gaccgggagg atcacagagc cagcatgtta caggatcctg acagtgatca 300
acctctgaac agcctcgatg tcaaaccctt gcgcaaacc cgtatcccca tggagacctt 360
cagaaagggtg gggatcccca tcatcatagc actactgagc ctggcgagta tcatcattgt 420
ggttgtctctc atcaagggtga ttctggataa atactacttc ctctgcgggc agcctctcca 480
cttcatcccg aggaagcagc tgtgtgacgg agagctggac tgtcccttgg gggaggacga 540
ggagcactgt gtcaagagct tccccgaagg gcctgcagtg gcagtcggcc tctccaagga 600
ccgateccaca ctgcagggtgc tggactcggc cacagggaac tggttctctg cctgtttcga 660
caacttcaca gaagctctcg ctgagacagc ctgtaggcag atgggctaca gcagcaaacc 720
cactttcaga gctgtggaga ttggcccaga ccaggatctg gatgttgttg aaatcacaga 780
aaacagccag gagcttcgca tgcggaactc aagtggggcc tgtctctcag gctccctggt 840
ctccctgcac tgtcttgctt gtgggaagag cctgaagacc ccccggtgtg tgggtgggga 900
ggaggcctct gtggattctt ggcttggca ggtcagcatc cagtacgaca aacagcacgt 960
ctgtggaggg agcatcctgg acccccactg ggtcctcagc gcagcccact gcttcaggaa 1020
acataccgat gtgttcaact ggaagggtgc ggcagggtca gacaaactgg gcagcttccc 1080
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc ccaaagacaa 1140
tgacatcgcc ctcatgaagc tgcagttccc actcactttc tcaggcacag tcaggcccat 1200
ctgtctgccc ttctttgatg aggagctcac tccagccacc ccaactctga tcattggatg 1260
gggctttacg aagcagaatg gaggggaagt gtctgacata ctgctgcagg cgtcagtcca 1320
ggtcattgac agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1380
gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg acagtgggtg 1440
gcccctgatg taccaatctg accagtggca tgtgggtggc atcgttagct ggggctatgg 1500
ctgcgggggc ccgagcacc caggagtata caccaaggtc tcagcctatc tcaactggat 1560
ctacaatgtc tggaaggctg agctgtaatg ctgctgcccc tttgcagtgc tgggagccgc 1620
ttccttctctg ccctgcccac ctggggatcc cccaaagtca gacacagagc aagagtcccc 1680
ttgggtacac nccctctngc ccacnagnnc ctncagnan ttttcttngg agncagcaaa 1740
ngggcnctc aattncctgt aagagaccn tcgncagccc agaggcgccc nagaggaagt 1800
cnagcagccc tagctcggcc nacacttggg gctcccangc atcccaggga gagacnacna 1860
gccnactga acaagggtct aggggtattg ctaagccaag aaggaaacnt tcccacacta 1920
ctgaatggaa gcaggctgtc ttgtaaaagc ccagatcanc tgtgggctgg agaggagaag 1980
gaaaggggtc gcgccangcc ctgtccgtct tncaccatc cccaagccta ctagagcnaa 2040
gaaaccagtt gtaatatata atgcactgcc ctactgttgg tatgactacc gttacctact 2100
gttgtcattg ttattacagc tatggccact attattaaag agnctgtgta acatcaaaaa 2160
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ataaataaaa aaaaactcga gggggggccc 2220
ggtacccaat tcgccctata gtgagtcgta ttacaattca ctggccgtcg ttttacaacg 2280
tcgtgactgg gaaaaccctg gcgttac 2307

```

<210> 218

<211> 428

<212> PRT

<213> Homo sapiens

<400> 218

```

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val
 1             5             10             15
Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val
          20          25          30
Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile Ile Ile
      35              40              45

```

```

Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys
  50                               55                               60
Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu
  65                               70                               75                               80
Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe
                               85                               90                               95
Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr
                               100                               105                               110
Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe
                               115                               120                               125
Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly
  130                               135                               140
Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln
  145                               150                               155                               160
Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met
                               165                               170                               175
Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His
                               180                               185                               190
Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly
                               195                               200                               205
Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr
  210                               215                               220
Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val
  225                               230                               235                               240
Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp
                               245                               250                               255
Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala
                               260                               265                               270
Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp
  275                               280                               285
Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly
  290                               295                               300
Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
  305                               310                               315                               320
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly
                               325                               330                               335
Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp
  340                               345                               350
Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu
  355                               360                               365
Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln
  370                               375                               380
Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val
  385                               390                               395                               400
Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro
                               405                               410                               415
Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp
                               420                               425

```

<210> 219

<211> 556

<212> DNA

<213> Homo sapiens

<400> 219

```

acaactcggt ggtggccact ggcgagacca gacttcgctc gtactcgtgc gcctcgcttc 60
gcttttcttc cgcaaccatg tctgacaaac ccgatatggc tgagatcgag aaattcgata 120
agtcgaaact gaagaagaca gagacgcaag agaaaaatcc actgccttcc aaagaaacga 180

```

```

ttgaacagga gaagcaagca ggogaatcgt aatgaggcgt gcgcgcgcaa tatgcactgt 240
acattccaca agcattgcct tottatttta cttcttttag ctgtttaact ttgtaagatg 300
caaagagggt ggatcaagtt taaatgactg tgctgcccct ttcacatcaa agaactactg 360
acaacgaagg ccgcgctgcc tttcccatct gtctatctat ctggctggca ggggaaggaaa 420
gaacttgcag gttggtgaag gaagaagtgg ggtggaagaa gtgggggtggg acgacagtga 480
aatctagagt aaaaccaagc tggcccaagt gtcctgcagg ctgtaatgca gtttaatcag 540
agtgccatth tttttt 556

```

<210> 220

<211> 44

<212> PRT

<213> Homo sapiens

<400> 220

```

Met Ser Asp Lys Pro Asp Met Ala Glu Ile Glu Lys Phe Asp Lys Ser
 1             5             10             15
Lys Leu Lys Lys Thr Glu Thr Gln Glu Lys Asn Pro Leu Pro Ser Lys
      20             25             30
Glu Thr Ile Glu Gln Glu Lys Gln Ala Gly Glu Ser
      35             40

```

<210> 221

<211> 4792

<212> DNA

<213> Homo sapiens

<400> 221

```

ggaccaccca gtaccgatcc cttcacgacc gtcaccatgg aagtgtcacc attgcagcct 60
gtaaataaaa atatgcaagt caacaaaata aagaaaaatg aagatgctaa gaaaagactg 120
tctgttgaaa gaattctatca aaagaaaaca caattggaac atattttgct ccgcccagac 180
acctacattg gttctgtgga attagtgacc cagcaaattgt gggtttacga tgaagatggt 240
ggcattaact atagggaagt cacttttgtt cctggtttgtt acaaaatctt tgatgagatt 300
ctagttaatg ctgcggacaa caaacaaaagg gacccaaaaa tgtcttgtat tagagtcaca 360
attgatccgg aaaacaattt aattagtata tggaataatg gaaaagggtat tctgttgtt 420
gaacacaaag ttgaaaagat gtatgtccca gctctcatat ttggacagct cctaacttct 480
agtaactatg atgatgatga aaagaaagtg acaggtggtc gaaatggcta tggagccaaa 540
ttgtgtaaca tattcagtac caaatttact gtggaaacag ccagtagaga atacaagaaa 600
atgttcaaac agacatggat ggataatatg ggaagagctg gtgagatgga actcaagccc 660
ttcaatggag aagattatac atgtatcacc tttcagcctg atttgtctaa gtttaaaatg 720
caaagcctgg acaagatat tgttgcaacta atggtcagaa gagcatatga tattgctgga 780
tccaccaaag atgtcaaagt ctttcttaat ggaaataaac tgccagtaaa aggatttcgt 840
agttatgtgg acatgtatth gaaggacaag ttggatgaaa ctggtaactc cttgaaagta 900
atacatgaac aagtaaacca caggtgggaa gtgtgtttta ctatgagtga aaaaggcttt 960
cagcaaatta gctttgtcaa cagcattgct acatccaagg gtggcagaca tgttgattat 1020
gtagctgata agattgtgac taaacttgtt gatgttgtga agaagaagaa caagggtggt 1080
gttgtagtaa aagcacatca ggtgaaaaat cacatgtgga tttttgtaaa tgccttaatt 1140
gaaaacccaa cttttgactc tcagacaaaa gaaaacatga ctttacaacc caagagcttt 1200
ggatcaacat gccaatggag tgaaaaattt atcaaagctg ccattggctg tggatttgta 1260
gaaagcatat taaactgggt gaagtttaag gcccaagtcc agttaacaa gaagtgttca 1320
gctgtaaaac ataatagaat caagggaatt cccaaactcg atgatgcaa tgatgcaggg 1380
ggccgaaact ccaactgagt tacgcttatc ctgactgagg gagattcagc caaaactttg 1440
gctgtttcag gccttggtgt ggttgggaga gacaaatatg gggttttccc tcttagagga 1500
aaaatactca atgttcgaga agcttctcat aagcagatca tggaaaatgc tgagattaac 1560
aatatcatca agattgtggg tcttcagtac aagaaaaact atgaagatga agattcattg 1620
aagacgcttc gttatgggaa gataatgatt atgacagatc aggaccaaga tggttcccac 1680
atcaaaggct tgctgattaa ttttatccat cacaactggc cctctcttct gcgacatcgt 1740
tttctggagg aatttatcac tcccattgta aaggtatcta aaaacaagca agaaatggca 1800
ttttacagcc ttctgaatt tgaagagtgg aagagttcta ctccaaatca taaaaaatgg 1860

```

```

aaagtcaaatt attacaaagg tttggggcacc agcacatcaa aggaagctaa agaatacttt 1920
gcagatatga aaagacatcg tatccagttc aaatatctctg gtcctgaaga tgatgctgct 1980
atcagcctgg ccttttagcaa aaaacagata gatgatcgaa aggaatgggtt aactaattttc 2040
atggaggata gaagacaacg aaagttactt gggcttcctg aggattactt gtatggacaa 2100
actaccacat atctgacata taatgacttc atcaacaagg aacttatctt gttctcaaatt 2160
tctgataacg agagatctat cccttctatg gtggatgggtt tgaaaccagg tcagagaaaag 2220
gttttgttta cttgcttcaa acggaatgac aagcgagaag taaagggttg ccaattagct 2280
ggatcagtggt ctgaaatgtc ttcttatcat catggtgaga tgtcactaat gatgaccatt 2340
atcaatttgg ctcagaattt tgtgggtagc aataatctaa acctcttgca gcccatgttg 2400
cagtttggtg ccaggctaca tgggtggcaag gattctgcta gtccacgata catctttaca 2460
atgctcagct ctttggctog attgttattt ccaccaaaaag atgatcacac gttgaagttt 2520
ttatatgatg acaaccagcg tgttgagcct gaatgggtaca ttcctattat tcccatgggtg 2580
ctgataaatg gtgctgaagg aatcgggtact ggggtggtcct gcaaaatccc caactttgat 2640
gtgctgtaaa ttgtaaataa catcaggcgt ttgatggatg gagaagaacc tttgccaatg 2700
cttccaagtt acaagaactt caaggggtact attgaagaac tggctccaaa tcaatatgtg 2760
attagtggtg aagtagctat tcttaattct acaaccattg aaatctcaga gcttcccgct 2820
agaacatgga cccagacata caaagaacaa gttctagaac ccatgttgaa tggcacccgag 2880
aagacacctc ctctcataac agactatagg gaataccata cagataccac tgtgaaattt 2940
gttggtgaaga tgactgaaga aaaactggca gaggcagaga gaggttggact acacaagtc 3000
ttcaaatccc aaactagctc cacatgcaac tctatggtgc tttttgacca cgtaggctgt 3060
ttaaagaaat atgacacggt gttggatatt ctaagagact tttttgaact cagacttaaa 3120
tattatggat taagaaaaga atggctccta ggaatgcttg gtgctgaatc tgctaaactg 3180
aataatcagg ctcgctttat cttagagaaa atagatggca aaataatcat tgaaaataag 3240
cctaagaaag aattaattaa agttctgatt cagaggggat atgattcgga tcctgtgaag 3300
gcctggaaaag aagcccagca aaaggttcca gatgaagaag aaaatgaaga gagtgaacaac 3360
gaaaaggaaa ctgaaaagag tgactccgta acagattctg gaccaacctt caactatctt 3420
cttgatatgc cccttttggt ttttaaccaag gaaaagaaaag atgaactctg caggctaaga 3480
aatgaaaaag aacaagagct ggacacatta aaaagaaaaga gtccatcaga tttgtggaaa 3540
gaagacttgg ctacatttat tgaagaattg gaggctgttg aagccaagga aaacaagat 3600
gaacaagtgc gacttctctg gaaagggggg aaggccaagg ggaaaaaaac acaaatggct 3660
gaagttttgc cttctccgct tgggtcaaaga gtcattccac gaataaccat agaaatgaaa 3720
gcagaggcag aaaagaaaaa taaaaagaaa attagaatg aaaatactga aggaagccct 3780
caagaagatg gtgtggaact agaaggcta aaacaaagat tagaaaagaa acagaaaaga 3840
gaaccaggta caaagacaaa gaaacaaact acattggcat ttaagccaat caaaaaagga 3900
aagaagagaa atccctggcc tgattcagaa tcagatagga gcagtgcga aagtaatttt 3960
gatgtccctc cagcagaaac agagccacgg agagcagcaa caaaaacaaa attcacaatg 4020
gatttggatt cagatgaaga tttctcagat tttgatgaaa aaactgatga tgaagatttt 4080
gtcccatcag atgctagtcc acctaaagacc aaaacttccc caaaacttag taacaaagaa 4140
ctgaaaccac agaaaagtgt cgtgtcagac cttgaagctg atgatgttaa gggcagtgta 4200
ccactgtctt caagccctcc tgctacacat ttcccagatg aaactgaaat tacaaacca 4260
gttcctaaaa agaattgtgac agtgaagaag acagcagcaa aaagtcagtc ttccacctcc 4320
actaccggtg ccaaaaaaag ggctgcccc aabggaacta aaagggatcc agctttgaat 4380
tctggtgtct ctcaaaagcc tgatcctgcc aaaaccaaga atcgccgcaa aaggaagcca 4440
tccacttctg atgattctga ctctaatttt gagaaaattg tttcgaaagc agtcacaagc 4500
aagaaatcca agggggagag tgatgacttc catatggact ttgactcagc tgtggctcct 4560
cgggcaaaat ctgtacgggc aaagaaacct ataaagtacc tggaagagtc agatgaagat 4620
gatctgtttt aaaatgtgag gcgattattt taagtaatta tcttaccaag cccaagactg 4680
gttttaaaagt tacctgaagc tcttaacttc ctcccctctg aatttagttt ggggaaggtg 4740
tttttagtac aagacatcaa agtgaagtaa agcccaagtg ttctttagct tt 4792

```

<210> 222

<211> 1531

<212> PRT

<213> Homo sapiens

<400> 222

Met Glu Val Ser Pro Leu Gln Pro Val Asn Glu Asn Met Gln Val Asn

1

5

10

15

Lys Ile Lys Lys Asn Glu Asp Ala Lys Lys Arg Leu Ser Val Glu Arg

Ser	His	Lys	Gln	Ile	Met	Glu	Asn	Ala	Glu	Ile	Asn	Asn	Ile	Ile	Lys	500	505	510
Ile	Val	Gly	Leu	Gln	Tyr	Lys	Lys	Asn	Tyr	Glu	Asp	Glu	Asp	Ser	Leu	515	520	525
Lys	Thr	Leu	Arg	Tyr	Gly	Lys	Ile	Met	Ile	Met	Thr	Asp	Gln	Asp	Gln	530	535	540
Asp	Gly	Ser	His	Ile	Lys	Gly	Leu	Leu	Ile	Asn	Phe	Ile	His	His	Asn	545	550	555
Trp	Pro	Ser	Leu	Leu	Arg	His	Arg	Phe	Leu	Glu	Glu	Phe	Ile	Thr	Pro	565	570	575
Ile	Val	Lys	Val	Ser	Lys	Asn	Lys	Gln	Glu	Met	Ala	Phe	Tyr	Ser	Leu	580	585	590
Pro	Glu	Phe	Glu	Glu	Trp	Lys	Ser	Ser	Thr	Pro	Asn	His	Lys	Lys	Trp	595	600	605
Lys	Val	Lys	Tyr	Tyr	Lys	Gly	Leu	Gly	Thr	Ser	Thr	Ser	Lys	Glu	Ala	610	615	620
Lys	Glu	Tyr	Phe	Ala	Asp	Met	Lys	Arg	His	Arg	Ile	Gln	Phe	Lys	Tyr	625	630	635
Ser	Gly	Pro	Glu	Asp	Ala	Ala	Ile	Ser	Leu	Ala	Phe	Ser	Lys	Lys		645	650	655
Gln	Ile	Asp	Asp	Arg	Lys	Glu	Trp	Leu	Thr	Asn	Phe	Met	Glu	Asp	Arg	660	665	670
Arg	Gln	Arg	Lys	Leu	Leu	Gly	Leu	Pro	Glu	Asp	Tyr	Leu	Tyr	Gly	Gln	675	680	685
Thr	Thr	Thr	Tyr	Leu	Thr	Tyr	Asn	Asp	Phe	Ile	Asn	Lys	Glu	Leu	Ile	690	695	700
Leu	Phe	Ser	Asn	Ser	Asp	Asn	Glu	Arg	Ser	Ile	Pro	Ser	Met	Val	Asp	705	710	715
Gly	Leu	Lys	Pro	Gly	Gln	Arg	Lys	Val	Leu	Phe	Thr	Cys	Phe	Lys	Arg	725	730	735
Asn	Asp	Lys	Arg	Glu	Val	Lys	Val	Ala	Gln	Leu	Ala	Gly	Ser	Val	Ala	740	745	750
Glu	Met	Ser	Ser	Tyr	His	His	Gly	Glu	Met	Ser	Leu	Met	Met	Thr	Ile	755	760	765
Ile	Asn	Leu	Ala	Gln	Asn	Phe	Val	Gly	Ser	Asn	Asn	Leu	Asn	Leu	Leu	770	775	780
Gln	Pro	Ile	Gly	Gln	Phe	Gly	Thr	Arg	Leu	His	Gly	Gly	Lys	Asp	Ser	785	790	795
Ala	Ser	Pro	Arg	Tyr	Ile	Phe	Thr	Met	Leu	Ser	Ser	Leu	Ala	Arg	Leu	805	810	815
Leu	Phe	Pro	Pro	Lys	Asp	Asp	His	Thr	Leu	Lys	Phe	Leu	Tyr	Asp	Asp	820	825	830
Asn	Gln	Arg	Val	Glu	Pro	Glu	Trp	Tyr	Ile	Pro	Ile	Ile	Pro	Met	Val	835	840	845
Leu	Ile	Asn	Gly	Ala	Glu	Gly	Ile	Gly	Thr	Gly	Trp	Ser	Cys	Lys	Ile	850	855	860
Pro	Asn	Phe	Asp	Val	Arg	Glu	Ile	Val	Asn	Asn	Ile	Arg	Arg	Leu	Met	865	870	875
Asp	Gly	Glu	Glu	Pro	Leu	Pro	Met	Leu	Pro	Ser	Tyr	Lys	Asn	Phe	Lys	885	890	895
Gly	Thr	Ile	Glu	Glu	Leu	Ala	Pro	Asn	Gln	Tyr	Val	Ile	Ser	Gly	Glu	900	905	910
Val	Ala	Ile	Leu	Asn	Ser	Thr	Thr	Ile	Glu	Ile	Ser	Glu	Leu	Pro	Val	915	920	925
Arg	Thr	Trp	Thr	Gln	Thr	Tyr	Lys	Glu	Gln	Val	Leu	Glu	Pro	Met	Leu	930	935	940
Asn	Gly	Thr	Glu	Lys	Thr	Pro	Pro	Leu	Ile	Thr	Asp	Tyr	Arg	Glu	Tyr	945	950	955
His	Thr	Asp	Thr	Thr	Val	Lys	Phe	Val	Val	Lys	Met	Thr	Glu	Glu	Lys			

				965					970				975		
Leu	Ala	Glu	Ala	Glu	Arg	Val	Gly	Leu	His	Lys	Val	Phe	Lys	Leu	Gln
			980					985					990		
Thr	Ser	Leu	Thr	Cys	Asn	Ser	Met	Val	Leu	Phe	Asp	His	Val	Gly	Cys
		995					1000					1005			
Leu	Lys	Lys	Tyr	Asp	Thr	Val	Leu	Asp	Ile	Leu	Arg	Asp	Phe	Phe	Glu
	1010					1015					1020				
Leu	Arg	Leu	Lys	Tyr	Tyr	Gly	Leu	Arg	Lys	Glu	Trp	Leu	Leu	Gly	Met
1025					1030					1035				1040	
Leu	Gly	Ala	Glu	Ser	Ala	Lys	Leu	Asn	Asn	Gln	Ala	Arg	Phe	Ile	Leu
				1045					1050					1055	
Glu	Lys	Ile	Asp	Gly	Lys	Ile	Ile	Ile	Glu	Asn	Lys	Pro	Lys	Lys	Glu
		1060						1065					1070		
Leu	Ile	Lys	Val	Leu	Ile	Gln	Arg	Gly	Tyr	Asp	Ser	Asp	Pro	Val	Lys
	1075						1080					1085			
Ala	Trp	Lys	Glu	Ala	Gln	Gln	Lys	Val	Pro	Asp	Glu	Glu	Glu	Asn	Glu
	1090					1095					1100				
Glu	Ser	Asp	Asn	Glu	Lys	Glu	Thr	Glu	Lys	Ser	Asp	Ser	Val	Thr	Asp
1105					1110						1115				1120
Ser	Gly	Pro	Thr	Phe	Asn	Tyr	Leu	Leu	Asp	Met	Pro	Leu	Trp	Tyr	Leu
				1125					1130					1135	
Thr	Lys	Glu	Lys	Lys	Asp	Glu	Leu	Cys	Arg	Leu	Arg	Asn	Glu	Lys	Glu
			1140					1145					1150		
Gln	Glu	Leu	Asp	Thr	Leu	Lys	Arg	Lys	Ser	Pro	Ser	Asp	Leu	Trp	Lys
	1155						1160					1165			
Glu	Asp	Leu	Ala	Thr	Phe	Ile	Glu	Glu	Leu	Glu	Ala	Val	Glu	Ala	Lys
	1170					1175					1180				
Glu	Lys	Gln	Asp	Glu	Gln	Val	Gly	Leu	Pro	Gly	Lys	Gly	Gly	Lys	Ala
1185					1190					1195					1200
Lys	Gly	Lys	Lys	Thr	Gln	Met	Ala	Glu	Val	Leu	Pro	Ser	Pro	Arg	Gly
				1205					1210					1215	
Gln	Arg	Val	Ile	Pro	Arg	Ile	Thr	Ile	Glu	Met	Lys	Ala	Glu	Ala	Glu
		1220						1225					1230		
Lys	Lys	Asn	Lys	Lys	Lys	Ile	Lys	Asn	Glu	Asn	Thr	Glu	Gly	Ser	Pro
	1235						1240					1245			
Gln	Glu	Asp	Gly	Val	Glu	Leu	Glu	Gly	Leu	Lys	Gln	Arg	Leu	Glu	Lys
	1250					1255					1260				
Lys	Gln	Lys	Arg	Glu	Pro	Gly	Thr	Lys	Thr	Lys	Lys	Gln	Thr	Thr	Leu
1265					1270					1275					1280
Ala	Phe	Lys	Pro	Ile	Lys	Lys	Gly	Lys	Lys	Arg	Asn	Pro	Trp	Pro	Asp
				1285					1290					1295	
Ser	Glu	Ser	Asp	Arg	Ser	Ser	Asp	Glu	Ser	Asn	Phe	Asp	Val	Pro	Pro
		1300						1305					1310		
Arg	Glu	Thr	Glu	Pro	Arg	Arg	Ala	Ala	Thr	Lys	Thr	Lys	Phe	Thr	Met
	1315						1320					1325			
Asp	Leu	Asp	Ser	Asp	Glu	Asp	Phe	Ser	Asp	Phe	Asp	Glu	Lys	Thr	Asp
	1330					1335					1340				
Asp	Glu	Asp	Phe	Val	Pro	Ser	Asp	Ala	Ser	Pro	Pro	Lys	Thr	Lys	Thr
1345					1350					1355				1360	
Ser	Pro	Lys	Leu	Ser	Asn	Lys	Glu	Leu	Lys	Pro	Gln	Lys	Ser	Val	Val
			1365						1370					1375	
Ser	Asp	Leu	Glu	Ala	Asp	Asp	Val	Lys	Gly	Ser	Val	Pro	Leu	Ser	Ser
		1380						1385					1390		
Ser	Pro	Pro	Ala	Thr	His	Phe	Pro	Asp	Glu	Thr	Glu	Ile	Thr	Asn	Pro
	1395						1400					1405			
Val	Pro	Lys	Lys	Asn	Val	Thr	Val	Lys	Lys	Thr	Ala	Ala	Lys	Ser	Gln
	1410					1415					1420				
Ser	Ser	Thr	Ser	Thr	Thr	Gly	Ala	Lys	Lys	Arg	Ala	Ala	Pro	Lys	Gly
1425					1430					1435					1440

```

Thr Lys Arg Asp Pro Ala Leu Asn Ser Gly Val Ser Gln Lys Pro Asp
      1445                      1450                      1455
Pro Ala Lys Thr Lys Asn Arg Arg Lys Arg Lys Pro Ser Thr Ser Asp
      1460                      1465                      1470
Asp Ser Asp Ser Asn Phe Glu Lys Ile Val Ser Lys Ala Val Thr Ser
      1475                      1480                      1485
Lys Lys Ser Lys Gly Glu Ser Asp Asp Phe His Met Asp Phe Asp Ser
      1490                      1495                      1500
Ala Val Ala Pro Arg Ala Lys Ser Val Arg Ala Lys Lys Pro Ile Lys
1505                      1510                      1515                      1520
Tyr Leu Glu Glu Ser Asp Glu Asp Asp Leu Phe
      1525                      1530

```

```

<210> 223
<211> 1111
<212> DNA
<213> Homo sapiens

```

```

<400> 223
ccgcgcgcgtc gccccgcgcgc tcctgctgca gccccaggcc cctcgccgcgc gccaccatgg 60
acgccatcaa gaagaagatg cagatgotga agctcgacaa ggagaacgcc ttggatcgag 120
ctgagcaggc ggaggccgac aagaaggcgg cggaagacag gagcaagcag ctggaagatg 180
agctggtgtc actgcaaaag aaactcaagg gcaccgaaga tgaactggac aaatactctg 240
aggctctcaa agatgcccgag gagaagctgg agctggcaga gaaaaaggcc accgatgctg 300
aagccgacgt agcttctctg aacagacgca tccagctggt tgaggaagag ttggatcgtg 360
cccaggagcg tctggcaaca gctttgcaga agctggagga agctgagaag gcagcagatg 420
agagtgagag aggcattgaaa gtcattgaga gtcagagccca aaaagatgaa gaaaaaatgg 480
aaattcagga gatccaactg aaagaggcca agcacattgc tgaagatgcc gaccgcaaat 540
acgaagaggt ggcccgtaaag ctggtcatca ttgagagcga cctggaacgt gcagaggagc 600
gggctgagct ctcaagaaggc aaatgtgccc agcttgaaga agaattgaaa actgtgacga 660
acaacttgaa gtcactggag gctcaggctg agaagtactc gcagaaggaa gacagatatg 720
aggaagagat caaggtcctt tccgacaagc tgaaggaggc tgagactcgg gctgagtttg 780
cggagaggctc agtaactaaa ttggagaaaa gcattgatga cttagaagac gagctgtacg 840
ctcagaaaact gaagtacaaa gccatcagcg aggagctgga ccacgctctc aacgatatga 900
cttccatata agtttctttg cttcacttct cccaagactc cctcgctcgag ctggatgtcc 960
cacctctctg agctctgcat ttgtctattc tccagctgac cctggttctc tctcttagca 1020
tctgcctta gagccaggca cacactgtgc tttctattgt acagaagctc ttcgtttcag 1080
tgtcaataaa acactgtgta agctaaaaaa a 1111

```

```

<210> 224
<211> 284
<212> PRT
<213> Homo sapiens

```

```

<400> 224
Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu
 1           5           10          15
Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala
      20           25           30
Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys
      35           40           45
Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu
      50           55           60
Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp
      65           70           75           80
Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
      85           90           95
Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys

```

<400> 225						
gaattcgctt	tggatccatt	tccatcggtc	cttacagccg	ctcgtcagac	tccagcagcc	60
aagatggtga	agcagatcga	gagcaagact	gcttttcagg	aagccttgga	cgctgcaggt	120
gataaaacttg	tagtagttga	cttctcagcc	acgtggtgtg	ggccttgcaa	aatgatcaac	180
cctttctttc	attccctctc	tgaaaagtat	tccaacgtga	tattccttga	agtagatgtg	240
gatgactgtc	aggatgttgc	ttcagagtgt	gaagtcaaat	gcacgccaac	attccagttt	300
tttaagaagg	gacaaaaggt	gggtgaattt	tctggagcca	ataaggaaaa	gcttgaagcc	360
accattaatg	aattagtcta	atcatgtttt	ctgaaaacat	aaccagccat	tggctattta	420
aacttgtatt	tttttattta	caaaaataaa	atatgaagac	ataaccagtt	gccatctgcg	480
tgacaataaa	cattatgcta	a				501

<400> 226															
Met	Val	Lys	Gln	Ile	Glu	Ser	Lys	Thr	Ala	Phe	Gln	Glu	Ala	Leu	Asp
1				5					10					15	
Ala	Ala	Gly	Asp	Lys	Leu	Val	Val	Val	Asp	Phe	Ser	Ala	Thr	Trp	Cys
			20					25					30		
Gly	Pro	Cys	Lys	Met	Ile	Asn	Pro	Phe	Phe	His	Ser	Leu	Ser	Glu	Lys
		35					40					45			
Tyr	Ser	Asn	Val	Ile	Phe	Leu	Glu	Val	Asp	Val	Asp	Asp	Cys	Gln	Asp
	50					55					60				
Val	Ala	Ser	Glu	Cys	Glu	Val	Lys	Cys	Thr	Pro	Thr	Phe	Gln	Phe	Phe
65					70					75				80	
Lys	Lys	Gly	Gln	Lys	Val	Gly	Glu	Phe	Ser	Gly	Ala	Asn	Lys	Glu	Lys
				85					90					95	

Leu Glu Ala Thr Ile Asn Glu Leu Val
100 105

<210> 227
<211> 783
<212> DNA
<213> Homo sapiens

<400> 227
ggcagcagcg agttcctgtc tctctgccaa cgccgcccgg atggccttccc aaaaccgcga 60
cccagccgcc actagcgtcg ccgcccggcg taaaggagct gagccgagcg ggggcgcccgc 120
ccgggggtccg gtggggcaaaa ggctacagca ggagctgatg accctcatga tgtctggcga 180
taaagggatt tctgccttcc ctgaatcaga caaccttttc aaatgggtag ggaccatcca 240
tggagcagct ggaacagtat atgaagacct gaggtataag ctctcgctag agttccccag 300
tggctaccct tacaatgcgc ccacagtga gttcctcacg ccctgctatc accccaacgt 360
ggacaccagc ggtaacatat gcctggacat cctgaaggaa aagtgggtctg ccctgtatga 420
tgtcaggacc attctgtctc ccatccagag ccttctagga gaaccaaca ttgatagtcc 480
cttgaacaca catgctgccg agctctggaa aaacccaca gcttttaaga agtacctgca 540
agaaacctac tcaaagcagg tcaccagcca ggagccctga ccaggctgc ccagcctgtc 600
cttgtgtcgt ctttttaatt tttccttaga tgggtctgtcc tttttgtgat ttctgtatag 660
gactctttat cttgagctgt ggtatttttg ttttgttttt gtctttttaa ttaagcctcg 720
gttgagccct tgtatattaa ataaatgcat ttttgcctt ttttaaaaaa aaaaaaaaaa 780
aaa 783

<210> 228
<211> 179
<212> PRT
<213> Homo sapiens

<400> 228
Met Ala Ser Gln Asn Arg Asp Pro Ala Ala Thr Ser Val Ala Ala Ala
1 5 10 15
Arg Lys Gly Ala Glu Pro Ser Gly Gly Ala Ala Arg Gly Pro Val Gly
20 25 30
Lys Arg Leu Gln Gln Glu Leu Met Thr Leu Met Met Ser Gly Asp Lys
35 40 45
Gly Ile Ser Ala Phe Pro Glu Ser Asp Asn Leu Phe Lys Trp Val Gly
50 55 60
Thr Ile His Gly Ala Ala Gly Thr Val Tyr Glu Asp Leu Arg Tyr Lys
65 70 75 80
Leu Ser Leu Glu Phe Pro Ser Gly Tyr Pro Tyr Asn Ala Pro Thr Val
85 90 95
Lys Phe Leu Thr Pro Cys Tyr His Pro Asn Val Asp Thr Gln Gly Asn
100 105 110
Ile Cys Leu Asp Ile Leu Lys Glu Lys Trp Ser Ala Leu Tyr Asp Val
115 120 125
Arg Thr Ile Leu Leu Ser Ile Gln Ser Leu Leu Gly Glu Pro Asn Ile
130 135 140
Asp Ser Pro Leu Asn Thr His Ala Ala Glu Leu Trp Lys Asn Pro Thr
145 150 155 160
Ala Phe Lys Lys Tyr Leu Gln Glu Thr Tyr Ser Lys Gln Val Thr Ser
165 170 175
Gln Glu Pro

<210> 229
<211> 777

<212> DNA

<213> Homo sapiens

<400> 229

```

ggcccccttgt ctgcagagat ggctcccaat gcttcctgcc tctgtgtgca tgtccgttcc 60
gaggaatggg atttaatgac ctttgatgcc aaccatgatg acagcgtgaa aaaaatcaaa 120
gaacatgtcc ggtctaagac caagggttcct gtgcaggacc aggttcctttt gctgggctcc 180
aagatcttaa agccacggag aagcctctca tcttatggca ttgacaaaga gaagaccatc 240
caccttacct tgaaagtggg gaagcccagt gatgaggagc tgcccttggt tcttgtggag 300
tcaggtgatg aggcaaagag gcacctcctc caggtgcgaa ggtccagctc agtggcacia 360
gtgaaagcaa tgatcgagac taagacgggt ataatccctg agaccagat tgtgacttgc 420
aatggaaaga gactggaaga tgggaagatg atggcagatt acggcatcag aaagggcaac 480
ttactcttcc tggcatctta ttgtattgga gggtagaccac cctgggggatg ggggtgttggc 540
aggggtcaaa aagcttatatt cttttaatct cttactcaac gaacacatct tctgatgatt 600
tcccaaaatt aatgagaatg agatgagtag agtaagattt gggtagggatg ggtaggatga 660
agtatatgtc ccaactctat gtttctttga ttctaacaca attaattaag tgacatgatt 720
tttactaatg tattactgag actagtaaataa aaatttttaa ggcaaaatag agcatc 777

```

<210> 230

<211> 165

<212> PRT

<213> Homo sapiens

<400> 230

```

Met Ala Pro Asn Ala Ser Cys Leu Cys Val His Val Arg Ser Glu Glu
1          5          10          15
Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys
20          25          30
Ile Lys Glu His Val Arg Ser Lys Thr Lys Val Pro Val Gln Asp Gln
35          40          45
Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser
50          55          60
Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His Leu Thr Leu Lys Val
65          70          75          80
Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Gly
85          90          95
Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg Arg Ser Ser Ser Val
100         105         110
Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu
115         120         125
Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu Glu Asp Gly Lys Met
130         135         140
Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu Leu Phe Leu Ala Ser
145         150         155         160
Tyr Cys Ile Gly Gly
165

```

<210> 231

<211> 4797

<212> DNA

<213> Homo sapiens

<400> 231

```

gcagtgaaca caacctttcc cctgagccac tggaattgga cagaatgccc cattctcctc 60
tgatctccat tctcatgtg tgggtgtcacc cagaagagga ggaaagaatg catgatgaac 120
ttctacaagc agtatccaag gggccggtga tgttcaggga tgtttccata gacttctctc 180
aagaggaatg ggaatgcctg gacgctgatc agatgaattt atacaaagaa gtgatgttgg 240
agaatttcag caacctgggt tcagtgggac tttccaattc taagccagct gtgatctcct 300

```

tattggaaca	aggaaaagag	ccctggatgg	ttgatagaga	gctgactaga	ggcctgtgtt	360
cagatctgga	atcaatgtgt	gagacccaaa	tattatctct	aaagaagaga	catttcagtc	420
aagtaataat	taccctgtgaa	gacatgtcta	cttttattca	gcccacattt	cttattccac	480
ctcaaaaaac	tatgagtga	gagaaacat	gggaatgtaa	gatatgtgga	aagaccttta	540
atcaaaactc	acaatttatc	caacatcaga	gaattcattt	tgggtgaaaa	cactatgaat	600
ctaaggagta	tgggaagtcc	tttagtcgtg	gctcactcgt	tactcgacat	cagaggatc	660
acactggtaa	aaaaccctat	gaatgtaagg	aatgtggcaa	ggcttttagt	tgtagtcat	720
atttttctca	acatcagagg	attcacactg	gtgagaaaac	ctatgaatgt	aaggaatgtg	780
gaaaagcctt	taagtattgc	tcaaaccctta	atgatcatca	gagaattcac	actggtgaga	840
aaccctatga	atgtaaagta	tgtggaaaag	cctttactaa	aagttcacaa	ctttttctac	900
atctgagaat	tcatactggg	gagaaacctt	atgaatgtaa	agaatgtggg	aaagccttta	960
ctcaacactc	aaggcttatt	cagcatcaga	gaatgcatac	tgggtgagaaa	ccttatgaat	1020
gtaagcagtg	tgggaaggcc	tttaatagtg	cctcaacact	tactaacat	cacagaattc	1080
atgctggtga	gaagctctat	gaatgtgaag	aatgtagaaa	ggcctttatt	cagagctcag	1140
aacttattca	acatcagaga	atccatacag	atgaaaaacc	atatgaatgt	aatgaatgtg	1200
ggaaggcctt	taataaaggc	tcaaactctta	ctcgacatca	gagaattcac	actggtgaga	1260
aaccctatga	ctgtaaggaa	tgtggaaaag	cttttggtag	tgcctctgac	ctcattcgcc	1320
ataggggaat	tcatactggg	tgaatgacag	taaagtaaga	ccattttgtt	aacctttata	1380
ataatttttt	taaaacagggt	aaggagaaca	aattaggata	catattatca	aaggttctcc	1440
tatgtattcg	tttttaaacg	atacgataac	aaagtaccaa	gtaccaaaac	cttggtggct	1500
taaaacaaga	gaaattttatt	ctctcatagt	ttagagcctg	gaaatctaaa	ctcaagggtg	1560
ctgatcgttt	tgggttccttc	tgaggactct	gaggatctgt	tctatgcctt	tttcctaacc	1620
tctgttaaca	gctggcagtc	cttggcattc	catggctttt	acatacacca	ttccaatctc	1680
tgccctccatc	ttcacattgc	attctcgtctg	tgtatctctg	tgtatgtcct	ttatttggac	1740
accagtcagg	ttagattggg	gctacctggg	gacctcatct	taacttgatt	atatctgcca	1800
agaccctggt	tccaagtaag	gtcacattta	ccggtaccag	gggttaggac	ttcagcatat	1860
cttttttaggg	gatacagttc	aacccataat	accctgtttag	aatgattttg	tctaataatat	1920
ttgtaatctc	cttttatata	taagttgtta	gtcaaattta	ttttatttta	ttttattttg	1980
agacagagtc	tgcctctggt	gcccaggctg	gagtgacgtg	gtgtgatctc	agctcactgc	2040
aacctccagc	tcctgagttc	aagcgattct	tgtgcctcag	cctctcaagt	agttgggatt	2100
acaygcattc	gccaccatgc	ccggctaatt	tttttttttt	tttttttgta	tttttagtag	2160
cgacgggggt	tcaccatggt	ggccaggctg	gtcttgaact	cctgacttca	agtgatctgc	2220
ccgcctcagc	ctcccaaagt	gctgggatta	cagacgtgag	ccaccgtgat	ggccaaaaca	2280
gactttatac	caacaaaaat	taaaaaggac	aaagaaggtc	atttataatg	ataaaggata	2340
aattcaacaa	gaagataaaa	caatcctaaa	tatgtatgca	cccaacactg	caacaccag	2400
atccataaca	cagatactac	tagacctaag	aaaagagata	gacagcaata	caacaatagc	2460
aggggacttc	accactccat	tgacagcact	agacagatca	ctgggacaga	aatcaacaaa	2520
gaaactctgg	acttaaatgt	gactctacac	caaatggacc	caacagacat	ctgaagaaca	2580
ttctacccaa	caaccacaga	atatatactc	ttctcttctg	tgcattggaac	attctcaaaa	2640
ataggtcata	tactggacca	caaagcaagt	atcaataaat	tttaaaaaaa	caaaatcata	2700
tctaacatct	tctctgacca	tagtggaata	aaactagata	tcaataccaa	gaggaactct	2760
caaaacagat	acatggaatt	taaacagctt	gctcctgaat	gattttttgga	tcaatgatga	2820
aactaagggt	gaaattttaa	attttttgaa	ataaatgaaa	atagagacaa	aacacatgaa	2880
aacatctgag	atacagcaaa	agcagtgtct	agagaggatt	ttatagcatt	aaatgcctac	2940
acaaaaaaga	tagaaaaatc	tcaaataaat	agcctaacgt	cacatctcaa	ggaactagga	3000
aaaaacaaaa	caaactcaac	ccaaagctgg	cagaagaaaa	gcaataacaa	atatcagagc	3060
aggcaaaaat	gagactgaga	acaaagggaat	gcaaaaagatc	aataaaaagaa	aaagttgggt	3120
ctttgtaaag	ataaaaactga	cagaccacta	gctagattaa	ccaagaaaaa	aagaagattc	3180
aaataaatac	aatcagaaat	gataagggtga	tattataact	gataacacag	acataataaa	3240
tatcagcaga	aactatatgc	acatattaga	aaacctagag	gaagtggata	aattcctaga	3300
aacacataac	cttccaagat	tgaaccaggg	agaaatagga	atcctcaaca	gactactgag	3360
tattgaaatt	gaatcagtaa	tagaaaaaaa	tcttgcaaaa	acaaaaagcc	caggaccaga	3420
cagattcaca	gctgaattct	actagacatg	caaggaagaa	ctagtaacag	cactattgaa	3480
actattccaa	aaattatagg	agggaatcct	ccctaactca	ttctacaaag	ccagtatcat	3540
cctgatactg	aagccaggca	aggataaaaac	acacaaaaaa	actacaagcc	aatatccctg	3600
atgaaaatag	acacaaaaat	cttcagcaaaa	atactagcaa	accaaataca	acagtacata	3660
aaaaagatag	taacagcaca	gtcaagtgga	ttttattcct	ggggtgtaag	gatggctcaa	3720
catatgcaac	tcaatacatg	attcatcaca	tacacagaat	taaaaaataag	ccaggcactc	3780
acacctgtaa	tcccagcact	ttgcaaggcc	aaggcgggca	gatcacatga	tgtcaagagt	3840


```

ttgagaccag tctggctgac atggcgaaac cctgtctcta ctaaaaatag aaaaattggc 3900
tgggcatggt ggcaggcact gtagtcccag ctacttggga ggctgaggca ggagaattac 3960
ttgaacctga gaagcggagg ttgcagttag ctgagatagt gccattgcac tccagcctgg 4020
gcaacagagc aaattgcttg aatgtgggag gtggagggtg cagttagccg agattatgcc 4080
attgcactcc agccggggga gcaacaaagc cagactccat ctcaaaaaaa aaccaaaaaa 4140
aatcctatth agtacaaggt acattattta ggtaatgagt ccattaaaag ccaacactth 4200
ccccactaca ctatatgtgt atgtaacaca actgcccttg taacttccta aacctataat 4260
taagaaacaa taaaaggcaa attaagaatg cttttttaaa aggtggggggc attatgctaa 4320
taagttactg tggatttcag agtgcagagt agaaagatca caagaattta gtgtggtagg 4380
tgggaacaga aaatgggtgt ataaatttta ttgacgtggg agtactggat attgtagaga 4440
cagatatcat cagggcaagg agattaaaga tttttgcatt gacggtttga cactatattg 4500
tggtaataac actgtatgtg ttgggagata gaacaggaaa catcttccct ggaatatgta 4560
tactatataa tgttttatca aacttttgat caaacagac agcacaattt ataatttcat 4620
ttctatttct atgttatgag aaactgatca tttattcaaa tgtttaacag gcatgttcat 4680
gttactataa actcttctgt ttctccatca cgttggttgg catctttact gattacaaat 4740
ttctttacat atttaagaaa tatatatatt tctttatata ttaaaaaaaa aaaaaaa 4797

```

<210> 232

<211> 433

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 433

<223> Xaa = Any Amino Acid

<400> 232

```

Met Pro His Ser Pro Leu Ile Ser Ile Pro His Val Trp Cys His Pro
 1          5          10          15
Glu Glu Glu Glu Arg Met His Asp Glu Leu Leu Gln Ala Val Ser Lys
 20          25          30
Gly Pro Val Met Phe Arg Asp Val Ser Ile Asp Phe Ser Gln Glu Glu
 35          40          45
Trp Glu Cys Leu Asp Ala Asp Gln Met Asn Leu Tyr Lys Glu Val Met
 50          55          60
Leu Glu Asn Phe Ser Asn Leu Val Ser Val Gly Leu Ser Asn Ser Lys
 65          70          75          80
Pro Ala Val Ile Ser Leu Leu Glu Gln Gly Lys Glu Pro Trp Met Val
 85          90          95
Asp Arg Glu Leu Thr Arg Gly Leu Cys Ser Asp Leu Glu Ser Met Cys
100          105          110
Glu Thr Lys Ile Leu Ser Leu Lys Lys Arg His Phe Ser Gln Val Ile
115          120          125
Ile Thr Arg Glu Asp Met Ser Thr Phe Ile Gln Pro Thr Phe Leu Ile
130          135          140
Pro Pro Gln Lys Thr Met Ser Glu Glu Lys Pro Trp Glu Cys Lys Ile
145          150          155          160
Cys Gly Lys Thr Phe Asn Gln Asn Ser Gln Phe Ile Gln His Gln Arg
165          170          175
Ile His Phe Gly Glu Lys His Tyr Glu Ser Lys Glu Tyr Gly Lys Ser
180          185          190
Phe Ser Arg Gly Ser Leu Val Thr Arg His Gln Arg Ile His Thr Gly
195          200          205
Lys Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ser Cys Ser
210          215          220
Ser Tyr Phe Ser Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr
225          230          235          240
Glu Cys Lys Glu Cys Gly Lys Ala Phe Lys Tyr Cys Ser Asn Leu Asn

```

```
<210> 233
<211> 1860
<212> DNA
<213> Homo sapiens
```

<400>	233					
tgcacccacg	cgtccggggcc	cgcgctgacg	gtgtccctgg	ggctctgcgc	tcgtccggcc	60
ggccccggcc	tcgccgcccc	gcgcagtacc	cagcccggcc	ccgccgaccc	gcctctactg	120
ccggctccgc	gcccttcccc	gagggctgga	tgatgggctg	tttcgccctg	caaacggtgg	180
acaccgagct	gaccgcggac	tcggtggagt	ggtgcccgct	gcaaggctgc	aggcacctgc	240
tggcgtgcgg	gacctaccag	ctgcggcggc	cggaggaccg	gcctgccggc	ccccagaaca	300
aggttggaat	ggaagttaag	gagcctcagg	tccgtttagg	ccgtctcttc	ctgtacagtt	360
tcaatgacaa	caactctatt	caccctctgg	tcgaggtcca	aagaaaagat	acttctgcaa	420
tcctggacat	gaaatggtgt	cacatccogg	tggctggaca	tgccctcttg	ggcttggcag	480
atgccagtgg	atccatacaa	ctgctccgcc	tggtggaatc	tgagaagagc	cacgtgctgg	540
agccattgtc	cagccttgcc	ctggaggagc	agtgtctggc	tttgtcccta	gatttgtcca	600
ctgggaaaac	tggaagggcc	ggggaccagc	ccttgaagat	catcagcagt	gactccacag	660
ggcagctcca	cctcctgatg	gtgaatgaga	cgaggcccag	gctgcagaaa	gtggcctcat	720
ggcaggcaca	tcaattcgag	gcctggattg	ctgotttcaa	ttactggcat	ccagaaattg	780
tgtattcaga	ggcgcacgat	ggccttctga	ggggtctggga	caccagggta	cccgggcaat	840
ttctcttcac	cagcaaaaaga	cacaccattg	gtgtgtgcag	catccagagc	agccctcatc	900
ggagcacat	cctggccacg	ggaagctatg	atgaacacat	cctactgtgg	gacacacgaa	960
acatgaagca	gccgttggca	gatacgcttg	tgcagggtgg	ggtatggaga	atcaagtggc	1020
accctttcca	ccaccacctg	ctcctggccg	cctgcatgca	cagtggcttt	aagatcctca	1080
actgccaaaa	ggcaatggag	gagaggcagg	aggcgacggt	cctgacatct	cacacattgc	1140
ccgactcgct	ggtgtatgga	gccgactggt	cctggctgct	cttcggttct	ctgcagcggg	1200
ccccctcgtg	gtccttttct	agcaacctag	gaaccaagac	ggcagacctg	aagggtgcaa	1260
gcgagttgcc	aacacctgtg	catgaatgca	gagaggataa	cgatggggag	ggccatgcca	1320
gacccacagc	tggaatgaag	ccactcacag	agggcattag	gaagaatggc	acctggtctc	1380
aggctacagc	agccaccaca	cgtgactgtg	gcgtgaacct	agaagaagca	gactcagcct	1440
tcagcctcct	ggccacctgc	tccttctatg	accatgcgct	ccacctctgg	gagtggggagg	1500
ggaactgagc	ttgaaatcat	gaagcccctt	cccacaagga	aaccaggagg	gagactgcga	1560

```

gtgagtgccccc gggaccacct catcagagat gcttactgca gccctgcagg tgcctgggca 1620
ctgatgggaat ccacagtgtgta gtcagaaaaag ctgttgactt ctcttaaatac agcttccctg 1680
ctggggccccc gaaagtggac tgggtgattc tgtctggcag agagtgggga aaagacgcgg 1740
tttccagctt gcagatttgt taagttttctc aggagattt tgacttttcag cctttcatac 1800
ttgtttaagc aactatttgt attaaatgaa gttttttgaa aaaaaaaaaa aaaaaaaaaa 1860

```

<210> 234
 <211> 501
 <212> PRT
 <213> Homo sapiens

<400> 234

Asp	Pro	Arg	Val	Arg	Ala	Arg	Ala	Asp	Gly	Val	Pro	Gly	Ala	Leu	Arg	1	5	10	15
Ser	Ser	Gly	Arg	Pro	Arg	Pro	Arg	Arg	Pro	Ala	Gln	Tyr	Pro	Ala	Arg	20	25	30	
Pro	Arg	Arg	Pro	Ala	Ser	Thr	Ala	Gly	Ser	Ala	Pro	Phe	Pro	Glu	Gly	35	40	45	
Trp	Met	Met	Gly	Cys	Phe	Ala	Leu	Gln	Thr	Val	Asp	Thr	Glu	Leu	Thr	50	55	60	
Ala	Asp	Ser	Val	Glu	Trp	Cys	Pro	Leu	Gln	Gly	Cys	Arg	His	Leu	Leu	65	70	75	80
Ala	Cys	Gly	Thr	Tyr	Gln	Leu	Arg	Arg	Pro	Glu	Asp	Arg	Pro	Ala	Gly	85	90	95	
Pro	Gln	Asn	Lys	Gly	Gly	Met	Glu	Val	Lys	Glu	Pro	Gln	Val	Arg	Leu	100	105	110	
Gly	Arg	Leu	Phe	Leu	Tyr	Ser	Phe	Asn	Asp	Asn	Asn	Ser	Ile	His	Pro	115	120	125	
Leu	Val	Glu	Val	Gln	Arg	Lys	Asp	Thr	Ser	Ala	Ile	Leu	Asp	Met	Lys	130	135	140	
Trp	Cys	His	Ile	Pro	Val	Ala	Gly	His	Ala	Leu	Leu	Gly	Leu	Ala	Asp	145	150	155	160
Ala	Ser	Gly	Ser	Ile	Gln	Leu	Leu	Arg	Leu	Val	Glu	Ser	Glu	Lys	Ser	165	170	175	
His	Val	Leu	Glu	Pro	Leu	Ser	Ser	Leu	Ala	Leu	Glu	Glu	Gln	Cys	Leu	180	185	190	
Ala	Leu	Ser	Leu	Asp	Trp	Ser	Thr	Gly	Lys	Thr	Gly	Arg	Ala	Gly	Asp	195	200	205	
Gln	Pro	Leu	Lys	Ile	Ile	Ser	Ser	Asp	Ser	Thr	Gly	Gln	Leu	His	Leu	210	215	220	
Leu	Met	Val	Asn	Glu	Thr	Arg	Pro	Arg	Leu	Gln	Lys	Val	Ala	Ser	Trp	225	230	235	240
Gln	Ala	His	Gln	Phe	Glu	Ala	Trp	Ile	Ala	Ala	Phe	Asn	Tyr	Trp	His	245	250	255	
Pro	Glu	Ile	Val	Tyr	Ser	Gly	Gly	Asp	Asp	Gly	Leu	Leu	Arg	Gly	Trp	260	265	270	
Asp	Thr	Arg	Val	Pro	Gly	Lys	Phe	Leu	Phe	Thr	Ser	Lys	Arg	His	Thr	275	280	285	
Met	Gly	Val	Cys	Ser	Ile	Gln	Ser	Ser	Pro	His	Arg	Glu	His	Ile	Leu	290	295	300	
Ala	Thr	Gly	Ser	Tyr	Asp	Glu	His	Ile	Leu	Leu	Trp	Asp	Thr	Arg	Asn	305	310	315	320
Met	Lys	Gln	Pro	Leu	Ala	Asp	Thr	Pro	Val	Gln	Gly	Gly	Val	Trp	Arg	325	330	335	
Ile	Lys	Trp	His	Pro	Phe	His	His	His	Leu	Leu	Leu	Ala	Ala	Cys	Met	340	345	350	
His	Ser	Gly	Phe	Lys	Ile	Leu	Asn	Cys	Gln	Lys	Ala	Met	Glu	Glu	Arg	355	360	365	

Gln	Glu	Ala	Thr	Val	Leu	Thr	Ser	His	Thr	Leu	Pro	Asp	Ser	Leu	Val
370						375					380				
Tyr	Gly	Ala	Asp	Trp	Ser	Trp	Leu	Leu	Phe	Arg	Ser	Leu	Gln	Arg	Ala
385					390					395					400
Pro	Ser	Trp	Ser	Phe	Pro	Ser	Asn	Leu	Gly	Thr	Lys	Thr	Ala	Asp	Leu
				405	.				410					415	
Lys	Gly	Ala	Ser	Glu	Leu	Pro	Thr	Pro	Cys	His	Glu	Cys	Arg	Glu	Asp
			420					425					430		
Asn	Asp	Gly	Glu	Gly	His	Ala	Arg	Pro	Gln	Ser	Gly	Met	Lys	Pro	Leu
		435					440					445			
Thr	Glu	Gly	Met	Arg	Lys	Asn	Gly	Thr	Trp	Leu	Gln	Ala	Thr	Ala	Ala
	450					455					460				
Thr	Thr	Arg	Asp	Cys	Gly	Val	Asn	Pro	Glu	Glu	Ala	Asp	Ser	Ala	Phe
465					470					475					480
Ser	Leu	Leu	Ala	Thr	Cys	Ser	Phe	Tyr	Asp	His	Ala	Leu	His	Leu	Trp
				485					490					495	
Glu	Trp	Glu	Gly	Asn											
			500												

<210> 235
 <211> 1614
 <212> DNA
 <213> Homo sapiens

<400> 235
 ggaaggaagt gaaaatgggt gtccctgctg cctcttagca acaagagggg tcaagtgaca 60
 caaccagctg actcccgtag aggaagacac tgtggaggcc agttctggag ctattgcagc 120
 ctcggttgcc cgccggggga cccgagccga aaagttagtc tcagaatgtc gggcaaagac 180
 cgaattgaaa tctttccctc gcgaatggca cagaccatca tgaaggctcg tttaaaggga 240
 gcacagacag gtcgaaacct cctgaagaaa aaatctgatg ccttaactct tcgatttcga 300
 cagatcctaa agaagataat agagactaaa atgttgatgg gcgaagtgat gagagaagct 360
 gcctttttcac tagctgaagc caagttcaca gcagggtgact tcagcactac agttatccaa 420
 aatgtcaata aagcgcaagt gaagattcga gcgaagaaaag ataatgtagc aggtgttact 480
 ttgccagtat ttgaacatta ccatgaagga actgacagtt atgaactgac tggtttagcc 540
 agaggtgggg aacagttggc taaattaaag aggaattatg ccaaagcagt ggaactactg 600
 gtggaaactag cttctctgca gacttctttt gttacttttg atgaagctat taagataacc 660
 aacaggcgtg taaatgccat tgaacatgtc atcattcccc ggattgaacg tactcttgct 720
 tatatcatca cagagctgga tgagagagag cgagaagagt tctatagggt aaagaaaata 780
 caagagaaga aaaagattct aaaggaaaaa tctgagaagg acttgagca aaggagagca 840
 gctggagagg tggtggagcc tgctaattct ctggctgaag agaaggacga ggatcttcta 900
 tttgaataat ctttcctggt ctgggtcttt gagaaaccct aacactggct tcattttaat 960
 tcacagtgtg taggtttgat ttgtgtggct attgattttt tggcctaaga atttactggt 1020
 ttgtaaaatt tacctagatg tctatttatg ggattacttt tgcagaatca taatttagca 1080
 accatttatc atggatgaaa gagatctgta aaacctgccc aggaacttac agaatttact 1140
 ttgcagaagc gttatcatat tccatttaca tctgtgttac acgtgatctg cttaccaagc 1200
 atattaggaa atacctctta ggaagcatta gcggtctcag gccaatctact gtggagcagc 1260
 tttcattcct acccacttgc aaaccttggc gctgttgtct gagattgctg cagccattct 1320
 tgttaccatg gtacttctca aactttgtga aaacctgcac ttttccttgc atgacagggt 1380
 cctgtcttgt ctgtcatggg agccattctg ccaattttaa tgcgactgtg gtataaacag 1440
 taaaatgatt taaaagtaag tcattccgtt tttattaatt tactgttaag tcatgttctc 1500
 atgctcagat cagtagtgtc agccagagct ttctctgcag acatgtagga agtgggtagc 1560
 tattttttccc actccatgta ttagagtttt acaaaaaggc ttacttttga gaca 1614

<210> 236
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 236

```

Met Ser Gly Lys Asp Arg Ile Glu Ile Phe Pro Ser Arg Met Ala Gln
 1           5           10          15
Thr Ile Met Lys Ala Arg Leu Lys Gly Ala Gln Thr Gly Arg Asn Leu
      20          25          30
Leu Lys Lys Lys Ser Asp Ala Leu Thr Leu Arg Phe Arg Gln Ile Leu
      35          40          45
Lys Lys Ile Ile Glu Thr Lys Met Leu Met Gly Glu Val Met Arg Glu
      50          55          60
Ala Ala Phe Ser Leu Ala Glu Ala Lys Phe Thr Ala Gly Asp Phe Ser
65          70          75          80
Thr Thr Val Ile Gln Asn Val Asn Lys Ala Gln Val Lys Ile Arg Ala
      85          90          95
Lys Lys Asp Asn Val Ala Gly Val Thr Leu Pro Val Phe Glu His Tyr
      100         105         110
His Glu Gly Thr Asp Ser Tyr Glu Leu Thr Gly Leu Ala Arg Gly Gly
      115         120         125
Glu Gln Leu Ala Lys Leu Lys Arg Asn Tyr Ala Lys Ala Val Glu Leu
      130         135         140
Leu Val Glu Leu Ala Ser Leu Gln Thr Ser Phe Val Thr Leu Asp Glu
145         150         155         160
Ala Ile Lys Ile Thr Asn Arg Arg Val Asn Ala Ile Glu His Val Ile
      165         170         175
Ile Pro Arg Ile Glu Arg Thr Leu Ala Tyr Ile Ile Thr Glu Leu Asp
      180         185         190
Glu Arg Glu Arg Glu Glu Phe Tyr Arg Leu Lys Lys Ile Gln Glu Lys
      195         200         205
Lys Lys Ile Leu Lys Glu Lys Ser Glu Lys Asp Leu Glu Gln Arg Arg
      210         215         220
Ala Ala Gly Glu Val Leu Glu Pro Ala Asn Leu Leu Ala Glu Glu Lys
225         230         235         240
Asp Glu Asp Leu Leu Phe Glu
      245

```

<210> 237

<211> 1658

<212> DNA

<213> Homo sapiens

<400> 237

```

ggcacgagct cggctcctgg aaagatggag gcagcggaga cagaggcgga agctgcagcc 60
ctagagggtcc tggctgaggt ggcaggcatc ttggaacctg taggcctgca ggaggaggca 120
gaactgccag ccaagatcct ggttgagttt gtggtggact ctcagaagaa agacaagctg 180
ctctgcagcc agcttcaggt agcggatttc ctgcagaaca tcctggctca ggaggacact 240
gctaagggtc tcgacccctt ggcttctgaa gacacgagcc gacagaaggc aattgcagct 300
aaggaacaat ggaaagagct gaaggccacc tacagggagc acgtagaggc catcaaaatt 360
ggcctcacca aggccctgac tcagatggag gaagcccaga ggaaacggac acaactccgg 420
gaagcctttg agcagctcca ggccaagaaa caaatggcca tggagaaacg cagagcagtc 480
cagaaccagt ggcagctaca acaggagaag catctgcagc atctggcgga ggtttctgca 540
gaggtgaggg agcgtaaagc agggactcag caggagcttg acggggtgtt tcagaaactt 600
ggaaacctga agcagcaggc agaacaggag cgggacaagc tgcagaggta tcagaccttc 660
ctccagcttc tgtataccct gcagggttaag ctgttggtcc ctgaggctga ggctgaggca 720
gagaatcttc cagatgataa accccagcag ccgactcgac ccaggagca gactacagga 780
gacaccatgg ggagagaccc tgggtgtgac ttcaaggctg ttggtctaca acctgctgga 840
gatgtaaatt tgccatgact tcctggagga cagcagcatg gagaaagatc ctagaaaagg 900
cctctgactt ccctcacctc ccaaccatca ttacaggaaa gactgtgaac tcctgagttc 960
agcttgattt ctgactacat cccagcaagc tctggcatct gtggattaaa atccctggat 1020
ctctctcagt tgtgtatttg ttcattctca tatgctggca ggaacaacta ttaatacaga 1080

```

```

tactcagaag ccaataacat gacaggagct gggactgggt tgaacacagg gtgtgcagat 1140
ggggaggggg tactggcctt gggcctccta tgatgcagac atggtgaatt taattcaagg 1200
aggaggagaa tgttttaggc aggtgggttat atgtgggaag ataattttat tcatggatcc 1260
aaatgtttgt tgagtccttt ctttgtgcta aggttcttgc ggtgaaccag aattataaca 1320
gtgagctcat ctgactgttt taggatgtac agcctagtgt taacattctt ggtatctttt 1380
tgtgccttat ctaaaacatt tctcgatcac tggtttcaga tgttcattta ttatattctt 1440
ttcaaagatt cagagattgg cttttgtcat coactattgt atgttttggt tcattgacct 1500
ctagtgtatc cttgatcttt ccacttttct gttttcggat tggagaagat gtaccttttt 1560
tgtcaactct tactttttatc agatgatcaa ctcacgtatt tggatcttta tttgttttct 1620
caaataaata ttttaaggta aaaaaaaaaa aaaaaaaa 1658

```

<210> 238

<211> 277

<212> PRT

<213> Homo sapiens

<400> 238

```

Met Glu Ala Ala Glu Thr Glu Ala Glu Ala Ala Leu Glu Val Leu
1      5      10      15
Ala Glu Val Ala Gly Ile Leu Glu Pro Val Gly Leu Gln Glu Ala
20     25     30
Glu Leu Pro Ala Lys Ile Leu Val Glu Phe Val Val Asp Ser Gln Lys
35     40     45
Lys Asp Lys Leu Leu Cys Ser Gln Leu Gln Val Ala Asp Phe Leu Gln
50     55     60
Asn Ile Leu Ala Gln Glu Asp Thr Ala Lys Gly Leu Asp Pro Leu Ala
65     70     75     80
Ser Glu Asp Thr Ser Arg Gln Lys Ala Ile Ala Ala Lys Glu Gln Trp
85     90     95
Lys Glu Leu Lys Ala Thr Tyr Arg Glu His Val Glu Ala Ile Lys Ile
100    105    110
Gly Leu Thr Lys Ala Leu Thr Gln Met Glu Glu Ala Gln Arg Lys Arg
115    120    125
Thr Gln Leu Arg Glu Ala Phe Glu Gln Leu Gln Ala Lys Lys Gln Met
130    135    140
Ala Met Glu Lys Arg Arg Ala Val Gln Asn Gln Trp Gln Leu Gln Gln
145    150    155    160
Glu Lys His Leu Gln His Leu Ala Glu Val Ser Ala Glu Val Arg Glu
165    170    175
Arg Lys Thr Gly Thr Gln Gln Glu Leu Asp Gly Val Phe Gln Lys Leu
180    185    190
Gly Asn Leu Lys Gln Gln Ala Glu Gln Glu Arg Asp Lys Leu Gln Arg
195    200    205
Tyr Gln Thr Phe Leu Gln Leu Leu Tyr Thr Leu Gln Gly Lys Leu Leu
210    215    220
Phe Pro Glu Ala Glu Ala Glu Ala Glu Asn Leu Pro Asp Asp Lys Pro
225    230    235    240
Gln Gln Pro Thr Arg Pro Gln Glu Gln Ser Thr Gly Asp Thr Met Gly
245    250    255
Arg Asp Pro Gly Val Ser Phe Lys Ala Val Gly Leu Gln Pro Ala Gly
260    265    270
Asp Val Asn Leu Pro
275

```